

142.2

- Best-BlastP=> >nrprot 62% Identities = 108/225 (48%), Positives = 144/225 (64%), Gaps = 1/225 (0%) ref|NP\_455898.1| D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi] pir|AE0669 D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi (strain CT18)] emb|CAD01726.1| D-alanyl-D-alanine dipeptidase [Salmonella enterica subsp. enterica serovar Typhi] Length = 256
- 1420.2 Best-BlastP=> >nrprot 80% Identities = 258/380 (67%), Positives = 309/380 (81%) ref|NP\_820998.1| cystathionine beta-lyase [Coxiella burnetii RSA 493] gb|AAO91512.1| cystathionine beta-lyase [Coxiella burnetii RSA 493] Length = 387
- 1421.3 Best-BlastP=> >nrprot 55% Identities = 280/736 (38%), Positives = 432/736 (58%), Gaps = 19/736 (2%) ref|NP\_900703.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 936
- 1423.2 Best-BlastP=> >nrprot 66% Identities = 226/450 (50%), Positives = 315/450 (70%), Gaps = 2/450 (0%) pir|JC5798 F0F1-ATPase (EC 3.4.-.-) beta chain - Methanosarcina barkeri gb|AAC38049.1| ATP synthase beta subunit [Methanosarcina barkeri] Length = 469
- 1424.2 Best-BlastP=> >nrprot 37% Identities = 27/106 (25%), Positives = 51/106 (48%) ref|ZP\_00090544.1| COG0355: F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit) [Azotobacter vinelandii] Length = 178
- 1425.2 Best-BlastP=> >nrprot 50% Identities = 25/88 (28%), Positives = 47/88 (53%), Gaps = 2/88 (2%) ref|NP\_661922.1| ATP synthase, putative [Chlorobium tepidum TLS] gb|AAM72264.1| ATP synthase, putative [Chlorobium tepidum TLS] Length = 107
- 1429.4 Best-BlastP=> >nrprot 26% Identities = 68/329 (20%), Positives = 131/329 (39%), Gaps = 32/329 (9%) emb|CAD27470.1| SPAPB18E9.04c [Schizosaccharomyces pombe] Length = 800
- 1432.3 Best-BlastP=> >nrprot 52% Identities = 105/294 (35%), Positives = 160/294 (54%), Gaps = 6/294 (2%) ref|NP\_745744.1| transcriptional regulator, LysR family [Pseudomonas putida KT2440] gb|AAN69208.1| AE016555\_6 transcriptional regulator, LysR family [Pseudomonas putida KT2440] Length = 309
- 1434.3 Best-BlastP=> >nrprot 52% Identities = 242/765 (31%), Positives = 388/765 (50%), Gaps = 49/765 (6%) ref|NP\_842403.1| DNA internalization-related competence protein ComEC/Rec2 [Nitrosomonas europaea ATCC 19718] emb|CAD86320.1| DNA internalization-related competence protein ComEC/Rec2 [Nitrosomonas europaea ATCC 19718] Length = 799
- 1438.4 Best-BlastP=> >nrprot 80% Identities = 428/631 (67%), Positives = 504/631 (79%), Gaps = 6/631 (0%) ref|NP\_245307.1| ParE [Pasteurella multocida] gb|AAK02454.1| ParE [Pasteurella multocida] Length = 632
- 144.3 Best-BlastP=> >nrprot 8% Identities = 21/50 (42%), Positives = 31/50 (62%), Gaps = 1/50 (2%) ref|NP\_618108.1| cysteine protease (papain C1 family) [Methanosarcina acetivorans str. C2A] gb|AAM06588.1| cysteine protease (papain C1 family) [Methanosarcina acetivorans str. C2A] Length = 340
- 1440.2 Best-BlastP=> >nrprot 55% Identities = 163/398 (40%), Positives = 231/398 (58%), Gaps = 45/398 (11%) ref|NP\_820093.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] gb|AAO90607.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] Length = 380
- 1444.3 Best-BlastP=> >nrprot 46% Identities = 189/523 (36%), Positives = 282/523 (53%), Gaps = 48/523 (9%) ref|NP\_775139.1| sphingosine-1-phosphate lyase 1 [Rattus norvegicus] emb|CAD55407.1| sphingosine-1-phosphate lyase [Rattus norvegicus] Length = 568

- 1446.3 Best-BlastP=> >nrprot 71% Identities = 143/246 (58%), Positives = 181/246 (73%) ref|NP\_793532.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 249
- 1448.2 Best-BlastP=> >nrprot 50% Identities = 109/334 (32%), Positives = 172/334 (51%), Gaps = 25/334 (7%) ref|NP\_106951.1| similar to oxidoreductase [Mesorhizobium loti] dbj|BAB52737.1| similar to oxidoreductase [Mesorhizobium loti] Length = 677
- 1449.3 Best-BlastP=> >nrprot 52% Identities = 209/735 (28%), Positives = 369/735 (50%), Gaps = 69/735 (9%) ref|ZP\_00042382.1| COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1] Length = 726
- 1450.2 Best-BlastP=> >nrprot 57% Identities = 168/388 (43%), Positives = 244/388 (62%), Gaps = 8/388 (2%) ref|NP\_407479.1| multidrug translocase [Yersinia pestis] ref|NP\_671360.1| proton motive force efflux pump protein [Yersinia pestis KIM] pir|AD0492 multidrug translocase [imported] - Yersinia pestis (strain CO92) emb|CAC93504.1| multidrug translocase [Yersinia pestis CO92] gb|AAM87611.1|AE014008\_5 proton motive force efflux pump protein [Yersinia pestis KIM] Length = 409
- 1451.4 Best-BlastP=> >nrprot 65% Identities = 188/426 (44%), Positives = 278/426 (65%), Gaps = 4/426 (0%) ref|ZP\_00034777.1| COG2252: Permeases [Burkholderia fungorum] Length = 433
- 1454.2 Best-BlastP=> >nrprot 88% Identities = 500/638 (78%), Positives = 568/638 (89%) ref|NP\_901459.1| protein kinase [Chromobacterium violaceum ATCC 12472] gb|AAQ59463.1| protein kinase [Chromobacterium violaceum ATCC 12472] Length = 642
- 1455.2 Best-BlastP=> >nrprot 47% Identities = 52/155 (33%), Positives = 81/155 (52%), Gaps = 10/155 (6%) ref|NP\_253150.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pir|D83087 conserved hypothetical protein PA4460 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07848.1|AE004860\_4 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 175
- 1456.2 Best-BlastP=> >nrprot 80% Identities = 165/238 (69%), Positives = 194/238 (81%) ref|NP\_719490.1| ABC transporter, ATP-binding protein [Shewanella oneidensis MR-1] gb|AAN56934.1|AE015827\_6 ABC transporter, ATP-binding protein [Shewanella oneidensis MR-1] Length = 243
- 1457.2 Best-BlastP=> >nrprot 73% Identities = 105/185 (56%), Positives = 141/185 (76%), Gaps = 1/185 (0%) ref|ZP\_00079751.1| COG0512: Anthranilate/para-aminobenzoate synthases component II [Geobacter metallireducens] Length = 189
- 1461.3 Best-BlastP=> >nrprot 68% Identities = 167/315 (53%), Positives = 214/315 (67%), Gaps = 20/315 (6%) ref|NP\_819187.1| UDP-N-acetylenolpyruvoylglucosamine reductase [Coxiella burnetii] RSA 493 gb|AAO89701.1| UDP-N-acetylenolpyruvoylglucosamine reductase [Coxiella burnetii] RSA 493 Length = 316
- 1463.2 Best-BlastP=> >nrprot 66% Identities = 170/375 (45%), Positives = 241/375 (64%), Gaps = 16/375 (4%) ref|NP\_773078.1| D-alanine--D-alanine ligase A [Bradyrhizobium japonicum] dbj|BAC51703.1| D-alanine--D-alanine ligase A [Bradyrhizobium japonicum USDA 110] Length = 373
- 1466.2 Best-BlastP=> >nrprot 71% Identities = 94/205 (45%), Positives = 152/205 (74%) ref|NP\_841948.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] emb|CAD85837.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] Length = 208
- 1467.5 Best-BlastP=> >nrprot 65% Identities = 90/186 (48%), Positives = 126/186 (67%), Gaps = 2/186 (1%) ref|NP\_691260.1| hypothetical protein [Oceanobacillus iheyensis HTE831] dbj|BAC12295.1| hypothetical conserved protein [Oceanobacillus iheyensis HTE831] Length = 189

- 1469.4 Best-BlastP=> >nrprot 20% Identities = 112/493 (22%), Positives = 217/493 (44%), Gaps = 44/493 (8%) ref|NP\_563924.1| nuclear matrix constituent protein -related [Arabidopsis thaliana] pir|G86266 hypothetical protein F3F19.25 - Arabidopsis thaliana gb|AAD31075.1|AC007357\_24 Similar to gb|D64087 nuclear matrix constituent protein 1 (NMCP1) from Daucus carota. [Arabidopsis thaliana] Length = 1128
- 1473.4 Best-BlastP=> >nrprot 49% Identities = 44/143 (30%), Positives = 75/143 (52%), Gaps = 4/143 (2%) ref|NP\_810648.1| chromate transport protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO76842.1| chromate transport protein [Bacteroides thetaiotaomicron VPI-5482] Length = 185
- 1474.4 Best-BlastP=> >nrprot 52% Identities = 125/314 (39%), Positives = 194/314 (61%), Gaps = 4/314 (1%) ref|NP\_103760.1| unknown protein [Mesorhizobium loti] dbj|BAB49546.1| unknown protein [Mesorhizobium loti] Length = 431
- 1475.2 Best-BlastP=> >nrprot No Hits found
- 1476.2 Best-BlastP=> >nrprot 81% Identities = 185/302 (61%), Positives = 246/302 (81%), Gaps = 1/302 (0%) ref|NP\_762779.1| Glutathione synthase; Ribosomal protein S6 modification enzyme [Vibrio vulnificus CMCP6] gb|AAO07769.1|AE016811\_10 Glutathione synthase; Ribosomal protein S6 modification enzyme [Vibrio vulnificus CMCP6] dbj|BAC97337.1| ribosomal protein S6 modification protein [Vibrio vulnificus YJ016] Length = 301
- 1479.3 Best-BlastP=> >nrprot 69% Identities = 223/407 (54%), Positives = 287/407 (70%), Gaps = 1/407 (0%) sp|Q8GDU5|ARLY\_HELMO Argininosuccinate lyase (Argininosuccinase) (ASAL) gb|AAN87483.1| Argininosuccinate lyase [Heliobacillus mobilis] Length = 458
- 148.2 Best-BlastP=> >nrprot 55% Identities = 186/450 (41%), Positives = 279/450 (62%), Gaps = 14/450 (3%) ref|ZP\_00060071.1| COG2200: FOG: EAL domain [Clostridium thermocellum ATCC 27405] Length = 862
- 1481.3 Best-BlastP=> >nrprot 51% Identities = 128/304 (42%), Positives = 191/304 (62%), Gaps = 9/304 (2%) ref|NP\_126998.1| ornithine carbamoyltransferase [Pyrococcus abyssi] sp|O93656|OTC\_PYRAB Ornithine carbamoyltransferase (OTCase) pir|G75041 ornithine carbamoyltransferase (argf) PAB1502 - Pyrococcus abyssi (strain Orsay) emb|CAB50228.1| argF ornithine carbamoyltransferase [Pyrococcus abyssi] Length = 317
- 1482.4 Best-BlastP=> >nrprot 22% Identities = 40/150 (26%), Positives = 71/150 (47%) ref|NP\_819099.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89613.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 250
- 1484.2 Best-BlastP=> >nrprot 72% Identities = 126/223 (56%), Positives = 164/223 (73%) ref|ZP\_00053873.1| COG1136: ABC-type antimicrobial peptide transport system, ATPase component [Magnetospirillum magnetotacticum] Length = 225
- 1485.4 Best-BlastP=> >nrprot 64% Identities = 171/414 (41%), Positives = 268/414 (64%), Gaps = 4/414 (0%) ref|NP\_436895.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] pir|C95886 conserved hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasamid pSymbB emb|CAC48755.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] Length = 413
- 1487.3 Best-BlastP=> >nrprot 99% Identities = 266/268 (99%), Positives = 268/268 (100%) emb|CAB65183.1| enoyl reductase [Legionella pneumophila] Length = 268
- 1488.2 Best-BlastP=> >nrprot No Hits found
- 1490.4 Best-BlastP=> >nrprot 72% Identities = 536/927 (57%), Positives = 679/927 (73%), Gaps = 9/927 (0%) ref|NP\_819435.1| isoleucyl-tRNA synthetase [Coxiella burnetii RSA 493] gb|AAO89949.1| isoleucyl-tRNA synthetase [Coxiella burnetii RSA 493] Length = 936

1493.6

Best-BlastP=> >nrprot 69% Identities = 822/1621 (50%), Positives = 1137/1621 (70%), Gaps = 3/1621 (0%) ref|NP\_820221.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90735.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 1619  
 Best-BlastP=> >nrprot 33% Identities = 58/170 (34%), Positives = 89/170 (52%), Gaps = 1/170 (0%) ref|ZP\_00081963.1| COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Geobacter metallireducens] Length = 234

1494.2

Best-BlastP=> >nrprot 72% Identities = 60/104 (57%), Positives = 78/104 (75%) ref|NP\_458777.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_463202.1| putative DMT superfamily transport protein [Salmonella typhimurium LT2] ref|NP\_807981.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|AE1046 SugE protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL23161.1| putative DMT superfamily transport protein [Salmonella typhimurium LT2] emb|CAD06818.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO71841.1| SugE protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 105

1495.1

Best-BlastP=> >nrprot 66% Identities = 189/335 (56%), Positives = 236/335 (70%) ref|ZP\_00125893.1| COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Pseudomonas syringae pv. syringae B728a] Length = 354

1497.2

Best-BlastP=> >nrprot 63% Identities = 181/393 (46%), Positives = 248/393 (63%), Gaps = 20/393 (5%) ref|NP\_890078.1| phage integrase [Bordetella bronchiseptica] emb|CAE34037.1| phage integrase [Bordetella bronchiseptica] Length = 407

15.1

Best-BlastP=> >nrprot 52% Identities = 130/266 (48%), Positives = 172/266 (64%), Gaps = 8/266 (3%) ref|ZP\_00029131.1| COG3243: Poly(3-hydroxyalkanoate) synthetase [Burkholderia fungorum] Length = 642

150.2

Best-BlastP=> >nrprot 72% Identities = 139/276 (50%), Positives = 200/276 (72%), Gaps = 2/276 (0%) ref|NP\_519387.1| PROBABLE SN-GLYCEROL-3-PHOSPHATE TRANSMEMBRANE ABC TRANSPORTER PROTEIN [Ralstonia solanacearum] emb|CAD14968.1| PROBABLE SN-GLYCEROL-3-PHOSPHATE TRANSMEMBRANE ABC TRANSPORTER PROTEIN [Ralstonia solanacearum] Length = 282

1501.3

Best-BlastP=> >nrprot 65% Identities = 183/364 (50%), Positives = 239/364 (65%), Gaps = 15/364 (4%) ref|NP\_407240.1| sn-glycerol-3-phosphate transport, ATP-binding protein [Yersinia pestis] pir|AH0461 sn-glycerol-3-phosphate transport, ATP-binding protein ugpc [imported] - Yersinia pestis (strain CO92) emb|CAC93260.1| sn-glycerol-3-phosphate transport, ATP-binding protein [Yersinia pestis CO92] Length = 357

1503.4

Best-BlastP=> >nrprot No Hits found

1505.4

Best-BlastP=> >nrprot 64% Identities = 226/496 (45%), Positives = 318/496 (64%), Gaps = 4/496 (0%) ref|NP\_231057.1| thermostable carboxypeptidase 1 [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82202 thermostable carboxypeptidase 1 VC1414 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94571.1| thermostable carboxypeptidase 1 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 524

1507.3

Best-BlastP=> >nrprot 38% Identities = 85/279 (30%), Positives = 141/279 (50%), Gaps = 9/279 (3%) ref|NP\_622993.1| predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA [Thermoanaerobacter tengcongensis] gb|AAM24597.1| predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA [Thermoanaerobacter tengcongensis] Length = 412

1508.4



- 151.2 Best-BlastP=> >nrprot 70% Identities = 128/248 (51%), Positives = 176/248 (70%), Gaps = 4/248 (1%) ref|NP\_902034.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ60036.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] Length = 246
- 1510.3 Best-BlastP=> >nrprot 64% Identities = 136/259 (52%), Positives = 177/259 (68%), Gaps = 1/259 (0%) ref|ZP\_00083725.1| COG3186: Phenylalanine-4-hydroxylase [Pseudomonas fluorescens PfO-1] Length = 263
- 1511.3 Best-BlastP=> >nrprot 99% Identities = 217/219 (99%), Positives = 218/219 (99%) gb|AAL79360.1| GacA regulatory protein [Legionella pneumophila] Length = 219
- 1513.4 Best-BlastP=> >nrprot 61% Identities = 181/448 (40%), Positives = 276/448 (61%), Gaps = 20/448 (4%) ref|NP\_820336.1| amino acid antiporter [Coxiella burnetii RSA 493] gb|AAO90850.1| amino acid antiporter [Coxiella burnetii RSA 493] Length = 474
- 1515.2 Best-BlastP=> >nrprot 73% Identities = 127/255 (49%), Positives = 188/255 (73%), Gaps = 1/255 (0%) ref|NP\_249886.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|F83497 hypothetical protein PA1195 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04584.1|AE004549\_11 hypothetical protein PA1195 [Pseudomonas aeruginosa PAO1] Length = 254
- 1516.3 Best-BlastP=> >nrprot 39% Identities = 69/269 (25%), Positives = 123/269 (45%), Gaps = 14/269 (5%) ref|NP\_826905.1| hypothetical protein [Streptomyces avermitilis MA-4680] dbj|BAC73440.1| hypothetical protein [Streptomyces avermitilis MA-4680] Length = 290
- 1517.3 Best-BlastP=> >nrprot 58% Identities = 164/368 (44%), Positives = 244/368 (66%), Gaps = 1/368 (0%) ref|ZP\_00034488.1| COG0156: 7-keto-8-aminopelargonate synthetase and related enzymes [Burkholderia fungorum] Length = 429
- 1519.2 Best-BlastP=> >nrprot 53% Identities = 126/333 (37%), Positives = 184/333 (55%), Gaps = 4/333 (1%) ref|ZP\_00034487.1| COG0784: FOG: CheY-like receiver [Burkholderia fungorum] Length = 333
- 152.3 Best-BlastP=> >nrprot 50% Identities = 33/120 (27%), Positives = 60/120 (50%), Gaps = 8/120 (6%) ref|NP\_459344.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] gb|AAL19303.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] Length = 119
- 1521.2 Best-BlastP=> >nrprot 56% Identities = 69/170 (40%), Positives = 107/170 (62%) ref|NP\_541215.1| HDED PROTEIN [Brucella melitensis] ref|NP\_700223.1| conserved hypothetical protein [Brucella suis 1330] pir|AD3539 hdeD protein [imported] - Brucella melitensis (strain 16M) gb|AAL53479.1| HDED PROTEIN [Brucella melitensis 16M] gb|AAN34228.1|AE014598\_9 conserved hypothetical protein [Brucella suis 1330] Length = 187
- 1522.2 Best-BlastP=> >nrprot 32% Identities = 77/231 (33%), Positives = 127/231 (54%), Gaps = 1/231 (0%) ref|NP\_691224.1| hypothetical protein [Oceanobacillus ihayensis HTE831] dbj|BAC12259.1| hypothetical conserved protein [Oceanobacillus ihayensis HTE831] Length = 243
- 1523.2 Best-BlastP=> >nrprot No Hits found
- 1524.3 Best-BlastP=> >nrprot 21% Identities = 48/129 (37%), Positives = 76/129 (58%), Gaps = 4/129 (3%) ref|NP\_561262.1| probable transcriptional regulator [Clostridium perfringens] dbj|BAB80052.1| probable transcriptional regulator [Clostridium perfringens str. 13] Length = 249
- 1525.3 Best-BlastP=> >nrprot 51% Identities = 137/384 (35%), Positives = 217/384 (56%), Gaps = 24/384 (6%) gb|AAM73854.1|AF454865\_1 putative phospholipase C [Legionella pneumophila] Length = 423

- 1528.4 Best-BlastP=> >nrprot 65% Identities = 214/446 (47%), Positives = 291/446 (65%), Gaps = 6/446 (1%) sp|Q8PMU6|RUMA\_XANAC 23S rRNA (Uracil-5-)-methyltransferase rumA (23S rRNA(M-5-U1939)-methyltransferase) Length = 444
- 1529.2 Best-BlastP=> >nrprot 77% Identities = 253/394 (64%), Positives = 309/394 (78%) ref|NP\_416880.1| putative aminotransferase [Escherichia coli K12] sp|P77434|YFDZ\_ECOLI Hypothetical aminotransferase yfdZ pir|H65011 probable transaminase (EC 2.6.1.-) b2379 [similarity] - Escherichia coli (strain K-12) gb|AAC75438.1| putative aminotransferase [Escherichia coli K12] dbj|BAA16249.1| PROBABLE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART) [Escherichia coli] Length = 412
- 153.2 Best-BlastP=> >nrprot 99% Identities = 436/437 (99%), Positives = 437/437 (100%) gb|AAM00622.1| chemiosmotic efflux system C protein C [Legionella pneumophila] Length = 445
- 1530.2 Best-BlastP=> >nrprot 52% Identities = 38/108 (35%), Positives = 64/108 (59%) ref|NP\_819878.1| conserved hypothetical protein. [Coxiella burnetii RSA 493] gb|AAO90392.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 123
- 1531.3 Best-BlastP=> >nrprot 71% Identities = 360/746 (48%), Positives = 523/746 (70%), Gaps = 17/746 (2%) ref|ZP\_00126361.1| COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Pseudomonas syringae pv. syringae B728a] Length = 747
- 1532.3 Best-BlastP=> >nrprot 52% Identities = 217/688 (31%), Positives = 341/688 (49%), Gaps = 49/688 (7%) ref|NP\_249777.1| flagellar hook-associated protein 1 FlgK [Pseudomonas aeruginosa PA01] pir|D83511 flagellar hook-associated protein 1 FlgK PA1086 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04475.1|AE004539\_17 flagellar hook-associated protein 1 FlgK [Pseudomonas aeruginosa PAO1] Length = 683
- 1533.1 Best-BlastP=> >nrprot 52% Identities = 120/413 (29%), Positives = 218/413 (52%), Gaps = 12/413 (2%) ref|NP\_718794.1| flagellar hook-associated protein FlgL [Shewanella oneidensis MR-1] gb|AAN56238.1|AE015761\_8 flagellar hook-associated protein FlgL [Shewanella oneidensis MR-1] Length = 403
- 1536.3 Best-BlastP=> >nrprot 59% Identities = 259/616 (42%), Positives = 374/616 (60%), Gaps = 9/616 (1%) ref|NP\_900243.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58249.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] Length = 621
- 1539.2 Best-BlastP=> >nrprot No Hits found
- 154.1 Best-BlastP=> >nrprot 98% Identities = 312/322 (96%), Positives = 317/322 (98%) gb|AAM00621.1| chemiosmotic efflux system C protein B [Legionella pneumophila] Length = 322
- 1542.2 Best-BlastP=> >nrprot 63% Identities = 161/342 (47%), Positives = 225/342 (65%), Gaps = 5/342 (1%) ref|NP\_820833.1| enoyl-CoA hydratase/isomerase family protein [Coxiella burnetii RSA 493] gb|AAO91347.1| enoyl-CoA hydratase/isomerase family protein [Coxiella burnetii RSA 493] Length = 356
- 1545.3 Best-BlastP=> >nrprot 74% Identities = 319/546 (58%), Positives = 411/546 (75%), Gaps = 7/546 (1%) ref|NP\_745048.1| glutaminyl-tRNA synthetase [Pseudomonas putida KT2440] gb|AAN68512.1|AE016483\_3 glutaminyl-tRNA synthetase [Pseudomonas putida KT2440] Length = 567
- 1547.2 Best-BlastP=> >nrprot 66% Identities = 132/266 (49%), Positives = 182/266 (68%), Gaps = 2/266 (0%) ref|NP\_520102.1| PROBABLE TRYPTOPHAN SYNTHASE (ALPHA CHAIN) PROTEIN [Ralstonia solanacearum] emb|CAD15683.1| PROBABLE TRYPTOPHAN SYNTHASE (ALPHA CHAIN) PROTEIN [Ralstonia solanacearum] Length = 265

- 1548.2 Best-BlastP=> >nrrprot 55% Identities = 83/198 (41%), Positives = 129/198 (65%), Gaps = 1/198 (0%) ref|NP\_866390.1| ATP synthase a subunit [Pirellula sp.] emb|CAD78171.1| ATP synthase a subunit [Pirellula sp.] Length = 228
- 1549.1 Best-BlastP=> >nrrprot 66% Identities = 46/73 (63%), Positives = 61/73 (83%) ref|ZP\_00034461.1| COG0636: F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K [Burkholderia fungorum] Length = 82
- 1550.2 Best-BlastP=> >nrrprot 50% Identities = 63/254 (24%), Positives = 125/254 (49%), Gaps = 10/254 (3%) ref|NP\_617341.1| H(+)-transporting ATP synthase, subunit B [Methanosarcina acetivorans str. C2A] gb|AAM05821.1| H(+)-transporting ATP synthase, subunit B [Methanosarcina acetivorans str. C2A] Length = 329
- 1552.3 Best-BlastP=> >nrrprot 87% Identities = 381/511 (74%), Positives = 452/511 (88%), Gaps = 1/511 (0%) ref|ZP\_00065462.1| COG0056: F0F1-type ATP synthase, alpha subunit [Microbulbifer degradans 2-40] Length = 513
- 1555.2 Best-BlastP=> >nrrprot 79% Identities = 189/288 (65%), Positives = 231/288 (80%), Gaps = 2/288 (0%) ref|NP\_254242.1| ATP synthase gamma chain [Pseudomonas aeruginosa PAO1] pir|D82952 ATP synthase gamma chain PA5555 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08940.1|AE004967\_11 ATP synthase gamma chain [Pseudomonas aeruginosa PAO1] Length = 286
- 1556.2 Best-BlastP=> >nrrprot 92% Identities = 395/458 (86%), Positives = 423/458 (92%), Gaps = 1/458 (0%) pir|D64071 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Haemophilus influenzae (strain Rd KW20) Length = 468
- 1557.3 Best-BlastP=> >nrrprot 90% Identities = 227/291 (78%), Positives = 265/291 (91%) ref|NP\_820381.1| succinyl-CoA synthetase, alpha subunit [Coxiella burnetii RSA 493] sp|P53591|SUCD\_COXBU Succinyl-CoA synthetase alpha chain (SCS-alpha) gb|AAO90895.1| succinyl-CoA synthetase, alpha subunit [Coxiella burnetii RSA 493] Length = 294
- 1559.2 Best-BlastP=> >nrrprot 80% Identities = 269/384 (70%), Positives = 314/384 (81%) ref|NP\_250279.1| succinyl-CoA synthetase beta chain [Pseudomonas aeruginosa PAO1] sp|P53593|SUCC\_PSEAE Succinyl-CoA synthetase beta chain (SCS-beta) pir|A83446 succinyl-CoA synthetase beta chain PA1588 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04977.1|AE004587\_1 succinyl-CoA synthetase beta chain [Pseudomonas aeruginosa PAO1] Length = 388
- 1560.2 Best-BlastP=> >nrrprot 59% Identities = 115/277 (41%), Positives = 166/277 (59%), Gaps = 11/277 (3%) ref|NP\_442598.1| PleD gene product homologue [Synechocystis sp. PCC 6803] pir|S76977 pleD-4 protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10669.1| slr0302 [Synechocystis sp. PCC 6803] Length = 768
- 1562.3 Best-BlastP=> >nrrprot 34% Identities = 51/213 (23%), Positives = 94/213 (44%), Gaps = 27/213 (12%) ref|NP\_705294.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD52531.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1936
- 1563.3 Best-BlastP=> >nrrprot 64% Identities = 95/200 (47%), Positives = 134/200 (67%), Gaps = 1/200 (0%) ref|ZP\_00087981.1| COG1335: Amidases related to nicotinamidase [Pseudomonas fluorescens PfO-1] Length = 208
- 1564.3 Best-BlastP=> >nrrprot 81% Identities = 321/467 (68%), Positives = 380/467 (81%) ref|NP\_820039.1| nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] gb|AAO90553.1| nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] Length = 468
- 1566.3 Best-BlastP=> >nrrprot 25% Identities = 34/120 (28%), Positives = 47/120 (39%), Gaps = 18/120 (15%) gb|AAQ23913.1| metallothionein IIE [Crassostrea virginica] Length = 149
- 1567.2 Best-BlastP=> >nrrprot 28% Identities = 58/293 (19%), Positives = 127/293 (43%), Gaps = 21/293 (7%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738

- 1569.6 Best-BlastP=> >nrprot 62% Identities = 310/738 (42%), Positives = 456/738 (61%), Gaps = 24/738 (3%) ref|NP\_796632.1| primosomal protein N' [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC58516.1| primosomal protein N' [Vibrio parahaemolyticus] Length = 734
- 157.2 Best-BlastP=> >nrprot 90% Identities = 886/1061 (83%), Positives = 973/1061 (91%) gb|AAM00612.1| chemiosmotic efflux system protein A-like protein [Legionella pneumophila] Length = 1066
- 1570.4 Best-BlastP=> >nrprot 74% Identities = 612/1047 (58%), Positives = 788/1047 (75%), Gaps = 9/1047 (0%) ref|ZP\_00034374.1| COG0841: Cation/multidrug efflux pump [Burkholderia fungorum] Length = 1098
- 1575.2 Best-BlastP=> >nrprot 50% Identities = 46/122 (37%), Positives = 71/122 (58%), Gaps = 7/122 (5%) ref|NP\_925923.1| MarR family transcriptional regulatory protein [Gloeobacter violaceus] dbj|BAC90918.1| MarR family transcriptional regulatory protein [Gloeobacter violaceus] Length = 143
- 1577.5 Best-BlastP=> >nrprot 63% Identities = 425/983 (43%), Positives = 617/983 (62%), Gaps = 35/983 (3%) ref|NP\_288121.1| putative oxidase [Escherichia coli O157:H7 EDL933] ref|NP\_310421.1| putative oxidase [Escherichia coli O157:H7] pir|B90928 probable oxidase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir|F85776 probable oxidase ydiJ [imported] - Escherichia coli (strain O157:H7, substrain EDL933) gb|AAG56674.1|AE005391\_11 putative oxidase [Escherichia coli O157:H7] Length = 1018
- 1578.3 Best-BlastP=> >nrprot 67% Identities = 135/246 (54%), Positives = 173/246 (70%), Gaps = 3/246 (1%) ref|NP\_436290.1| Hypothetical protein [Sinorhizobium meliloti] pir|D95392 protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasamid pSymA gb|AAK65702.1| Hypothetical protein [Sinorhizobium meliloti] Length = 408
- 1579.4 Best-BlastP=> >nrprot 44% Identities = 36/124 (29%), Positives = 68/124 (54%), Gaps = 5/124 (4%) ref|NP\_635420.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM39344.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 143
- 158.2 Best-BlastP=> >nrprot 74% Identities = 139/205 (67%), Positives = 165/205 (80%), Gaps = 1/205 (0%) ref|NP\_478237.1| ORF\_ID:all7590~unknown protein [Nostoc sp. PCC 7120] pir|AC2538 hypothetical protein all7590 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta dbj|BAB77233.1| ORF\_ID:all7590~unknown protein [Nostoc sp. PCC 7120] Length = 217
- 1581.4 Best-BlastP=> >nrprot No Hits found
- 1582.2 Best-BlastP=> >nrprot 76% Identities = 99/138 (71%), Positives = 115/138 (83%), Gaps = 2/138 (1%) ref|NP\_233004.1| peptide methionine sulfoxide reductase [Vibrio cholerae O1 biovar eltor str. N16961] pir|C82439 peptide methionine sulfoxide reductase VCA0615 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96516.1| peptide methionine sulfoxide reductase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 394
- 1584.3 Best-BlastP=> >nrprot 79% Identities = 574/901 (63%), Positives = 711/901 (78%), Gaps = 7/901 (0%) ref|NP\_285794.1| preprotein translocase; secretion protein [Escherichia coli O157:H7 EDL933] ref|NP\_308129.1| preprotein translocase SecA [Escherichia coli O157:H7] ref|NP\_752070.1| Preprotein translocase secA subunit [Escherichia coli CFT073] pir|F90641 preprotein translocase SecA [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir|F85492 preprotein translocase, secretion protein [imported] - Escherichia coli (strain O157:H7, substrain EDL933) gb|AAG54402.1|AE005186\_8 preprotein translocase; secretion protein [Escherichia coli O157:H7 EDL933] dbj|BAB33525.1| preprotein translocase SecA [Escherichia coli O157:H7] gb|AAN78614.1|AE016755\_114 Preprotein translocase secA subunit [Escherichia coli CFT073] Length = 901

- 1585.2 Best-BlastP=> >nrrprot 54% Identities = 115/350 (32%), Positives = 194/350 (55%), Gaps = 31/350 (8%) ref[NP\_642273.1] flagellar protein [Xanthomonas axonopodis pv. citri str. 306] Length = 337  
Best-BlastP=> >nrrprot No Hits found
- 1586.2 Best-BlastP=> >nrrprot 43% Identities = 139/387 (35%), Positives = 203/387 (52%), Gaps = 19/387 (4%) ref[NP\_643897.1] oxidoreductase [Xanthomonas axonopodis pv. citri str. 306] Length = 443
- 1589.3 Best-BlastP=> >nrrprot 79% Identities = 138/220 (62%), Positives = 179/220 (81%), Gaps = 2/220 (0%) ref[NP\_820222.1] DNA-binding response regulator [Coxiella burnetii RSA 493] Length = 223
- 159.1 Best-BlastP=> >nrrprot 54% Identities = 44/97 (45%), Positives = 57/97 (58%), Gaps = 14/97 (14%) ref[NP\_747491.1] hypothetical protein [Pseudomonas putida KT2440] Length = 91  
Best-BlastP=> >nrrprot 69% Identities = 92/172 (53%), Positives = 126/172 (73%) ref[NP\_819923.1] intracellular septation protein A [Coxiella burnetii RSA 493] Length = 181
- 1591.4 Best-BlastP=> >nrrprot 56% Identities = 183/441 (41%), Positives = 275/441 (62%), Gaps = 13/441 (2%) ref[YP\_00065233.1] COG0741: Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) [Microbulbifer degradans 2-40] Length = 543
- 1592.3 Best-BlastP=> >nrrprot 62% Identities = 130/295 (44%), Positives = 191/295 (64%) ref[NP\_406039.1] putative membrane protein [Yersinia pestis] ref[NP\_669001.1] hypothetical [Yersinia pestis KIM] pir[AB0306 probable membrane protein YPO2505 [imported] - Yersinia pestis (strain CO92) emb[CAC91310.1] putative membrane protein [Yersinia pestis CO92] gb|AAM85252.1|AE013771\_7 hypothetical [Yersinia pestis KIM] Length = 312
- 1594.2 Best-BlastP=> >nrrprot 57% Identities = 83/248 (33%), Positives = 138/248 (55%), Gaps = 14/248 (5%) ref[NP\_842295.1] possible BioH, catalyzes some early step in biotin biosynthesis [Nitrosomonas europaea ATCC 19718] emb|CAD86210.1| possible BioH, catalyzes some early step in biotin biosynthesis [Nitrosomonas europaea ATCC 19718] Length = 259
- 1595.3 Best-BlastP=> >nrrprot 52% Identities = 130/329 (39%), Positives = 199/329 (60%), Gaps = 2/329 (0%) ref[NP\_790344.1] 8-amino-7-oxononanoate synthase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54039.1| 8-amino-7-oxononanoate synthase [Pseudomonas syringae pv. tomato str. DC3000] Length = 396
- 1598.6 Best-BlastP=> >nrrprot 75% Identities = 189/307 (61%), Positives = 240/307 (78%) gb|AAG47791.1|AF311738\_7 BioB [Mesorhizobium loti] emb|CAD31399.1| BIOTIN SYNTHASE PROTEIN [Mesorhizobium loti] Length = 331
- 1599.4 Best-BlastP=> >nrrprot 48% Identities = 481/1746 (27%), Positives = 836/1746 (47%), Gaps = 149/1746 (8%) ref[NP\_932226.1] putative conjugative transfer protein Tral [Vibrio vulnificus YJ016] dbj|BAC97749.1| putative conjugative transfer protein Tral [Vibrio vulnificus YJ016] Length = 1924
- 16.1 Best-BlastP=> >nrrprot 60% Identities = 34/55 (61%), Positives = 42/55 (76%) ref[NP\_890077.1] putative phage excisionase [Bordetella bronchiseptica] emb|CAE34036.1| putative phage excisionase [Bordetella bronchiseptica] Length = 84

- 160.1 Best-BlastP=> >nrprot 35% Identities = 36/95 (37%), Positives = 43/95 (45%), Gaps = 7/95 (7%) gb|AAF86199.1|AF238885\_2 VrrB [Bacillus anthracis] Length = 265
- 1601.3 Best-BlastP=> >nrprot 61% Identities = 166/370 (44%), Positives = 236/370 (63%), Gaps = 17/370 (4%) refNP\_660996.1| glycosyl hydrolase, family 3 [Chlorobium tepidum TLS] gb|AAM71338.1| glycosyl hydrolase, family 3 [Chlorobium tepidum TLS] Length = 372
- 1602.2 Best-BlastP=> >nrprot 52% Identities = 133/394 (33%), Positives = 207/394 (52%), Gaps = 17/394 (4%) refNP\_798008.1| putative SAM-dependent methyltransferase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC59892.1| putative SAM-dependent methyltransferase [Vibrio parahaemolyticus] Length = 418
- 1603.3 Best-BlastP=> >nrprot 10% Identities = 40/105 (38%), Positives = 55/105 (52%), Gaps = 5/105 (4%) pdb|1N0R|A Chain A, 4ank: A Designed Ankyrin Repeat Protein With Four Identical Consensus Repeats Length = 126
- 1606.2 Best-BlastP=> >nrprot 64% Identities = 136/270 (50%), Positives = 178/270 (65%) refZP\_00065849.1| COG0266: Formamidopyrimidine-DNA glycosylase [Microbulbifer degradans 2-40] Length = 271
- 1607.2 Best-BlastP=> >nrprot 55% Identities = 24/78 (30%), Positives = 43/78 (55%), Gaps = 1/78 (1%) refNP\_820114.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90628.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 105
- 1608.2 Best-BlastP=> >nrprot 70% Identities = 201/383 (52%), Positives = 279/383 (72%) refNP\_903067.1| probable stearyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] gb|AAQ61061.1| probable stearyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] Length = 405
- 1611.5 Best-BlastP=> >nrprot 75% Identities = 206/338 (60%), Positives = 260/338 (76%), Gaps = 1/338 (0%) refZP\_00085994.1| COG0128: 5-enolpyruvylshikimate-3-phosphate synthase [Pseudomonas fluorescens PfO-1] Length = 679
- 1615.2 Best-BlastP=> >nrprot 64% Identities = 291/607 (47%), Positives = 389/607 (64%), Gaps = 17/607 (2%) refNP\_826054.1| putative oxidoreductase [Streptomyces avermitilis MA-4680] dbj|BAC72589.1| putative oxidoreductase [Streptomyces avermitilis MA-4680] Length = 642
- 1617.3 Best-BlastP=> >nrprot 62% Identities = 77/167 (46%), Positives = 107/167 (64%), Gaps = 3/167 (1%) refNP\_820461.1| alkylhydroperoxidase AhpD family core domain protein [Coxiella burnetii RSA 493] gb|AAO90975.1| alkylhydroperoxidase AhpD family core domain protein [Coxiella burnetii RSA 493] Length = 177
- 1618.3 Best-BlastP=> >nrprot 97% Identities = 159/162 (98%), Positives = 159/162 (98%) sp|P53637|SODC\_LEGPN Superoxide dismutase [Cu-Zn] precursor dbj|BAA06223.1| [Cu,Zn]-superoxide dismutase [Legionella pneumophila] gb|AAB36467.1| periplasmic copper-zinc superoxide dismutase; CuZnSOD [Legionella pneumophila] Length = 162
- 1623.4 Best-BlastP=> >nrprot 46% Identities = 115/438 (26%), Positives = 202/438 (46%), Gaps = 28/438 (6%) refNP\_873416.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] gb|AAP95805.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] Length = 665
- 1624.4 Best-BlastP=> >nrprot 42% Identities = 121/543 (22%), Positives = 225/543 (41%), Gaps = 73/543 (13%) refZP\_00089633.1| hypothetical protein [Azotobacter vinelandii] Length = 642
- 1625.3 Best-BlastP=> >nrprot 90% Identities = 317/379 (83%), Positives = 345/379 (91%) gb|AAP88975.1| S-adenosylmethionine synthetase [Amoeba proteus symbiotic bacterium] Length = 381

- 1626.3 Best-BlastP=> >nrprot 83% Identities = 321/427 (75%), Positives = 368/427 (86%) ref|NP\_821004.1| adenosylhomocysteinase [Coxiella burnetii RSA 493] gb|AAO91518.1| adenosylhomocysteinase [Coxiella burnetii RSA 493] Length = 429
- 1628.3 Best-BlastP=> >nrprot 56% Identities = 118/268 (44%), Positives = 154/268 (57%), Gaps = 21/268 (7%) ref|NP\_771454.1| bl|4814 [Bradyrhizobium japonicum] dbj|BAC50079.1| bl|4814 [Bradyrhizobium japonicum USDA 110] Length = 262
- 1629.1 Best-BlastP=> >nrprot 54% Identities = 88/251 (35%), Positives = 138/251 (54%), Gaps = 19/251 (7%) ref|NP\_771455.1| bl|4815 [Bradyrhizobium japonicum] dbj|BAC50080.1| bl|4815 [Bradyrhizobium japonicum USDA 110] Length = 235
- 163.1 Best-BlastP=> >nrprot 74% Identities = 237/426 (55%), Positives = 324/426 (76%) ref|ZP\_00072043.1| COG0334: Glutamate dehydrogenase/leucine dehydrogenase [Trichodesmium erythraeum IMS101] Length = 428
- 1631.3 Best-BlastP=> >nrprot 60% Identities = 264/625 (42%), Positives = 366/625 (58%), Gaps = 65/625 (10%) ref|NP\_771456.1| bl|4816 [Bradyrhizobium japonicum] dbj|BAC50081.1| bl|4816 [Bradyrhizobium japonicum USDA 110] Length = 649
- 1632.3 Best-BlastP=> >nrprot 69% Identities = 276/567 (48%), Positives = 411/567 (72%), Gaps = 4/567 (0%) ref|NP\_819875.1| ABC transporter, ATP-binding/permease protein [Coxiella burnetii RSA 493] gb|AAO90389.1| ABC transporter, ATP-binding/permease protein [Coxiella burnetii RSA 493] Length = 589
- 1633.2 Best-BlastP=> >nrprot 63% Identities = 142/305 (46%), Positives = 203/305 (66%), Gaps = 11/305 (3%) ref|NP\_438232.1| tetraacyldisaccharide 4'-kinase-like protein [Haemophilus influenzae Rd] sp|P44491|LPXK\_HAEIN Tetraacyldisaccharide 4'-kinase (Lipid A 4'-kinase) pir|G64141 probable tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) H10059 [similarity] - Haemophilus influenzae (strain Rd KW20) gb|AAC21737.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 332
- 1635.4 Best-BlastP=> >nrprot 16% Identities = 86/371 (23%), Positives = 164/371 (44%), Gaps = 39/371 (10%) pir|T24806 hypothetical protein T10G3.5 - Caenorhabditis elegans Length = 1164
- 1636.2 Best-BlastP=> >nrprot 73% Identities = 660/1159 (56%), Positives = 841/1159 (72%), Gaps = 16/1159 (1%) ref|NP\_454838.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_804113.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|A10530 DNA polymerase III, alpha chain [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) emb|CAD08689.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO67962.1| DNA polymerase III, alpha chain [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 1160
- 1638.2 Best-BlastP=> >nrprot 76% Identities = 256/395 (64%), Positives = 304/395 (76%), Gaps = 3/395 (0%) ref|NP\_642338.1| 3-ketoacyl-CoA thiolase [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36874.1| 3-ketoacyl-CoA thiolase [Xanthomonas axonopodis pv. citri str. 306] Length = 401
- 1639.4 Best-BlastP=> >nrprot No Hits found
- 1641.5 Best-BlastP=> >nrprot 63% Identities = 190/434 (43%), Positives = 282/434 (64%), Gaps = 5/434 (1%) ref|NP\_793501.1| trigger factor [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57196.1| trigger factor [Pseudomonas syringae pv. tomato str. DC3000] Length = 436



- 1642.3 Best-BlastP=> >nrprot 82% Identities = 150/203 (73%), Positives = 178/203 (87%), Gaps = 1/203 (0%) ref|NP\_455045.1| ATP-dependent clp protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_459444.1| proteolytic subunit of clpA-clpP ATP-dependent serine protease, heat shock protein F21.5 [Salmonella typhimurium LT2] ref|NP\_806142.1| ATP-dependent clp protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2] sp|Q9LC07|CLPP\_SALTY ATP-dependent Clp protease proteolytic subunit [Endopeptidase Clp] pir|IAC0558 ATP-dependent clp protease proteolytic chain [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) dbj|BAA94668.1| serine protease subunit [Salmonella typhimurium] gb|AAL19403.1| proteolytic subunit of clpA-clpP ATP-dependent serine protease [Salmonella typhimurium LT2] emb|CAD08907.1| ATP-dependent clp protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70002.1| ATP-dependent clp protease proteolytic subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 207
- 1643.4 Best-BlastP=> >nrprot 97% Identities = 791/816 (96%), Positives = 800/816 (98%) gb|AAM00615.1| response regulator TutC-like protein [Legionella pneumophila] Length = 816
- 1644.6 Best-BlastP=> >nrprot 59% Identities = 171/417 (41%), Positives = 246/417 (58%), Gaps = 9/417 (2%) ref|NP\_772134.1| bl|5494 [Bradyrhizobium japonicum] dbj|BAC50759.1| bl|5494 [Bradyrhizobium japonicum USDA 110] Length = 415
- 1645.1 Best-BlastP=> >nrprot 59% Identities = 76/172 (44%), Positives = 110/172 (63%) ref|NP\_717325.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN54769.1|AE015617\_4 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 183
- 1647.2 Best-BlastP=> >nrprot 67% Identities = 101/180 (56%), Positives = 127/180 (70%), Gaps = 1/180 (0%) ref|NP\_715765.1| acyltransferase family protein [Shewanella oneidensis MR-1] gb|AAN53210.1|AE015463\_7 acyltransferase family protein [Shewanella oneidensis MR-1] Length = 186
- 1649.3 Best-BlastP=> >nrprot 53% Identities = 276/732 (37%), Positives = 397/732 (54%), Gaps = 63/732 (8%) ref|NP\_832882.1| hypothetical protein [Bacillus cereus ATCC 14579] gb|AAP10083.1| hypothetical protein [Bacillus cereus ATCC 14579] Length = 854
- 1650.2 Best-BlastP=> >nrprot 35% Identities = 119/317 (37%), Positives = 181/317 (57%), Gaps = 6/317 (1%) ref|NP\_832883.1| NADH-quinone oxidoreductase chain L [Bacillus cereus ATCC 14579] gb|AAP10084.1| NADH-quinone oxidoreductase chain L [Bacillus cereus ATCC 14579] Length = 510
- 1652.4 Best-BlastP=> >nrprot 35% Identities = 37/135 (27%), Positives = 67/135 (49%), Gaps = 11/135 (8%) pir|I40884 cytotoxin L - Clostridium sordellii emb|CAA57959.1| cytotoxin L [Clostridium sordellii] Length = 2364
- 1653.3 Best-BlastP=> >nrprot 63% Identities = 142/281 (50%), Positives = 195/281 (69%), Gaps = 1/281 (0%) pir|A42928 plasminogen activator precursor - Yersinia pestis Length = 312
- 1655.2 Best-BlastP=> >nrprot 81% Identities = 41/60 (68%), Positives = 49/60 (81%), Gaps = 2/60 (3%) ref|NP\_842168.1| Tetraacyldisaccharide-1-P 4'-kinase [Nitrosomonas europaea ATCC 19718] emb|CAD86075.1| Tetraacyldisaccharide-1-P 4'-kinase [Nitrosomonas europaea ATCC 19718] Length = 396
- 1657.1 Best-BlastP=> >nrprot 64% Identities = 124/250 (49%), Positives = 163/250 (65%), Gaps = 7/250 (2%) ref|NP\_872922.1| 3-deoxy-manno-oculosonate cytidyltransferase [Haemophilus ducreyi 35000HP] gb|AAP95311.1| 3-deoxy-manno-oculosonate cytidyltransferase [Haemophilus ducreyi 35000HP] Length = 253
- 1658.2 Best-BlastP=> >nrprot 33% Identities = 96/392 (24%), Positives = 148/392 (37%), Gaps = 116/392 (29%) ref|ZP\_00067367.1| COG2730: Endoglucanase [Microbulbifer degradans 2-40] Length = 725

- 1659.4 Best-BlastP=> >nrprot 25% Identities = 156/726 (21%), Positives = 334/726 (46%), Gaps = 107/726 (14%) pir||A47297 myosin heavy chain form B, nonmuscle - African clawed frog gb|AAA49915.1| nonmuscle myosin heavy chain b Length = 1992
- 166.2 Best-BlastP=> >nrprot 96% Identities = 1010/1064 (94%), Positives = 1030/1064 (96%), Gaps = 4/1064 (0%) gb|AAM00617.1| putative copper efflux ATPase [Legionella pneumophila] Length = 1060
- 1660.2 Best-BlastP=> >nrprot No Hits found
- 1661.3 Best-BlastP=> >nrprot 61% Identities = 110/213 (51%), Positives = 140/213 (65%), Gaps = 1/213 (0%) sp|Q8DDY0|RAD\_C\_VIBU DNA repair protein radC homolog dbj|BAC93049.1| DNA repair protein [Vibrio vulnificus YJ016] Length = 224
- 1663.6 Best-BlastP=> >nrprot 86% Identities = 1036/1406 (73%), Positives = 1216/1406 (86%), Gaps = 14/1406 (0%) ref|NP\_742614.1| DNA-directed RNA polymerase, beta' subunit [Pseudomonas putida KT2440] gb|AAN66078.1| AE016237\_2 DNA-directed RNA polymerase, beta' subunit [Pseudomonas putida KT2440] Length = 1399
- 1664.2 Best-BlastP=> >nrprot 29% Identities = 47/193 (24%), Positives = 80/193 (41%), Gaps = 13/193 (6%) ref|ZP\_00046942.1| COG3064: Membrane protein involved in colicin uptake [Lactobacillus gasseri] Length = 962
- 1666.3 Best-BlastP=> >nrprot No Hits found
- 1669.3 Best-BlastP=> >nrprot 68% Identities = 177/313 (56%), Positives = 220/313 (70%) ref|NP\_617527.1| triacylglycerol lipase [Methanosarcina acetivorans str. C2A] gb|AAM06007.1| triacylglycerol lipase [Methanosarcina acetivorans str. C2A] Length = 321
- 1670.3 Best-BlastP=> >nrprot 16% Identities = 43/147 (29%), Positives = 74/147 (50%), Gaps = 6/147 (4%) ref|XP\_323831.1| predicted protein [Neurospora crassa] gb|EAA27811.1| predicted protein [Neurospora crassa] Length = 554
- 1671.3 Best-BlastP=> >nrprot No Hits found
- 1673.5 Best-BlastP=> >nrprot 31% Identities = 97/388 (25%), Positives = 174/388 (44%), Gaps = 42/388 (10%) pir||F86291 hypothetical protein F7H2.8 [imported] - Arabidopsis thaliana gb|AAF82144.1| AC034256\_8 Contains similarity to F-box protein FBL2 from Homo sapiens gb|AF176518 and contains multiple Leucine Rich PF|00560 repeats. ESTs gb|Z34572, gb|Z34571, gb|A1100681, gb|A1100675, gb|AA395320, gb|A1100674, gb|AA651378, gb|AA007067, gb|T46145, gb|T22090, gb|A1995016, gb|H36884, gb|A1995066, gb|H37061, gb|T43537 come from this gene. [Arabidopsis thaliana] Length = 568
- 1675.3 Best-BlastP=> >nrprot 39% Identities = 20/67 (29%), Positives = 42/67 (62%) ref|NP\_439878.1| hypothetical protein [Haemophilus influenzae Rd] sp|P44300|YH36\_HAEIN Hypothetical protein H1736 pir||D64041 hypothetical protein H1736 - Haemophilus influenzae (strain Rd KW20) gb|AAC23384.1| H. influenzae predicted coding region H1736 [Haemophilus influenzae Rd] Length = 77
- 168.1 Best-BlastP=> >nrprot 42% Identities = 43/160 (26%), Positives = 75/160 (46%), Gaps = 25/160 (15%) ref|NP\_437473.1| hypothetical membrane protein [Sinorhizobium meliloti] pir||E95958 hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC49333.1| hypothetical membrane protein [Sinorhizobium meliloti] Length = 172
- 1681.5 Best-BlastP=> >nrprot 65% Identities = 432/984 (43%), Positives = 629/984 (63%), Gaps = 47/984 (4%) ref|NP\_927961.1| RNA polymerase associated protein (ATP-dependent helicase) [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE12910.1| RNA polymerase associated protein (ATP-dependent helicase) [Photobacterium luminescens subsp. laumondii TTO1] Length = 970
- 1682.4 Best-BlastP=> >nrprot 35% Identities = 63/190 (33%), Positives = 105/190 (55%), Gaps = 8/190 (4%) ref|ZP\_00065413.1| COG3000: Sterol desaturase [Microbulbifer degradans 2-40] Length = 273

- 1683.2 Best-BlastP=> >nrprot No Hits found
- 1684.3 Best-BlastP=> >nrprot No Hits found
- 1685.3 Best-BlastP=> >nrprot 72% Identities = 199/372 (53%), Positives = 270/372 (72%), Gaps = 3/372 (0%) ref|ZP\_00016064.1| COG0842: ABC-type multidrug transport system, permease component [Rhodospirillum rubrum] Length = 376
- 1689.3 Best-BlastP=> >nrprot 68% Identities = 207/377 (54%), Positives = 275/377 (72%), Gaps = 9/377 (2%) ref|NP\_720122.1| cytochrome c oxidase, subunit II [Shewanella oneidensis MR-1] gb|AAN57566.1|AE015892\_6 cytochrome c oxidase, subunit II [Shewanella oneidensis MR-1] Length = 513
- 169.1 Best-BlastP=> >nrprot 86% Identities = 55/68 (80%), Positives = 60/68 (88%) gb|AAM00618.1| unknown [Legionella pneumophila] Length = 68
- 1691.3 Best-BlastP=> >nrprot 84% Identities = 388/528 (73%), Positives = 458/528 (86%), Gaps = 8/528 (1%) ref|NP\_720123.1| cytochrome c oxidase, subunit I [Shewanella oneidensis MR-1] gb|AAN57567.1|AE015892\_7 cytochrome c oxidase, subunit I [Shewanella oneidensis MR-1] Length = 530
- 1692.2
- 1693.2 Best-BlastP=> >nrprot 86% Identities = 473/671 (70%), Positives = 577/671 (85%), Gaps = 7/671 (1%) ref|NP\_819550.1| excinuclease ABC, B subunit [Coxiella burnetii RSA 493] gb|AAO90064.1| excinuclease ABC, B subunit [Coxiella burnetii RSA 493] Length = 672
- 1695.2 Best-BlastP=> >nrprot 56% Identities = 27/75 (36%), Positives = 45/75 (60%) ref|NP\_754358.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN80925.1|AE016762\_178 Hypothetical protein [Escherichia coli CFT073] Length = 82
- Best-BlastP=> >nrprot 56% Identities = 118/355 (33%), Positives = 189/355 (53%), Gaps = 47/355 (13%) ref|NP\_884030.1| conserved hypothetical protein [Bordetella parapertussis] emb|CAE37058.1| conserved hypothetical protein [Bordetella parapertussis] Length = 392
- 1697.2 Best-BlastP=> >nrprot 56% Identities = 66/174 (37%), Positives = 104/174 (59%), Gaps = 2/174 (1%) ref|ZP\_00013244.1| COG3038: Cytochrome B561 [Rhodospirillum rubrum] Length = 188
- 1698.2 Best-BlastP=> >nrprot 35% Identities = 84/273 (30%), Positives = 130/273 (47%), Gaps = 17/273 (6%) ref|ZP\_00085491.1| COG0354: Predicted aminomethyltransferase related to GovT [Pseudomonas fluorescens PfO-1] Length = 313
- 1699.4 Best-BlastP=> >nrprot 58% Identities = 130/277 (46%), Positives = 176/277 (63%), Gaps = 6/277 (2%) ref|ZP\_00090118.1| COG0771: UDP-N-acetylmutamoylalanine-D-glutamate ligase [Azotobacter vinelandii] Length = 448
- 1701.5 Best-BlastP=> >nrprot 66% Identities = 192/359 (53%), Positives = 262/359 (72%) ref|NP\_819182.1| cell division protein FtsW [Coxiella burnetii RSA 493] gb|AAD39750.1|AF123260\_1 FtsW [Coxiella burnetii] gb|AAO89696.1| cell division protein FtsW [Coxiella burnetii RSA 493] Length = 372
- 1703.1 Best-BlastP=> >nrprot 36% Identities = 57/215 (26%), Positives = 93/215 (43%), Gaps = 32/215 (14%) ref|NP\_780971.1| DNA helicase [Clostridium tetani E88] gb|AAO34908.1| DNA helicase [Clostridium tetani E88] Length = 1352
- 1704.4 Best-BlastP=> >nrprot 8% Identities = 33/108 (30%), Positives = 55/108 (50%), Gaps = 5/108 (4%) ref|NP\_266277.1| hypothetical protein [Lactococcus lactis subsp. lactis] pir|A86640 hypothetical protein ybcH [imported] - Lactococcus lactis subsp. lactis (strain IL1403) gb|AAK04219.1|AE006250\_6 HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 311
- 1705.2 Best-BlastP=> >nrprot No Hits found

- 1706.2 Best-BlastP=> >nrprot 56% Identities = 62/148 (41%), Positives = 86/148 (58%), Gaps = 7/148 (4%) ref|ZP\_00054547.1| COG0350: Methylated DNA-protein cysteine methyltransferase [Magnetospirillum magnetotacticum] Length = 183
- 1707.2 Best-BlastP=> >nrprot 85% Identities = 96/117 (82%), Positives = 104/117 (88%), Gaps = 2/117 (1%) ref|ZP\_00091602.1| COG0335: Ribosomal protein L19 [Azotobacter vinelandii] Length = 116
- 1708.4 Best-BlastP=> >nrprot 52% Identities = 44/123 (35%), Positives = 65/123 (52%), Gaps = 6/123 (4%) ref|ZP\_00134742.1| COG3109: Activator of osmotectant transporter ProP [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 182
- 1709.1 Best-BlastP=> >nrprot 65% Identities = 114/228 (50%), Positives = 152/228 (66%), Gaps = 2/228 (0%) ref|NP\_819391.1| 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] gb|AAO89905.1| 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] Length = 234
- 1711.2 Best-BlastP=> >nrprot 36% Identities = 49/177 (27%), Positives = 88/177 (49%), Gaps = 15/177 (8%) gb|EAA36774.1| GLP\_193\_16037\_16813 [Giardia lamblia ATCC 50803] Length = 258
- 1713.2 Best-BlastP=> >nrprot 64% Identities = 314/686 (45%), Positives = 445/686 (64%), Gaps = 3/686 (0%) ref|NP\_820891.1| glycyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] sp|P45651|SYGB\_COXBU Glycyl-tRNA synthetase beta chain (Glycine-tRNA ligase beta chain) (GlyRS) gb|AAO91405.1| glycyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] Length = 689
- 1714.4 Best-BlastP=> >nrprot 85% Identities = 224/291 (76%), Positives = 258/291 (88%) ref|NP\_820890.1| glycyl-tRNA synthetase, alpha subunit [Coxiella burnetii RSA 493] sp|P94616|SYGA\_COXBU Glycyl-tRNA synthetase alpha chain (Glycine-tRNA ligase alpha chain) (GlyRS) emb|CAA71456.1| unnamed protein product [Coxiella burnetii] gb|AAO91404.1| glycyl-tRNA synthetase, alpha subunit [Coxiella burnetii RSA 493] Length = 319
- 172.1 Best-BlastP=> >nrprot 69% Identities = 28/58 (48%), Positives = 44/58 (75%) ref|ZP\_00053249.1| hypothetical protein [Magnetospirillum magnetotacticum] ref|ZP\_00101210.1| hypothetical protein [Desulfiobacterium hafniense] Length = 60
- 1720.3 Best-BlastP=> >nrprot 24% Identities = 37/126 (29%), Positives = 64/126 (50%), Gaps = 3/126 (2%) ref|NP\_371995.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus Mu50] ref|NP\_374585.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus N315] ref|NP\_646177.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus MW2] pir|G89925| menaquinone biosynthesis methyltransferase [imported] - Staphylococcus aureus (strain N315) dbj|BAB42564.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus N315] dbj|BAB57633.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus Mu50] dbj|BAB95225.1| menaquinone biosynthesis methyltransferase [Staphylococcus aureus subsp. aureus MW2] Length = 241
- 1722.2 Best-BlastP=> >nrprot 55% Identities = 123/307 (40%), Positives = 173/307 (56%), Gaps = 9/307 (2%) ref|NP\_781246.1| glutaminase [Clostridium tetani E88] gb|AAO35183.1| glutaminase [Clostridium tetani E88] Length = 306
- 1723.5 Best-BlastP=> >nrprot 59% Identities = 71/181 (39%), Positives = 111/181 (61%), Gaps = 9/181 (4%) ref|NP\_346734.1| D-3 phosphoglycerate dehydrogenase [Clostridium acetobutylicum] pir|G96910| D-3 phosphoglycerate dehydrogenase [imported] - Clostridium acetobutylicum gb|AAK78074.1| AE007521\_8 D-3 phosphoglycerate dehydrogenase [Clostridium acetobutylicum] Length = 318

- 1724.3 Best-BlastP=> >nrprot 35% Identities = 62/241 (25%), Positives = 104/241 (43%), Gaps = 20/241 (8%) ref[NP\_102317.1] probable hydrolase [Mesorhizobium loti] dbj[BAB48103.1] probable hydrolase [Mesorhizobium loti] Length = 248
- 1725.3 Best-BlastP=> >nrprot 74% Identities = 172/279 (61%), Positives = 212/279 (75%) ref[NP\_747209.1] RNA polymerase sigma-32 factor [Pseudomonas putida KT2440] gb|AAF80334.1|AF157048.1 heat shock sigma factor RpoH [Pseudomonas putida] gb|AAN70673.1|AE016711.1 RNA polymerase sigma-32 factor [Pseudomonas putida KT2440] Length = 284
- 1726.4 Best-BlastP=> >nrprot 14% Identities = 50/174 (28%), Positives = 82/174 (47%), Gaps = 18/174 (10%) ref[NP\_473239.1] hypothetical protein [Plasmodium falciparum 3D7] pir|T18459 hypothetical protein C0515c - malaria parasite (Plasmodium falciparum) emb|CAA15601.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1236
- 1730.3 Best-BlastP=> >nrprot 72% Identities = 498/899 (55%), Positives = 632/899 (70%), Gaps = 39/899 (4%) ref[NP\_668025.1] protein chain initiation factor IF-2 [Yersinia pestis KIM] sp|Q8ZBC2|IF2\_YERPE Translation initiation factor IF-2 gb|AAM84276.1|AE013671.3 protein chain initiation factor IF-2 [Yersinia pestis KIM] Length = 892
- 1733.3 Best-BlastP=> >nrprot 70% Identities = 225/399 (56%), Positives = 293/399 (73%), Gaps = 1/399 (0%) ref[NP\_653663.1] SDF, Sodium:dicarboxylate symporter family [Bacillus anthracis A2012] ref[NP\_847618.1] proton/glutamate symporter family protein, putative [Bacillus anthracis str. Ames] gb|AAP29104.1|proton/glutamate symporter family protein, putative [Bacillus anthracis str. Ames] Length = 405
- 1734.2 Best-BlastP=> >nrprot No Hits found
- 1735.1 Best-BlastP=> >nrprot No Hits found
- 1737.2 Best-BlastP=> >nrprot 34% Identities = 88/258 (34%), Positives = 129/258 (50%), Gaps = 30/258 (11%) ref[NP\_052868.1] hypothetical protein [Coxiella burnetii] gb|AAD33500.1|AF131076.26 hypothetical protein [Coxiella burnetii] Length = 361
- 1738.3 Best-BlastP=> >nrprot 84% Identities = 284/394 (72%), Positives = 339/394 (86%) ref[ZP\_00065178.1] COG0133: Tryptophan synthase beta chain [Microbulbifer degradans 2-40] Length = 403
- 1739.2 Best-BlastP=> >nrprot 65% Identities = 95/197 (48%), Positives = 136/197 (69%) ref[NP\_902433.1] phosphoribosylanthranilate isomerase [Chromobacterium violaceum ATCC 12472] gb|AAQ60431.1|phosphoribosylanthranilate isomerase [Chromobacterium violaceum ATCC 12472] Length = 206
- 174.1
- Best-BlastP=> >nrprot 71% Identities = 165/284 (58%), Positives = 206/284 (72%) ref[NP\_820298.1] peptide methionine sulfoxide reductase [Coxiella burnetii RSA 493] gb|AAO90812.1|peptide methionine sulfoxide reductase [Coxiella burnetii RSA 493] Length = 284
- 1740.3 Best-BlastP=> >nrprot 73% Identities = 148/259 (57%), Positives = 193/259 (74%), Gaps = 1/259 (0%) ref[ZP\_00087161.1] COG0101: Pseudouridylylate synthase [Pseudomonas fluorescens PfO-1] Length = 313
- 1742.3 Best-BlastP=> >nrprot 79% Identities = 163/239 (68%), Positives = 198/239 (82%), Gaps = 1/239 (0%) ref[ZP\_00091549.1] COG0528: Uridylate kinase [Azotobacter vinelandii] Length = 249
- 1743.4 Best-BlastP=> >nrprot 84% Identities = 118/184 (64%), Positives = 158/184 (85%) ref[NP\_928020.1] ribosome releasing factor [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE12970.1|ribosome releasing factor [Photobacterium luminescens subsp. laumondii TTO1] Length = 185

- 1746.2 Best-BlastP=> >nrprot 47% Identities = 71/209 (33%), Positives = 100/209 (47%), Gaps = 8/209 (3%) ref|NP\_233145.1| arginine ABC transporter, periplasmic arginine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|H82420 arginine ABC transporter, periplasmic arginine-binding protein VCA0759 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96657.1| arginine ABC transporter, periplasmic arginine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 243
- 1747.2 Best-BlastP=> >nrprot No Hits found
- 1748.3 Best-BlastP=> >nrprot 57% Identities = 160/430 (37%), Positives = 244/430 (56%), Gaps = 14/430 (3%) ref|NP\_662910.1| threonine synthase [Chlorobium tepidum TLS] gb|AAM73252.1| threonine synthase [Chlorobium tepidum TLS] Length = 441
- 1749.2 Best-BlastP=> >nrprot 29% Identities = 48/192 (25%), Positives = 77/192 (40%), Gaps = 21/192 (10%) ref|NP\_698612.1| outer membrane protein, 31 kDa [Brucella suis 1330] gb|AAN30527.1|AE014455\_11 outer membrane protein, 31 kDa [Brucella suis 1330] Length = 261
- 1750.3 Best-BlastP=> >nrprot 69% Identities = 162/295 (54%), Positives = 201/295 (68%), Gaps = 6/295 (2%) ref|NP\_742276.1| cytochrome c oxidase, subunit III [Pseudomonas putida KT2440] gb|AAN65740.1|AE016200\_4 cytochrome c oxidase, subunit III [Pseudomonas putida KT2440] Length = 295
- 1752.2 Best-BlastP=> >nrprot 66% Identities = 83/173 (47%), Positives = 120/173 (69%), Gaps = 2/173 (1%) ref|NP\_720124.1| cytochrome c oxidase assembly protein coxG [Shewanella oneidensis MR-1] gb|AAN57568.1|AE015892\_8 cytochrome c oxidase assembly protein coxG [Shewanella oneidensis MR-1] Length = 193
- 1754.3 Best-BlastP=> >nrprot 49% Identities = 174/422 (41%), Positives = 252/422 (59%), Gaps = 9/422 (2%) ref|NP\_820704.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] gb|AAO91218.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] Length = 584
- 1755.3 Best-BlastP=> >nrprot No Hits found
- 1756.4 Best-BlastP=> >nrprot 63% Identities = 133/271 (49%), Positives = 181/271 (66%) ref|NP\_902359.1| probable oxidoreductase, short-chain dehydrogenase/reductase family [Chromobacterium violaceum ATCC 12472] gb|AAQ60359.1| probable oxidoreductase, short-chain dehydrogenase/reductase family [Chromobacterium violaceum ATCC 12472] Length = 278
- 1759.4 Best-BlastP=> >nrprot 43% Identities = 55/224 (24%), Positives = 102/224 (45%), Gaps = 3/224 (1%) ref|NP\_746234.1| conserved hypothetical protein [Pseudomonas putida KT2440] gb|AAN69698.1|AE016606\_1 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 267
- 176.1 Best-BlastP=> >nrprot No Hits found
- 1760.4 Best-BlastP=> >nrprot 75% Identities = 116/223 (52%), Positives = 170/223 (76%) ref|XP\_306643.1| ENSANGP00000000843 [Anopheles gambiae] gb|EAA02110.1| ENSANGP00000000843 [Anopheles gambiae str. PEST] Length = 228
- 1761.4 Best-BlastP=> >nrprot 9% Identities = 54/209 (25%), Positives = 100/209 (47%), Gaps = 38/209 (18%) ref|ZP\_00010059.1| COG1680: Beta-lactamase class C and other penicillin binding proteins [Rhodopseudomonas palustris] Length = 395
- 1762.2 Best-BlastP=> >nrprot 39% Identities = 66/245 (26%), Positives = 125/245 (51%), Gaps = 9/245 (3%) ref|NP\_834835.1| Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] gb|AAP12036.1| Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] Length = 254

- 1764.3 Best-BlastP=> >nrprot 99% Identities = 377/377 (100%), Positives = 377/377 (100%) emb|CAB65211.1| N-acylglucosamine 2-epimerase [Legionella pneumophila] Length = 377
- 1765.4 Best-BlastP=> >nrprot 99% Identities = 201/201 (100%), Positives = 201/201 (100%) emb|CAB65210.1| putative acetyl transferase [Legionella pneumophila] Length = 419
- 1767.2 Best-BlastP=> >nrprot 56% Identities = 103/234 (44%), Positives = 135/234 (57%), Gaps = 1/234 (0%) prf|1712315B glycerophosphoryl diester esterase Length = 247
- 1768.3 Best-BlastP=> >nrprot 52% Identities = 150/405 (37%), Positives = 216/405 (53%), Gaps = 12/405 (2%) ref|NP\_519385.1| PROBABLE GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC LIPOPROTEIN SIGNAL PEPTIDE [Ralstonia solanacearum] emb|CAD14966.1| PROBABLE GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC LIPOPROTEIN SIGNAL PEPTIDE [Ralstonia solanacearum] Length = 438
- 1770.2 Best-BlastP=> >nrprot 99% Identities = 1034/1035 (99%), Positives = 1034/1035 (99%) gb|AAF32510.1|AF095231\_1 defect in organelle trafficking protein [Legionella pneumophila] Length = 1035
- 1772.1 Best-BlastP=> >nrprot 94% Identities = 135/151 (89%), Positives = 144/151 (95%) gb|AAC35591.1| lcmV [Legionella pneumophila] Length = 151
- 1773.1 Best-BlastP=> >nrprot 99% Identities = 150/151 (99%), Positives = 151/151 (100%) pir|S61384 lcmW protein - Legionella pneumophila gb|AAC35589.1| lcmW [Legionella pneumophila] Length = 151
- 1774.2 Best-BlastP=> >nrprot 90% Identities = 411/472 (87%), Positives = 426/472 (90%), Gaps = 6/472 (1%) gb|AAC35590.1| lcmX [Legionella pneumophila] Length = 466
- 1775.3 Best-BlastP=> >nrprot No Hits found
- 1778.5 Best-BlastP=> >nrprot 52% Identities = 63/115 (54%), Positives = 82/115 (71%), Gaps = 4/115 (3%) ref|NP\_215343.1| hypothetical protein Rv0828c [Mycobacterium tuberculosis H37Rv] ref|NP\_854509.1| POSSIBLE DEAMINASE [Mycobacterium bovis subsp. bovis AF2122/97] pir|D70811 hypothetical protein Rv0828c - Mycobacterium tuberculosis (strain H37Rv) emb|CAA17634.1| hypothetical protein Rv0828c [Mycobacterium tuberculosis H37Rv] emb|CAD93713.1| POSSIBLE DEAMINASE [Mycobacterium bovis subsp. bovis AF2122/97] Length = 140
- 1779.3 Best-BlastP=> >nrprot No Hits found
- 178.1 Best-BlastP=> >nrprot No Hits found
- 1780.3 Best-BlastP=> >nrprot 80% Identities = 51/69 (73%), Positives = 56/69 (81%) ref|ZP\_00067276.1| COG1278: Cold shock proteins [Microbulifer degradans 2-40] Length = 71
- 1781.4 Best-BlastP=> >nrprot 72% Identities = 245/436 (56%), Positives = 318/436 (72%), Gaps = 1/436 (0%) ref|ZP\_00031144.1| COG0513: Superfamily II DNA and RNA helicases [Burkholderia fungorum] Length = 534
- 1782.3 Best-BlastP=> >nrprot 51% Identities = 134/404 (33%), Positives = 216/404 (53%), Gaps = 3/404 (0%) ref|NP\_819935.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO90449.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 437
- 1784.2 Best-BlastP=> >nrprot No Hits found
- 1786.2 Best-BlastP=> >nrprot 99% Identities = 123/123 (100%), Positives = 123/123 (100%) gb|AAN08839.1| transmission trait enhancer protein LetE [Legionella pneumophila] Length = 123



- 1787.4 Best-BlastP=> >nrprot 26% Identities = 131/667 (19%), Positives = 275/667 (41%), Gaps = 111/667 (16%) ref|NP\_082559.1| nuclear membrane binding protein NUCLING [Mus musculus] gb|AAH42415.1| Nuclear membrane binding protein NUCLING [Mus musculus] Length = 1413
- 1788.3 Best-BlastP=> >nrprot 62% Identities = 208/445 (46%), Positives = 285/445 (64%), Gaps = 6/445 (1%) ref|ZP\_00118630.1| hypothetical protein [Cytophaga hutchinsonii] Length = 452
- 179.1 Best-BlastP=> >nrprot 97% Identities = 85/89 (95%), Positives = 88/89 (98%) emb|CAC34415.1| putative TatB protein [Legionella pneumophila] Length = 89
- 1792.2 Best-BlastP=> >nrprot 46% Identities = 70/254 (27%), Positives = 121/254 (47%), Gaps = 13/254 (5%) ref|NP\_421699.1| hypothetical protein [Caulobacter crescentus CB15] pir|G87608 hypothetical protein CC2905 [imported] - Caulobacter crescentus gb|AAK24867.1| hypothetical protein [Caulobacter crescentus CB15] Length = 261
- 1793.3 Best-BlastP=> >nrprot 65% Identities = 133/262 (50%), Positives = 182/262 (69%), Gaps = 1/262 (0%) ref|NP\_819072.1| xanthosine phosphorylase [Coxiella burnetii RSA 493] gb|AAO89586.1| xanthosine phosphorylase [Coxiella burnetii RSA 493] Length = 273
- 1794.3 Best-BlastP=> >nrprot 51% Identities = 88/257 (34%), Positives = 132/257 (51%), Gaps = 21/257 (8%) ref|NP\_671037.1| 2-deoxyribose-5-phosphate aldolase [Yersinia pestis KIM] gb|AAM87288.1| AE013977\_7 2-deoxyribose-5-phosphate aldolase [Yersinia pestis KIM] Length = 270
- 1795.3 Best-BlastP=> >nrprot 19% Identities = 101/385 (26%), Positives = 172/385 (44%), Gaps = 54/385 (14%) ref|NP\_220907.1| unknown [Rickettsia prowazekii] pir|E71657 hypothetical protein RP534 - Rickettsia prowazekii emb|CAA14983.1| unknown [Rickettsia prowazekii] Length = 598
- 1797.4 Best-BlastP=> >nrprot 66% Identities = 123/252 (48%), Positives = 174/252 (69%), Gaps = 8/252 (3%) dbj|BAA20497.1| 27kDa outer membrane protein [Coxiella burnetii] Length = 252
- 18.1 Best-BlastP=> >nrprot No Hits found
- 180.1 Best-BlastP=> >nrprot 98% Identities = 60/61 (98%), Positives = 61/61 (100%) emb|CAC34414.1| putative TatA protein [Legionella pneumophila] Length = 61
- 1800.4 Best-BlastP=> >nrprot 74% Identities = 417/723 (57%), Positives = 543/723 (75%), Gaps = 7/723 (0%) ref|NP\_407289.1| DNA helicase II [Yersinia pestis] pir|AI0467 DNA helicase II (EC 3.6.1.-) [imported] - Yersinia pestis (strain CO92) emb|CAC93309.1| DNA helicase II [Yersinia pestis CO92] Length = 720
- 1803.2 Best-BlastP=> >nrprot 45% Identities = 30/59 (50%), Positives = 40/59 (67%) ref|ZP\_00021376.1| COG0477: Permeases of the major facilitator superfamily [Ralstonia metallidurans] Length = 120
- 1804.2 Best-BlastP=> >nrprot 88% Identities = 320/414 (77%), Positives = 367/414 (88%) gb|AAO92282.1| Hel Length = 414
- 1805.3 Best-BlastP=> >nrprot 27% Identities = 39/113 (34%), Positives = 59/113 (52%), Gaps = 5/113 (4%) ref|NP\_811310.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO77504.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 207
- 1806.2 Best-BlastP=> >nrprot 80% Identities = 90/151 (59%), Positives = 121/151 (80%), Gaps = 3/151 (1%) ref|NP\_820500.1| RNA methyltransferase, TrmH family, group 2 [Coxiella burnetii RSA 493] gb|AAO91014.1| RNA methyltransferase, TrmH family, group 2 [Coxiella burnetii RSA 493] Length = 152

- 1807.3 Best-BlastP=> >nrprot 65% Identities = 221/460 (48%), Positives = 309/460 (67%), Gaps = 2/460 (0%) ref|NP\_841539.1| putative homospemidine synthase protein [Nitrosomonas europaea ATCC 19718] Length = 472
- 1809.4 Best-BlastP=> >nrprot 42% Identities = 190/572 (33%), Positives = 326/572 (56%), Gaps = 4/572 (0%) ref|NP\_902623.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 1390
- 1812.4 Best-BlastP=> >nrprot 42% Identities = 88/335 (26%), Positives = 168/335 (50%), Gaps = 2/335 (0%) ref|ZP\_00092491.1| COG0477: Permeases of the major facilitator superfamily [Azotobacter vinelandii] Length = 432
- 1815.2 Best-BlastP=> >nrprot 45% Identities = 49/148 (33%), Positives = 80/148 (54%) ref|ZP\_00087676.1| COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Pseudomonas fluorescens PfO-1] Length = 167
- 1817.2 Best-BlastP=> >nrprot No Hits found
- 1818.4 Best-BlastP=> >nrprot 55% Identities = 280/280 (100%), Positives = 280/280 (100%) emb|CAB65209.1| hypothetical protein [Legionella pneumophila] Length = 280
- 1819.6 Best-BlastP=> >nrprot 58% Identities = 819/859 (95%), Positives = 836/859 (97%), Gaps = 1/859 (0%) gb|AAD47371.1| LigA [Legionella pneumophila] Length = 869
- 182.3 Best-BlastP=> >nrprot 66% Identities = 272/471 (57%), Positives = 367/471 (77%), Gaps = 2/471 (0%) ref|NP\_820993.1| ubiquinone biosynthesis protein AarF, putative [Coxiella burnetii RSA 493] gb|AAO91507.1| ubiquinone biosynthesis protein AarF, putative [Coxiella burnetii RSA 493] Length = 541
- 1823.5 Best-BlastP=> >nrprot 66% Identities = 206/419 (49%), Positives = 287/419 (68%) ref|NP\_252387.1| hypothetical protein [Pseudomonas aeruginosa PAO1] pir|A83183 hypothetical protein PA3697 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07085.1|AE004789\_5 hypothetical protein PA3697 [Pseudomonas aeruginosa PAO1] Length = 431
- 1826.2 Best-BlastP=> >nrprot No Hits found
- 1827.3 Best-BlastP=> >nrprot No Hits found
- 1831.3 Best-BlastP=> >nrprot 73% Identities = 235/399 (58%), Positives = 297/399 (74%) ref|NP\_819677.1| riboflavin biosynthesis protein RibA [Coxiella burnetii RSA 493] gb|AAO90191.1| riboflavin biosynthesis protein RibA [Coxiella burnetii RSA 493] Length = 406
- 1832.4 Best-BlastP=> >nrprot 58% Identities = 82/191 (42%), Positives = 120/191 (62%) ref|NP\_819676.1| riboflavin synthase, alpha subunit [Coxiella burnetii RSA 493] gb|AAO90190.1| riboflavin synthase, alpha subunit [Coxiella burnetii RSA 493] Length = 202
- 1834.4 Best-BlastP=> >nrprot 49% Identities = 144/439 (32%), Positives = 228/439 (51%), Gaps = 14/439 (3%) ref|NP\_484368.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AC1847 hypothetical protein all0324 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB72282.1| ORF\_ID:all0324-hypothetical protein [Nostoc sp. PCC 7120] Length = 447
- 1838.2 Best-BlastP=> >nrprot 52% Identities = 170/486 (34%), Positives = 256/486 (52%), Gaps = 27/486 (5%) ref|ZP\_00110911.1| COG1816: Adenosine deaminase [Nostoc punctiforme] Length = 523
- 1839.2 Best-BlastP=> >nrprot 57% Identities = 157/414 (37%), Positives = 230/414 (55%), Gaps = 33/414 (7%) ref|NP\_711587.1| sterol desaturase-related protein [Leptospira interrogans serovar lai str. 56601] gb|AAN48605.1|AE011320\_5 sterol desaturase-related protein [Leptospira interrogans serovar lai str. 56601] Length = 442
- 184.2 Best-BlastP=> >nrprot No Hits found

- 1840.3 Best-BlastP=> >nprot 53% Identities = 138/380 (36%), Positives = 220/380 (57%), Gaps = 7/380 (1%) ref|NP\_820736.1| drug resistance transporter, Bcr/CflA family [Coxiella burnetii RSA 493] gb|AAO91250.1| drug resistance transporter, Bcr/CflA family [Coxiella burnetii RSA 493] Length = 393
- 1841.2 Best-BlastP=> >nprot 58% Identities = 215/536 (40%), Positives = 327/536 (61%), Gaps = 9/536 (1%) ref|NP\_715995.1| AMP-binding protein [Shewanella oneidensis MR-1] gb|AAN53440.1|AE015483\_6 AMP-binding protein [Shewanella oneidensis MR-1] Length = 554
- 1844.3 Best-BlastP=> >nprot 54% Identities = 120/330 (36%), Positives = 193/330 (58%), Gaps = 3/330 (0%) ref|NP\_925659.1| UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Gloeobacter violaceus] dbj|BAC90654.1| UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Gloeobacter violaceus] Length = 345
- 1845.3 Best-BlastP=> >nprot No Hits found
- 1846.3 Best-BlastP=> >nprot 62% Identities = 181/411 (44%), Positives = 255/411 (62%), Gaps = 4/411 (0%) gb|AAN87389.1| 3-oxoacyl-[acyl-carrier-protein] synthase [Helicobacter mobilis] Length = 415
- 1847.3 Best-BlastP=> >nprot 19% Identities = 77/190 (40%), Positives = 110/190 (57%), Gaps = 5/190 (2%) ref|NP\_253486.1| hypothetical protein [Pseudomonas aeruginosa PAO1] sp|Q9HV11|YBJ8\_PSEAE Hypothetical protein PA4798 pir|C83045 hypothetical protein PA4798 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08184.1|AE004893\_2 hypothetical protein PA4798 [Pseudomonas aeruginosa PAO1] Length = 242
- 1848.4 Best-BlastP=> >nprot 31% Identities = 77/258 (29%), Positives = 129/258 (50%), Gaps = 21/258 (8%) ref|NP\_832609.1| Methyltransferase [Bacillus cereus ATCC 14579] gb|AAP09810.1| Methyltransferase [Bacillus cereus ATCC 14579] Length = 253
- 1849.3 Best-BlastP=> >nprot 40% Identities = 45/134 (33%), Positives = 73/134 (54%), Gaps = 4/134 (2%) ref|NP\_636084.1| acetyltransferase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM40008.1| acetyltransferase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 157
- 185.1 Best-BlastP=> >nprot 69% Identities = 141/253 (55%), Positives = 182/253 (71%), Gaps = 1/253 (0%) ref|NP\_484519.1| probable short-chain dehydrogenase [Nostoc sp. PCC 7120] pir|AB1866 hypothetical protein all0475 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB72433.1| ORF\_ID:all0475~probable short-chain dehydrogenase [Nostoc sp. PCC 7120] Length = 257
- 1852.2 Best-BlastP=> >nprot 54% Identities = 43/110 (39%), Positives = 65/110 (59%), Gaps = 6/110 (5%) ref|NP\_900345.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58351.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 128
- 1853.2 Best-BlastP=> >nprot 58% Identities = 65/127 (51%), Positives = 79/127 (62%), Gaps = 9/127 (7%) ref|NP\_459344.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] gb|AAL19303.1| putative outer membrane lipoprotein [Salmonella typhimurium LT2] Length = 119
- 1856.3 Best-BlastP=> >nprot No Hits found
- 1858.1 Best-BlastP=> >nprot No Hits found
- 1859.2 Best-BlastP=> >nprot 51% Identities = 85/271 (31%), Positives = 139/271 (51%), Gaps = 21/271 (7%) ref|NP\_219985.1| hypothetical protein [Chlamydia trachomatis] pir|E71509 hypothetical protein CT472 - Chlamydia trachomatis (serotype D, strain UW3/Cx) gb|AAC68072.1| hypothetical protein [Chlamydia trachomatis] Length = 264

- 1860.2 Best-BlastP=> >nrprot 47% Identities = 104/344 (30%), Positives = 174/344 (50%), Gaps = 38/344 (11%) gb|AAAF86695.1|AF180956\_1 AMPC cephalosporinase precursor protein ACC-3a [Hafnia alvei] Length = 377
- 1861.2 Best-BlastP=> >nrprot No Hits found
- 1862.2
- Best-BlastP=> >nrprot 63% Identities = 206/470 (43%), Positives = 279/470 (59%), Gaps = 41/470 (8%) ref|NP\_249771.1| flagellar hook protein FigE [Pseudomonas aeruginosa PAO1] pir|F83510 flagellar hook protein FigE PA1080 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04469.1|AE004539\_11 flagellar hook protein FigE [Pseudomonas aeruginosa PAO1] Length = 462
- 1863.2 Best-BlastP=> >nrprot 64% Identities = 97/223 (43%), Positives = 145/223 (65%), Gaps = 2/223 (0%) ref|ZP\_00138665.1| COG1843: Flagellar hook capping protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 237
- 1864.3 Best-BlastP=> >nrprot 73% Identities = 273/454 (60%), Positives = 346/454 (76%), Gaps = 5/454 (1%) ref|NP\_638130.1| succinyl-diaminopimelate desuccinylase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42054.1| succinyl-diaminopimelate desuccinylase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 497
- 1865.3 Best-BlastP=> >nrprot 72% Identities = 175/353 (49%), Positives = 263/353 (74%), Gaps = 1/353 (0%) ref|NP\_562979.1| UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl N-acetylglucosamine transferase [Clostridium perfringens] sp|Q8XIQ1|MURG\_CLOPE UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Undecaprenyl-PP-MurNAC-pentapeptide-UDP-GlcNAc transferase) dbj|BAB81769.1| UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl N-acetylglucosamine transferase [Clostridium perfringens str. 13] Length = 357
- 187.1 Best-BlastP=> >nrprot No Hits found
- 1870.3
- Best-BlastP=> >nrprot 60% Identities = 152/349 (43%), Positives = 223/349 (63%), Gaps = 19/349 (5%) ref|NP\_767636.1| HlyD family secretion protein [Bradyrhizobium japonicum] dbj|BAC46261.1| HlyD family secretion protein [Bradyrhizobium japonicum USDA 110] Length = 410
- 1871.2 Best-BlastP=> >nrprot 99% Identities = 348/348 (100%), Positives = 348/348 (100%) emb|CAC33484.1| RecA protein [Legionella pneumophila] Length = 348
- 1873.2 Best-BlastP=> >nrprot 99% Identities = 150/150 (100%), Positives = 150/150 (100%) sp|P37864|RECX\_LEGPN Regulatory protein recX emb|CAC33485.1| RecX protein [Legionella pneumophila] Length = 150
- 1875.2 Best-BlastP=> >nrprot 75% Identities = 234/379 (61%), Positives = 294/379 (77%) ref|NP\_842481.1| General substrate transporters [Nitrosomonas europaea ATCC 19718] emb|CAD86404.1| General substrate transporters [Nitrosomonas europaea ATCC 19718] Length = 391
- 1878.3
- Best-BlastP=> >nrprot 63% Identities = 130/311 (41%), Positives = 199/311 (63%), Gaps = 7/311 (2%) ref|NP\_520407.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD15993.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 317
- 188.1 Best-BlastP=> >nrprot No Hits found
- 1880.3 Best-BlastP=> >nrprot 79% Identities = 208/324 (64%), Positives = 262/324 (80%) ref|NP\_820236.1| malate dehydrogenase [Coxiella burnetii RSA 493] gb|AAO90750.1| malate dehydrogenase [Coxiella burnetii RSA 493] Length = 328

- 1882.2 Best-BlastP=> >nrprot 52% Identities = 116/255 (45%), Positives = 165/255 (64%), Gaps = 12/255 (4%) ref|NP\_819457.1| polysaccharide deacetylase-related protein [Coxiella burnetii RSA 493] gb|AAO89971.1| polysaccharide deacetylase-related protein [Coxiella burnetii RSA 493] Length = 276
- 1883.4 Best-BlastP=> >nrprot No Hits found
- 1885.3 Best-BlastP=> >nrprot 67% Identities = 221/446 (49%), Positives = 307/446 (68%), Gaps = 5/446 (1%) ref|NP\_252709.1| UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [Pseudomonas aeruginosa PAO1] pir|A83145 UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) PA4020 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07407.1|AE004818\_13 UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase [Pseudomonas aeruginosa PAO1] Length = 451
- 1886.2 Best-BlastP=> >nrprot No Hits found
- 1887.2 Best-BlastP=> >nrprot 37% Identities = 126/504 (25%), Positives = 205/504 (40%), Gaps = 128/504 (25%) ref|NP\_905954.1| leucine-rich protein [Porphyromonas gingivalis W83] gb|AAQ66853.1| leucine-rich protein [Porphyromonas gingivalis W83] Length = 1266
- 1889.2 Best-BlastP=> >nrprot 30% Identities = 64/297 (21%), Positives = 122/297 (41%), Gaps = 33/297 (11%) ref|NP\_764683.1| ebhA protein [Staphylococcus epidermidis ATCC 12228] gb|AAO04725.1|AE016747\_222 ebhA protein [Staphylococcus epidermidis ATCC 12228] Length = 9439
- 189.3 Best-BlastP=> >nrprot 81% Identities = 272/394 (69%), Positives = 330/394 (83%) dbj|BAB55449.1| NAD+-dependent formate dehydrogenase [Hyphomicrobium sp. JC17] Length = 399
- 1891.2 Best-BlastP=> >nrprot 47% Identities = 72/239 (30%), Positives = 123/239 (51%) ref|NP\_812276.1| hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO78470.1| hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 247
- 1893.2 Best-BlastP=> >nrprot 64% Identities = 98/218 (44%), Positives = 142/218 (65%), Gaps = 2/218 (0%) ref|NP\_820819.1| ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5 [Coxiella burnetii RSA 493] gb|AAO91333.1| ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5 [Coxiella burnetii RSA 493] Length = 244
- 1894.2 Best-BlastP=> >nrprot 73% Identities = 63/101 (62%), Positives = 76/101 (75%) ref|NP\_00086202.1| COG0261: Ribosomal protein L21 [Pseudomonas fluorescens PfO-1] Length = 103
- 1895.6 Best-BlastP=> >nrprot 47% Identities = 59/173 (34%), Positives = 100/173 (57%), Gaps = 14/173 (8%) ref|NP\_842310.1| putative type 4 fimbrial biogenesis protein PilP [Nitrosomonas europaea ATCC 19718] emb|CAD86225.1| putative type 4 fimbrial biogenesis protein PilP [Nitrosomonas europaea ATCC 19718] Length = 176
- 1896.5 Best-BlastP=> >nrprot 61% Identities = 282/695 (40%), Positives = 430/695 (61%), Gaps = 40/695 (5%) ref|NP\_715925.1| type IV pilus biogenesis protein PilQ [Shewanella oneidensis MR-1] gb|AAN53370.1|AE015476\_11 type IV pilus biogenesis protein PilQ [Shewanella oneidensis MR-1] Length = 684
- 19.1 Best-BlastP=> >nrprot 37% Identities = 48/174 (27%), Positives = 80/174 (45%), Gaps = 14/174 (8%) ref|NP\_820400.1| peptidase, family S24 [Coxiella burnetii RSA 493] gb|AAO90914.1| peptidase, family S24 [Coxiella burnetii RSA 493] Length = 216
- 190.3 Best-BlastP=> >nrprot No Hits found
- 1902.5 Best-BlastP=> >nrprot 79% Identities = 205/338 (60%), Positives = 264/338 (78%), Gaps = 5/338 (1%) ref|NP\_00086819.1| COG0533: Metal-dependent proteases with possible chaperone activity [Pseudomonas fluorescens PfO-1] Length = 341

- 1903.4 Best-BlastP=> >nrprot 58% Identities = 119/287 (41%), Positives = 161/287 (56%), Gaps = 14/287 (4%) ref|NP\_821016.1| chitinase domain protein [Coxiella burnetii RSA 493] gb|AAO91530.1| chitinase domain protein [Coxiella burnetii RSA 493] Length = 593
- 1905.2 Best-BlastP=> >nrprot 77% Identities = 248/422 (58%), Positives = 328/422 (77%), Gaps = 1/422 (0%) ref|NP\_718455.1| conserved hypothetical protein [Shewanella oneidensis MR-1] sp|P59352|YS83\_SHEON Hypothetical UPF0229 protein SO2883 gb|AAN55899.1|AE015726\_7 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 422
- 1906.2 Best-BlastP=> >nrprot 83% Identities = 347/504 (68%), Positives = 425/504 (84%), Gaps = 1/504 (0%) ref|NP\_790392.1| SpoVR like family protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54087.1| SpoVR like family protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 520
- 1908.4 Best-BlastP=> >nrprot 60% Identities = 348/811 (42%), Positives = 495/811 (61%), Gaps = 14/811 (1%) emb|CAD58321.1| Long chain acyl-CoA dehydrogenase [Azoarcus sp. EbN1] Length = 829
- 191.1 Best-BlastP=> >nrprot 50% Identities = 76/297 (25%), Positives = 144/297 (48%), Gaps = 33/297 (11%) ref|NP\_832129.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] gb|AAP09330.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] Length = 300
- 1910.6 Best-BlastP=> >nrprot 12% Identities = 92/441 (20%), Positives = 185/441 (41%), Gaps = 64/441 (14%) gb|AAB70839.1| ZipA [Dictyostelium discoideum] Length = 924
- 1911.4 Best-BlastP=> >nrprot 41% Identities = 37/110 (33%), Positives = 64/110 (58%), Gaps = 6/110 (5%) ref|ZP\_00054083.1| COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Magnetospirillum magnetotacticum] Length = 282
- 1913.2 Best-BlastP=> >nrprot 61% Identities = 41/91 (45%), Positives = 61/91 (67%) ref|NP\_819252.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89766.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 130
- 1915.3 Best-BlastP=> >nrprot 56% Identities = 237/625 (37%), Positives = 364/625 (58%), Gaps = 18/625 (2%) ref|NP\_518200.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD13607.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 795
- 1918.3 Best-BlastP=> >nrprot 74% Identities = 142/226 (62%), Positives = 176/226 (77%), Gaps = 1/226 (0%) ref|NP\_384333.1| PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Sinorhizobium meliloti] emb|CAC41614.1| PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Sinorhizobium meliloti] Length = 230
- 1920.3 Best-BlastP=> >nrprot 66% Identities = 198/345 (57%), Positives = 239/345 (69%), Gaps = 9/345 (2%) emb|CAB82454.1| CnrT protein [Ralstonia metallidurans] Length = 351
- 1923.2 Best-BlastP=> >nrprot No Hits found
- 1924.4 Best-BlastP=> >nrprot 62% Identities = 75/165 (45%), Positives = 106/165 (64%), Gaps = 6/165 (3%) ref|NP\_840350.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] emb|CAD84171.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] Length = 171
- 1926.2 Best-BlastP=> >nrprot 71% Identities = 121/188 (64%), Positives = 150/188 (79%), Gaps = 1/188 (0%) ref|NP\_405720.1| thymidine kinase [Yersinia pestis] ref|NP\_669456.1| thymidine kinase [Yersinia pestis KIM] sp|Q8ZEJ1|KITH\_YERPE Thymidine kinase pir|AD0265 thymidine kinase [EC 2.7.1.21] [similarity] - Yersinia pestis (strain CO92) emb|CAC90984.1| thymidine kinase [Yersinia pestis CO92] gb|AAM85707.1|AE013818\_1 thymidine kinase [Yersinia pestis KIM] Length = 196

- 1928.2 Best-BlastP=> >nrprot 60% Identities = 181/408 (44%), Positives = 254/408 (62%), Gaps = 8/408 (1%) ref|NP\_821038.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO91552.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 446
- 193.3 Best-BlastP=> >nrprot 56% Identities = 132/320 (41%), Positives = 199/320 (62%), Gaps = 17/320 (5%) gb|AAC21671.1| PvcA [Pseudomonas aeruginosa] Length = 327
- 1930.3 Best-BlastP=> >nrprot No Hits found
- 1933.4 Best-BlastP=> >nrprot 14% Identities = 109/524 (20%), Positives = 228/524 (43%), Gaps = 74/524 (14%) ref|NP\_010225.1| involved intracellular protein transport, coiled-coil protein necessary for protein transport from ER to Golgi; Uso1p [Saccharomyces cerevisiae] pir|S67593 transport protein USO1 - yeast (Saccharomyces cerevisiae) emb|CAA98621.1| USO1 [Saccharomyces cerevisiae] Length = 1790
- 1934.4 Best-BlastP=> >nrprot 97% Identities = 310/333 (93%), Positives = 324/333 (97%) emb|CAB65198.1| hypothetical protein [Legionella pneumophila] Length = 333
- 1935.4 Best-BlastP=> >nrprot 96% Identities = 348/372 (93%), Positives = 360/372 (96%), Gaps = 3/372 (0%) emb|CAB65199.1| hypothetical protein [Legionella pneumophila] Length = 369
- 1937.4 Best-BlastP=> >nrprot No Hits found
- 1939.5 Best-BlastP=> >nrprot No Hits found
- 1940.2 Best-BlastP=> >nrprot 53% Identities = 153/524 (29%), Positives = 286/524 (54%), Gaps = 30/524 (5%) ref|NP\_922967.1| HlyB/MsbA family ABC transporter [Gloeobacter violaceus] dbj|BAC87962.1| HlyB/MsbA family ABC transporter [Gloeobacter violaceus] Length = 605
- 1943.3 Best-BlastP=> >nrprot 55% Identities = 136/303 (44%), Positives = 183/303 (60%), Gaps = 3/303 (0%) ref|ZP\_00095364.1| COG0845: Membrane-fusion protein [Novosphingobium aromaticivorans] Length = 371
- 1945.4 Best-BlastP=> >nrprot 80% Identities = 408/591 (69%), Positives = 473/591 (80%), Gaps = 5/591 (0%) ref|NP\_706511.1| succinate dehydrogenase flavoprotein subunit [Shigella flexneri 2a str. 301] gb|AAN42218.1| AE015088\_5 succinate dehydrogenase flavoprotein subunit [Shigella flexneri 2a str. 301] Length = 592
- 1946.2 Best-BlastP=> >nrprot 78% Identities = 156/227 (68%), Positives = 188/227 (82%), Gaps = 1/227 (0%) emb|CAA74088.1| succinate dehydrogenase putative iron sulphur subunit [Shewanella frigidimarina] Length = 235
- 1947.3 Best-BlastP=> >nrprot 45% Identities = 76/274 (27%), Positives = 133/274 (48%), Gaps = 12/274 (4%) ref|ZP\_00069289.1| COG1577: Mevalonate kinase [Oenococcus oeni MCW] Length = 306
- 1949.4 Best-BlastP=> >nrprot 67% Identities = 38/83 (45%), Positives = 61/83 (73%) ref|NP\_252324.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] pir|G83191 conserved hypothetical protein PA3634 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07022.1| AE004783\_7 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 94
- 195.3 Best-BlastP=> >nrprot 79% Identities = 181/278 (65%), Positives = 223/278 (80%) ref|NP\_231578.1| PvcB protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82137 PvcB protein VC1944 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95092.1| PvcB protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 287



- 1950.2 Best-BlastP=> >nrprot 55% Identities = 159/405 (39%), Positives = 239/405 (59%), Gaps = 13/405 (3%) ref|NP\_820347.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90861.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 426
- 1951.4 Best-BlastP=> >nrprot 81% Identities = 170/245 (69%), Positives = 205/245 (83%) ref|NP\_924317.1| probable ABC transporter ATP-binding protein [Gloeobacter violaceus] dbj|BAC89312.1| glr1371 [Gloeobacter violaceus] Length = 252
- 1955.3 Best-BlastP=> >nrprot 46% Identities = 141/475 (29%), Positives = 221/475 (46%), Gaps = 64/475 (13%) ref|ZP\_00015335.1| COG2067: Long-chain fatty acid transport protein [Rhodospirillum rubrum] Length = 436
- 1960.2 Best-BlastP=> >nrprot No Hits found
- 1961.3 Best-BlastP=> >nrprot 96% Identities = 283/293 (96%), Positives = 284/293 (96%) gb|AAM00623.1| unknown [Legionella pneumophila] Length = 293
- 1966.2 Best-BlastP=> >nrprot 84% Identities = 131/188 (69%), Positives = 160/188 (85%) ref|NP\_820795.1| translation elongation factor P [Coxiella burnetii RSA 493] gb|AAO91309.1| translation elongation factor P [Coxiella burnetii RSA 493] Length = 188
- 1968.1 Best-BlastP=> >nrprot 41% Identities = 25/64 (39%), Positives = 32/64 (50%), Gaps = 13/64 (20%) ref|ZP\_00011706.1| hypothetical protein [Rhodopseudomonas palustris] Length = 150
- 197.3 Best-BlastP=> >nrprot 80% Identities = 324/474 (68%), Positives = 389/474 (82%) ref|NP\_231579.1| FAD monooxygenase, PheA/TfdB family [Vibrio cholerae O1 biovar eltor str. N16961] pir|C82137 FAD monooxygenase, PheA/TfdB family VC1945 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95093.1| FAD monooxygenase, PheA/TfdB family [Vibrio cholerae O1 biovar N16961] Length = 487
- 1972.3 Best-BlastP=> >nrprot 62% Identities = 158/342 (46%), Positives = 216/342 (63%), Gaps = 3/342 (0%) gb|AAP58486.1| putative phosphoribosylformylglycinamide cyclo ligase [uncultured Acidobacteria bacterium] Length = 343
- 1976.2 Best-BlastP=> >nrprot 79% Identities = 427/626 (68%), Positives = 497/626 (79%), Gaps = 6/626 (0%) ref|NP\_720274.1| glucose-inhibited division protein A [Shewanella oneidensis MR-1] gb|AAN57717.1| AE015908\_2 glucose-inhibited division protein A [Shewanella oneidensis MR-1] Length = 629
- 1978.1 Best-BlastP=> >nrprot 63% Identities = 94/201 (46%), Positives = 133/201 (66%), Gaps = 6/201 (2%) ref|NP\_246425.1| GidB [Pasteurella multocida] sp|P57946|GIDB\_PASMU Methyltransferase gidB (Glucose inhibited division protein B) gb|AAK03570.1| GidB [Pasteurella multocida] Length = 210
- 1979.1 Best-BlastP=> >nrprot 79% Identities = 163/254 (64%), Positives = 204/254 (80%) ref|NP\_820903.1| sporulation initiation inhibitor protein soj [Coxiella burnetii RSA 493] gb|AAO91417.1| sporulation initiation inhibitor protein soj [Coxiella burnetii RSA 493] Length = 256
- 1983.1 Best-BlastP=> >nrprot 63% Identities = 138/265 (52%), Positives = 175/265 (66%), Gaps = 1/265 (0%) ref|NP\_820962.1| bis(5'-nucleosyl)-tetraphosphatase, symmetrical [Coxiella burnetii RSA 493] sp|Q83AB7|APAH\_COXBU Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5''-P1,P4-tetraphosphate pyrophosphohydrolase) gb|AAO91476.1| bis(5'-nucleosyl)-tetraphosphatase, symmetrical [Coxiella burnetii RSA 493] Length = 291
- 1986.2 Best-BlastP=> >nrprot 24% Identities = 56/235 (23%), Positives = 111/235 (47%), Gaps = 11/235 (4%) gb|AAP84130.1| putative pathogenesis-related protein [Pseudomonas aeruginosa] Length = 639

- 1989.2 Best-BlastP=> >nrprot 70% Identities = 263/481 (54%), Positives = 348/481 (72%), Gaps = 1/481 (0%) sp|P37986|G6PD\_ERWCH Glucose-6-phosphate 1-dehydrogenase (G6PD) pir|S37053 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Erwinia chrysanthemi emb|CAA52858.1| glucose-6-phosphate 1-dehydrogenase [Erwinia chrysanthemi] Length = 491
- 199.1 Best-BlastP=> >nrprot 45% Identities = 105/371 (28%), Positives = 173/371 (46%), Gaps = 13/371 (3%) ref|ZP\_00014611.1| COG2814: Arabinose efflux permease [Rhodospirillum rubrum] Length = 411
- 1990.1 Best-BlastP=> >nrprot 55% Identities = 102/228 (44%), Positives = 136/228 (59%), Gaps = 2/228 (0%) gb|AAL76390.1| 6-phosphogluconolactonase [uncultured proteobacterium] Length = 226
- 1992.2 Best-BlastP=> >nrprot No Hits found
- 1998.3 Best-BlastP=> >nrprot 51% Identities = 119/265 (44%), Positives = 170/265 (64%), Gaps = 9/265 (3%) ref|ZP\_00089281.1| COG1295: Predicted membrane protein [Azotobacter vinelandii] Length = 408
- 2.1 Best-BlastP=> >nrprot 59% Identities = 70/170 (41%), Positives = 102/170 (60%), Gaps = 2/170 (1%) ref|NP\_907750.1| HYPOTHETICAL PROTEIN-RecB family exonuclease [Wolinella succinogenes] emb|CAE10650.1| HYPOTHETICAL PROTEIN-RecB family exonuclease [Wolinella succinogenes] Length = 193
- 20.1 Best-BlastP=> >nrprot No Hits found
- 2000.1 Best-BlastP=> >nrprot 99% Identities = 149/149 (100%), Positives = 149/149 (100%) gb|AAC38305.1| type IV pilin; competence and adherence associated pilin; CAP [Legionella pneumophila] Length = 149
- 2006.2 Best-BlastP=> >nrprot 46% Identities = 64/229 (27%), Positives = 102/229 (44%), Gaps = 27/229 (11%) ref|NP\_762597.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO07587.1| AE016810\_90 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 232
- 2007.1 Best-BlastP=> >nrprot 72% Identities = 173/298 (58%), Positives = 220/298 (73%) ref|NP\_792548.1| hydroxymethylglutaryl-CoA lyase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO56243.1| hydroxymethylglutaryl-CoA lyase [Pseudomonas syringae pv. tomato str. DC3000] Length = 299
- 201.2 Best-BlastP=> >nrprot 50% Identities = 139/407 (34%), Positives = 209/407 (51%), Gaps = 9/407 (2%) dbj|BAB69410.1| hypothetical protein [Streptomyces avermitilis] Length = 468
- 2016.2 Best-BlastP=> >nrprot 64% Identities = 54/141 (38%), Positives = 90/141 (63%), Gaps = 4/141 (2%) ref|NP\_820504.1| rhodanese domain protein [Coxiella burnetii RSA 493] gb|AAO91018.1| rhodanese domain protein [Coxiella burnetii RSA 493] Length = 144
- 2017.1 Best-BlastP=> >nrprot 52% Identities = 70/179 (39%), Positives = 99/179 (55%), Gaps = 7/179 (3%) ref|ZP\_00124407.1| COG2840: Uncharacterized protein conserved in bacteria [Pseudomonas syringae pv. syringae B728a] Length = 185
- 2019.2 Best-BlastP=> >nrprot 61% Identities = 112/266 (42%), Positives = 153/266 (57%), Gaps = 28/266 (10%) ref|NP\_253119.1| probable cytochrome c1 precursor [Pseudomonas aeruginosa PAO1] pir|E83092 probable cytochrome c1 precursor PA4429 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07817.1| AE004857\_8 probable cytochrome c1 precursor [Pseudomonas aeruginosa PAO1] Length = 260
- 202.3 Best-BlastP=> >nrprot 57% Identities = 299/765 (39%), Positives = 444/765 (58%), Gaps = 17/765 (2%) ref|NP\_519533.1| PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] emb|CAD15114.1| PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] Length = 765

- 2020.1 Best-BlastP=> >nrprot 78% Identities = 128/206 (62%), Positives = 163/206 (79%), Gaps = 2/206 (0%) ref|NP\_716244.1| stringent starvation protein a [Shewanella oneidensis MR-1] Length = 209
- 2021.1 Best-BlastP=> >nrprot 67% Identities = 68/134 (50%), Positives = 89/134 (66%), Gaps = 5/134 (3%) ref|NP\_820726.1| stringent starvation protein B [Coxiella burnetii RSA 493] Length = 138
- 2022.1 Best-BlastP=> >nrprot No Hits found
- 2024.2 Best-BlastP=> >nrprot 58% Identities = 66/177 (37%), Positives = 105/177 (59%) ref|ZP\_00065967.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 183
- 2026.1 Best-BlastP=> >nrprot No Hits found
- 2027.2 Best-BlastP=> >nrprot 50% Identities = 140/413 (33%), Positives = 215/413 (52%), Gaps = 13/413 (3%) ref|NP\_215111.1| hypothetical protein Rv0597c [Mycobacterium tuberculosis H37Rv] ref|NP\_335037.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] ref|NP\_854272.1| CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pir||H70908 hypothetical protein Rv0597c - Mycobacterium tuberculosis (strain H37RV) emb|CAB09957.1| hypothetical protein Rv0597c [Mycobacterium tuberculosis H37RV] gb|AAK44851.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] emb|CAD93475.1| CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 411
- 2029.2 Best-BlastP=> >nrprot No Hits found
- 2030.2 Best-BlastP=> >nrprot No Hits found
- 2031.2 Best-BlastP=> >nrprot 31% Identities = 24/63 (38%), Positives = 36/63 (57%) ref|NP\_051664.1| transposase, putative [Deinococcus radiodurans] pir||A75633 probable transposase - Deinococcus radiodurans (strain R1) gb|AAF12606.1|AE001826\_75 transposase, putative [Deinococcus radiodurans] Length = 327
- 2034.2 Best-BlastP=> >nrprot 40% Identities = 65/223 (29%), Positives = 110/223 (49%), Gaps = 13/223 (5%) ref|ZP\_00009418.1| COG1647: Esterase/lipase [Rhodopseudomonas palustris] Length = 263
- 2037.3 Best-BlastP=> >nrprot 97% Identities = 453/469 (96%), Positives = 459/469 (97%) gb|AAM00645.1| Zn metalloprotein [Legionella pneumophila] Length = 469
- 2039.1 Best-BlastP=> >nrprot No Hits found
- 204.1 Best-BlastP=> >nrprot 63% Identities = 199/448 (44%), Positives = 288/448 (64%), Gaps = 1/448 (0%) ref|NP\_459228.1| putative membrane-associated Zn-dependent protease [Salmonella typhimurium LT2] sp|Q8ZRP1|ECFE\_SALTY Protease ecfe gb|AAL19187.1| putative membrane-associated Zn-dependent protease [Salmonella typhimurium LT2] Length = 450
- 2041.2 Best-BlastP=> >nrprot 36% Identities = 74/238 (31%), Positives = 119/238 (50%), Gaps = 4/238 (1%) gb|AAK19894.1| O-methyltransferase [Polyangium cellulorum] Length = 346
- 2044.2 Best-BlastP=> >nrprot 59% Identities = 274/627 (43%), Positives = 384/627 (61%), Gaps = 9/627 (1%) sp|Q59118|AMOH\_ARTGO Histamine oxidase (Copper amine oxidase) pir||A56102 amine oxidase (copper-containing) (EC 1.4.3.6) - Arthrobacter globiformis dbj|BAA07517.1| Copper amine oxidase, Monoamine oxidase, Histamine oxidase [Arthrobacter globiformis] Length = 684

- 2049.2 Best-BlastP=> >nrprot 26% Identities = 57/288 (19%), Positives = 112/288 (38%), Gaps = 32/288 (11%) pir||T13030 microtubule binding protein D-CLIP-190 - fruit fly (*Drosophila melanogaster*) gb|AAB96783.1| microtubule binding protein D-CLIP-190 [*Drosophila melanogaster*] Length = 1690
- 205.1 Best-BlastP=> >nrprot 59% Identities = 103/267 (38%), Positives = 158/267 (59%), Gaps = 15/267 (5%) ref|NP\_820370.1| phosphatidate cytidyltransferase [*Coxiella burnetii* RSA 493] gb|AAO90884.1| phosphatidate cytidyltransferase [*Coxiella burnetii* RSA 493] Length = 272
- 2051.2 Best-BlastP=> >nrprot 37% Identities = 34/108 (31%), Positives = 63/108 (58%), Gaps = 2/108 (1%) ref|NP\_932218.1| putative conjugative transfer protein TrbB [*Vibrio vulnificus* YJ016] dbj|BAC97741.1| putative conjugative transfer protein TrbB [*Vibrio vulnificus* YJ016] Length = 137
- 2053.2 Best-BlastP=> >nrprot 55% Identities = 146/331 (44%), Positives = 180/331 (54%), Gaps = 57/331 (17%) gb|AAC83331.1| major outer membrane protein precursor [*Legionella pneumophila*] Length = 288
- 2054.2 Best-BlastP=> >nrprot 54% Identities = 128/296 (43%), Positives = 184/296 (62%), Gaps = 17/296 (5%) ref|NP\_442548.1| unknown protein [*Synechocystis* sp. PCC 6803] pir||S76674 hypothetical protein - *Synechocystis* sp. (strain PCC 6803) dbj|BAA10618.1| slr0619 [*Synechocystis* sp. PCC 6803] Length = 348
- 2056.1 Best-BlastP=> >nrprot 55% Identities = 109/292 (37%), Positives = 165/292 (56%), Gaps = 8/292 (2%) ref|ZP\_00134420.1| COG0500: SAM-dependent methyltransferases [*Actinobacillus pleuropneumoniae* serovar 1 str. 4074] Length = 290
- 2057.3 Best-BlastP=> >nrprot 59% Identities = 145/350 (41%), Positives = 208/350 (59%), Gaps = 17/350 (4%) ref|ZP\_00097544.1| COG0722: 3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase [*Desulfitobacterium hafniense*] Length = 342
- 206.3 Best-BlastP=> >nrprot 66% Identities = 120/227 (52%), Positives = 150/227 (66%) ref|NP\_252342.1| undecaprenyl pyrophosphate synthetase [*Pseudomonas aeruginosa* PA01] pir||G83188 undecaprenyl pyrophosphate synthetase PA3652 [imported] - *Pseudomonas aeruginosa* (strain PA01) gb|AAG07040.1|AE004785\_4 undecaprenyl pyrophosphate synthetase [*Pseudomonas aeruginosa* PA01] Length = 251
- 2060.3 Best-BlastP=> >nrprot 32% Identities = 71/221 (32%), Positives = 123/221 (55%), Gaps = 24/221 (10%) ref|ZP\_00082359.1| COG2199: FOG: GGDEF domain [*Geobacter metallireducens*] Length = 353
- 2062.2 Best-BlastP=> >nrprot No Hits found
- 2064.3 Best-BlastP=> >nrprot No Hits found
- 2065.2 Best-BlastP=> >nrprot No Hits found
- 2066.5 Best-BlastP=> >nrprot No Hits found
- 2067.5 Best-BlastP=> >nrprot 61% Identities = 151/349 (43%), Positives = 215/349 (61%), Gaps = 19/349 (5%) ref|NP\_660996.1| glycosyl hydrolase, family 3 [*Chlorobium tepidum* TLS] gb|AAM71338.1| glycosyl hydrolase, family 3 [*Chlorobium tepidum* TLS] Length = 372
- 2068.3 Best-BlastP=> >nrprot 27% Identities = 71/336 (21%), Positives = 133/336 (39%), Gaps = 67/336 (19%) emb|CAE02882.1| OSJNBb0022F23.19 [*Oryza sativa* (japonica cultivar-group)] Length = 2391
- 207.3 Best-BlastP=> >nrprot 98% Identities = 418/423 (98%), Positives = 419/423 (99%) gb|AAM73854.1|AF454865\_1 putative phospholipase C [*Legionella pneumophila*] Length = 423

- 2070.4 Best-BlastP=> >nprot 49% Identities = 166/568 (29%), Positives = 274/568 (48%), Gaps = 46/568 (8%) ref|NP\_251765.1| hypothetical protein [Pseudomonas aeruginosa PA01] ref|ZP\_00136432.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] pir|D83262 hypothetical protein PA3075 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06463.1|AE004731\_11 hypothetical protein PA3075 [Pseudomonas aeruginosa PAO1] Length = 543
- 2073.4 Best-BlastP=> >nprot 37% Identities = 49/192 (25%), Positives = 85/192 (44%), Gaps = 23/192 (11%) ref|NP\_929249.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE14276.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 231
- 2075.1 Best-BlastP=> >nprot No Hits found
- 2078.2 Best-BlastP=> >nprot No Hits found
- 2079.2 Best-BlastP=> >nprot No Hits found
- 2080.3 Best-BlastP=> >nprot 57% Identities = 88/221 (39%), Positives = 128/221 (57%), Gaps = 1/221 (0%) ref|NP\_925444.1| hypothetical protein gl|2498 [Gloeobacter violaceus] dbj|BAC90439.1| gl|2498 [Gloeobacter violaceus] Length = 222
- 2082.2 Best-BlastP=> >nprot 75% Identities = 34/66 (51%), Positives = 51/66 (77%) ref|NP\_768003.1| bs|1363 [Bradyrhizobium japonicum] dbj|BAC46628.1| bs|1363 [Bradyrhizobium japonicum USDA 110] Length = 73
- 2083.2 Best-BlastP=> >nprot 98% Identities = 224/227 (98%), Positives = 226/227 (99%) gb|AAM00399.1|AF386079\_9 CcmH [Legionella pneumophila] Length = 360
- 2085.2 Best-BlastP=> >nprot 99% Identities = 132/133 (99%), Positives = 133/133 (100%) gb|AAM00399.1|AF386079\_9 CcmH [Legionella pneumophila] Length = 360
- 2087.2 Best-BlastP=> >nprot 36% Identities = 88/166 (53%), Positives = 116/166 (69%) ref|NP\_819420.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89934.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 176
- 209.2 Best-BlastP=> >nprot 24% Identities = 41/135 (30%), Positives = 61/135 (45%), Gaps = 36/135 (26%) gb|AAO49307.1| outer surface protein precursor [Wolbachia pipientis] Length = 186
- 2091.1 Best-BlastP=> >nprot 39% Identities = 60/226 (26%), Positives = 99/226 (43%), Gaps = 8/226 (3%) gb|AAK31375.1|AC084329\_1 ppg3 [Leishmania major] Length = 1325
- 2092.2 Best-BlastP=> >nprot 86% Identities = 634/850 (74%), Positives = 741/850 (87%) ref|NP\_457131.1| ClpB protein (heat shock protein f84.1) [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_461591.1| ATP-dependent protease, Hsp 100, part of novel multi-chaperone system with DnaK, DnaJ, and GrpE [Salmonella typhimurium LT2] ref|NP\_806327.1| ClpB protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|A10831 ClpB protein (heat shock protein f84.1) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL21550.1| ATP-dependent protease [Salmonella typhimurium LT2] emb|CAD05840.1| ClpB protein (heat shock protein f84.1) [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70187.1| ClpB protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 857
- 2095.2 Best-BlastP=> >nprot 72% Identities = 218/393 (55%), Positives = 285/393 (72%), Gaps = 1/393 (0%) ref|ZP\_00125180.1| COG2081: Predicted flavoproteins [Pseudomonas syringae pv. syringae B728a] Length = 392
- 2098.2 Best-BlastP=> >nprot No Hits found

- 2103.2 Best-BlastP=> >nrprot 69% Identities = 424/791 (53%), Positives = 552/791 (69%), Gaps = 3/791 (0%) ref|NP\_637344.1| 3-hydroxyacyl-CoA dehydrogenase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM41268.1| 3-hydroxyacyl-CoA dehydrogenase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 790
- 2104.1 Best-BlastP=> >nrprot 85% Identities = 91/127 (71%), Positives = 108/127 (85%), Gaps = 1/127 (0%) ref|NP\_878931.1| 50S ribosomal protein L7/L12 [Bordetella pertussis] ref|NP\_882379.1| 50S ribosomal protein L7/L12 [Bordetella pertussis] ref|NP\_885666.1| 50S ribosomal protein L7/L12 [Bordetella bronchiseptica] emb|CAE39754.1| 50S ribosomal protein L7/L12 [Bordetella pertussis] emb|CAE40393.1| 50S ribosomal protein L7/L12 [Bordetella pertussis] emb|CAE30515.1| 50S ribosomal protein L7/L12 [Bordetella bronchiseptica] Length = 127
- 2106.2 Best-BlastP=> >nrprot 73% Identities = 89/173 (51%), Positives = 131/173 (75%) ref|NP\_819272.1| ribosomal protein L10 [Coxiella burnetii RSA 493] gb|AAO89786.1| ribosomal protein L10 [Coxiella burnetii RSA 493] Length = 174
- 2108.2 Best-BlastP=> >nrprot 45% Identities = 81/300 (27%), Positives = 142/300 (47%), Gaps = 14/300 (4%) ref|NP\_561674.1| conserved hypothetical protein [Clostridium perfringens] dbj|BAB80464.1| conserved hypothetical protein [Clostridium perfringens str. 13] Length = 308
- 211.1 Best-BlastP=> >nrprot 58% Identities = 118/341 (34%), Positives = 204/341 (59%), Gaps = 13/341 (3%) ref|NP\_882114.1| putative membrane protein [Bordetella pertussis] ref|NP\_882789.1| putative membrane protein [Bordetella pertussis] ref|NP\_886988.1| putative membrane protein [Bordetella bronchiseptica] emb|CAE43862.1| putative membrane protein [Bordetella pertussis] emb|CAE36021.1| putative membrane protein [Bordetella pertussis] emb|CAE30937.1| putative membrane protein [Bordetella bronchiseptica] Length = 367
- 2112.2 Best-BlastP=> >nrprot 28% Identities = 83/302 (27%), Positives = 137/302 (45%), Gaps = 15/302 (4%) ref|NP\_772278.1| blf5638 [Bradyrhizobium japonicum] dbj|BAC50903.1| blf5638 [Bradyrhizobium japonicum USDA 110] Length = 500
- 2116.2 Best-BlastP=> >nrprot 26% Identities = 23/73 (31%), Positives = 42/73 (57%), Gaps = 1/73 (1%) ref|NP\_391095.1| transcriptional regulator [Bacillus subtilis] sp|P21340|PAIA\_BACSU Protease synthase and sporulation negative regulatory protein PAI 1 emb|CAB15205.1| transcriptional regulator [Bacillus subtilis subsp. subtilis str. 168] Length = 172
- 2119.2 Best-BlastP=> >nrprot 47% Identities = 175/527 (33%), Positives = 263/527 (49%), Gaps = 77/527 (14%) dbj|BAB86344.1| metalloprotease [Vibrio fluvialis] Length = 610
- 212.1 Best-BlastP=> >nrprot 68% Identities = 83/152 (54%), Positives = 110/152 (72%), Gaps = 2/152 (1%) ref|NP\_742683.1| phosphatidylglycerophosphatase A [Pseudomonas putida KT2440] gb|AAN66147.1|AE016242\_15 phosphatidylglycerophosphatase A [Pseudomonas putida KT2440] Length = 167
- 2120.2 Best-BlastP=> >nrprot No Hits found
- 2121.2 Best-BlastP=> >nrprot 60% Identities = 108/221 (48%), Positives = 148/221 (66%), Gaps = 1/221 (0%) ref|NP\_251544.1| conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir|B83288 conserved hypothetical protein PA2854 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06242.1|AE004712\_2 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 323
- 2122.2 Best-BlastP=> >nrprot 43% Identities = 100/377 (26%), Positives = 171/377 (45%), Gaps = 29/377 (7%) ref|NP\_820237.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90751.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 408

- 2127.2 Best-BlastP=> >nrprot 62% Identities = 56/112 (50%), Positives = 74/112 (66%), Gaps = 3/112 (2%) ref|NP\_840790.1| Uncharacterised protein family UPF0102 [Nitrosomonas europaea ATCC 19718] emb|CAD84622.1| Uncharacterised protein family UPF0102 [Nitrosomonas europaea ATCC 19718] Length = 118
- 2129.1 Best-BlastP=> >nrprot 70% Identities = 98/192 (51%), Positives = 141/192 (73%) ref|NP\_743483.1| phosphoheptose isomerase [Pseudomonas putida KT2440] gb|AAN66947.1|AE016322\_14 phosphoheptose isomerase [Pseudomonas putida KT2440] Length = 195
- 213.1 Best-BlastP=> >nrprot 56% Identities = 141/268 (52%), Positives = 180/268 (67%), Gaps = 4/268 (1%) ref|NP\_406655.1| thiamine-monophosphate kinase [Yersinia pestis] ref|NP\_668333.1| thiamin-monophosphate kinase [Yersinia pestis KIM] pir|AD0386 thiamine-phosphate kinase (EC 2.7.4.16) [imported] - Yersinia pestis (strain CO92) emb|CAC92415.1| thiamine-monophosphate kinase [Yersinia pestis CO92] gb|AAM84584.1|AE013704\_1 thiamin-monophosphate kinase [Yersinia pestis KIM] Length = 329
- 2130.1 Best-BlastP=> >nrprot 62% Identities = 88/188 (46%), Positives = 120/188 (63%), Gaps = 7/188 (3%) ref|NP\_820724.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91238.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 191
- 2132.2 Best-BlastP=> >nrprot 47% Identities = 53/181 (29%), Positives = 96/181 (53%), Gaps = 7/181 (3%) ref|NP\_715937.1| lipoprotein, putative [Shewanella oneidensis MR-1] gb|AAN53382.1|AE015477\_12 lipoprotein, putative [Shewanella oneidensis MR-1] Length = 188
- 2133.1 Best-BlastP=> >nrprot No Hits found
- 2135.1 Best-BlastP=> >nrprot 53% Identities = 55/118 (46%), Positives = 70/118 (59%), Gaps = 1/118 (0%) ref|NP\_254248.1| ATP synthase protein I [Pseudomonas aeruginosa PA01] pir|B82953 ATP synthase protein I PA5561 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08946.1|AE004967\_17 ATP synthase protein I [Pseudomonas aeruginosa PAO1] Length = 126
- 2136.1 Best-BlastP=> >nrprot 75% Identities = 176/277 (63%), Positives = 210/277 (75%), Gaps = 19/277 (6%) ref|NP\_720269.1| ATP synthase F0, A subunit [Shewanella oneidensis MR-1] gb|AAN57712.1|AE015907\_10 ATP synthase F0, A subunit [Shewanella oneidensis MR-1] Length = 264
- 2137.1 Best-BlastP=> >nrprot 81% Identities = 72/80 (90%), Positives = 75/80 (93%) ref|ZP\_00124678.1| COG0636: F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K [Pseudomonas syringae pv. syringae B728a] ref|NP\_795322.1| ATP synthase F0, C subunit [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO59017.1| ATP synthase F0, C subunit [Pseudomonas syringae pv. tomato str. DC3000] Length = 85
- 2138.2 Best-BlastP=> >nrprot 72% Identities = 85/156 (54%), Positives = 114/156 (73%) ref|NP\_820917.1| ATP synthase F0, B subunit [Coxiella burnetii RSA 493] gb|AAO91431.1| ATP synthase F0, B subunit [Coxiella burnetii RSA 493] Length = 156
- 214.1 Best-BlastP=> >nrprot 66% Identities = 61/140 (43%), Positives = 99/140 (70%) ref|NP\_252741.1| NusB protein [Pseudomonas aeruginosa PA01] sp|Q9HWW6|NUSB\_PSEAE N utilization substance protein B homolog (NusB protein) pir|G83140 NusB protein PA4052 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07439.1|AE004821\_12 NusB protein [Pseudomonas aeruginosa PAO1] Length = 159
- 2140.2 Best-BlastP=> >nrprot 64% Identities = 86/178 (48%), Positives = 116/178 (65%), Gaps = 2/178 (1%) ref|NP\_254244.1| ATP synthase delta chain [Pseudomonas aeruginosa PA01] pir|F82952 ATP synthase delta chain PA5557 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08942.1|AE004967\_13 ATP synthase delta chain [Pseudomonas aeruginosa PAO1] Length = 178



- 2141.2 Best-BlastP=> >nrprot No Hits found
- 2143.5 Best-BlastP=> >nrprot 21% Identities = 66/242 (27%), Positives = 110/242 (45%), Gaps = 32/242 (13%) ref|NP\_819452.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89966.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 262
- 2144.3 Best-BlastP=> >nrprot 59% Identities = 133/308 (43%), Positives = 196/308 (63%), Gaps = 1/308 (0%) ref|NP\_716251.1| arginine N-succinyltransferase [Shewanella oneidensis MR-1] gb|AAN53696.1| arginine N-succinyltransferase [Shewanella oneidensis MR-1] Length = 339
- 2146.2 Best-BlastP=> >nrprot 60% Identities = 151/363 (41%), Positives = 224/363 (61%), Gaps = 5/363 (1%) ref|NP\_251855.1| histidinol-phosphate aminotransferase [Pseudomonas aeruginosa PAO1] sp|Q9HZ68|H182\_PSEAE Histidinol-phosphate aminotransferase 2 [imidazole acetol-phosphate transaminase 2] pir|F83250 histidinol-phosphate aminotransferase PA3165 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06553.1|AE004740\_6 histidinol-phosphate aminotransferase [Pseudomonas aeruginosa PAO1] Length = 369
- 2147.1 Best-BlastP=> >nrprot 70% Identities = 58/107 (54%), Positives = 80/107 (74%), Gaps = 2/107 (1%) ref|NP\_840178.1| Pterin 4 alpha carbinolamine dehydratase [Nitrosomonas europaea ATCC 19718] emb|CAD83988.1| Pterin 4 alpha carbinolamine dehydratase [Nitrosomonas europaea ATCC 19718] Length = 113
- 2148.1 Best-BlastP=> >nrprot 75% Identities = 172/305 (56%), Positives = 230/305 (75%), Gaps = 1/305 (0%) ref|NP\_820140.1| protein-export membrane protein SecF [Coxiella burnetii RSA 493] gb|AAO90654.1| protein-export membrane protein SecF [Coxiella burnetii RSA 493] Length = 304
- 2149.4 Best-BlastP=> >nrprot 99% Identities = 427/431 (99%), Positives = 430/431 (99%) sp|Q8RNM2|PURA\_LEGPN Adenylosuccinate synthetase (IMP--aspartate ligase) (AdSS) (AMPSase) gb|AAM00648.1| adenylosuccinate synthetase [Legionella pneumophila] Length = 431
- 215.1 Best-BlastP=> >nrprot 79% Identities = 97/150 (64%), Positives = 124/150 (82%) ref|ZP\_00126026.1| COG1327: Predicted transcriptional regulator, consists of a Zn-ribbon and ATP-cone domains [Pseudomonas syringae pv. syringae B728a] Length = 165
- 2150.1 Best-BlastP=> >nrprot 39% Identities = 37/148 (25%), Positives = 64/148 (43%), Gaps = 19/148 (12%) ref|NP\_799791.1| hypothetical protein VPA0281 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61624.1| hypothetical protein [Vibrio parahaemolyticus] Length = 133
- 2151.2 Best-BlastP=> >nrprot 14% Identities = 39/144 (27%), Positives = 67/144 (46%), Gaps = 24/144 (16%) sp|Q9U7E0|ATRX\_CAEEL Transcriptional regulator ATRX homolog (X-linked nuclear protein-1) gb|AAD55361.1|AF134186\_1 XNP-1 [Caenorhabditis elegans] Length = 1359
- 2152.2 Best-BlastP=> >nrprot 83% Identities = 127/176 (72%), Positives = 150/176 (85%) ref|NP\_820460.1| antioxidant, AhpC/TSA family [Coxiella burnetii RSA 493] gb|AAO90974.1| antioxidant, AhpC/TSA family [Coxiella burnetii RSA 493] Length = 179
- 2153.3 Best-BlastP=> >nrprot No Hits found
- 2156.3 Best-BlastP=> >nrprot 45% Identities = 126/444 (28%), Positives = 197/444 (44%), Gaps = 30/444 (6%) ref|NP\_436941.1| putative oxidoreductase protein [Sinorhizobium meliloti] pir|A95892 probable oxidoreductase protein Smb20415 [imported] - Sinorhizobium (strain 1021) magaplasmid pSymB emb|CAC48801.1| putative oxidoreductase protein [Sinorhizobium meliloti] Length = 429

2159.2

Best-BlastP=> >nrprot 76% Identities = 163/238 (68%), Positives = 191/238 (80%) ref|NP\_249464.1| pyridoxal phosphate biosynthetic protein PdxJ [Pseudomonas aeruginosa PA01] sp|Q915G5|PDXJ\_PSEAE Pyridoxal phosphate biosynthetic protein pdxJ (PNP synthase) pir|H83548 pyridoxal phosphate biosynthetic protein PdxJ PA0773 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04162.1|AE004512\_5 pyridoxal phosphate biosynthetic protein PdxJ [Pseudomonas aeruginosa PAO1] Length = 248

216.2 Best-BlastP=> >nrprot 83% Identities = 296/416 (71%), Positives = 351/416 (84%), Gaps = 1/416 (0%) ref|ZP\_00138159.1| COG0112: Glycine/serine hydroxymethyltransferase [Pseudomonas aeruginosa UCBPP-PA14] Length = 421

2160.2 Best-BlastP=> >nrprot 70% Identities = 166/329 (50%), Positives = 227/329 (68%), Gaps = 15/329 (4%) ref|NP\_867540.1| 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Pirellula sp.] emb|CAD75087.1| 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Pirellula sp.] Length = 353

2162.2 Best-BlastP=> >nrprot 52% Identities = 153/496 (30%), Positives = 247/496 (49%), Gaps = 41/496 (8%) ref|NP\_478172.1| amidase [Nostoc sp. PCC 7120] pir|AB2530 amidase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta dbj|BAB77168.1| amidase [Nostoc sp. PCC 7120] Length = 507

2164.2 Best-BlastP=> >nrprot 48% Identities = 91/191 (47%), Positives = 135/191 (70%), Gaps = 1/191 (0%) ref|NP\_820234.1| membrane protein, putative [Coxiella burnetii RSA 493] sp|Q83C89|YC39\_COXBU Hypothetical UPF0078 protein CBU1239 gb|AAO90748.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 193

2166.2 Best-BlastP=> >nrprot No Hits found

2167.2 Best-BlastP=> >nrprot 65% Identities = 230/469 (49%), Positives = 315/469 (67%), Gaps = 5/469 (1%) ref|NP\_819701.1| mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase [Coxiella burnetii RSA 493] gb|AAO90215.1| mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase [Coxiella burnetii RSA 493] Length = 477

2169.2 Best-BlastP=> >nrprot 69% Identities = 77/136 (56%), Positives = 95/136 (69%), Gaps = 4/136 (2%) ref|ZP\_00067440.1| COG4969: Tfp pilus assembly protein, major pilin PilA [Microbulbifer degradans 2-40] Length = 164

2170.1 Best-BlastP=> >nrprot 60% Identities = 67/136 (49%), Positives = 84/136 (61%), Gaps = 5/136 (3%) ref|ZP\_00067440.1| COG4969: Tfp pilus assembly protein, major pilin PilA [Microbulbifer degradans 2-40] Length = 164

2172.2 Best-BlastP=> >nrprot 52% Identities = 47/147 (31%), Positives = 81/147 (55%), Gaps = 1/147 (0%) ref|NP\_717367.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN5481.1|AE015620\_3 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 159

2173.2 Best-BlastP=> >nrprot 52% Identities = 59/125 (47%), Positives = 75/125 (60%), Gaps = 1/125 (0%) sp|Q45292|YOUUG\_BACLI Hypothetical 17.3 kDa protein in GNTR 5'region pir|JC2302 oug protein - Bacillus licheniformis dbj|BAA06500.1| hypothetical protein [Bacillus licheniformis] Length = 147

2174.1 Best-BlastP=> >nrprot 50% Identities = 37/71 (52%), Positives = 50/71 (70%) ref|NP\_840482.1| DUF167 [Nitrosomonas europaea ATCC 19718] emb|CAD84306.1| DUF167 [Nitrosomonas europaea ATCC 19718] Length = 100

2175.3 Best-BlastP=> >nrprot No Hits found

2176.3 Best-BlastP=> >nrprot 52% Identities = 35/119 (29%), Positives = 64/119 (53%), Gaps = 6/119 (5%) ref|NP\_784901.1| unknown [Lactobacillus plantarum WCFS1] emb|CAD63748.1| unknown [Lactobacillus plantarum WCFS1] Length = 269

- 2177.2 Best-BlastP=> >nrprot 53% Identities = 71/181 (39%), Positives = 104/181 (57%), Gaps = 1/181 (0%) ref|ZP\_00052983.1| COG0582: Integrase [Magnetospirillum magnetotacticum] Length = 193
- 2180.2 Best-BlastP=> >nrprot 19% Identities = 68/171 (39%), Positives = 95/171 (55%), Gaps = 5/171 (2%) ref|NP\_814807.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] gb|AAO80877.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] Length = 168
- 2188.2 Best-BlastP=> >nrprot 45% Identities = 64/241 (26%), Positives = 113/241 (46%), Gaps = 17/241 (7%) ref|NP\_719332.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56776.1|AE015813\_4 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 250
- 2191.4 Best-BlastP=> >nrprot 74% Identities = 88/168 (52%), Positives = 127/168 (75%) ref|NP\_709074.1| peptide deformylase [Shigella flexneri 2a str. 301] ref|NP\_838779.1| peptide deformylase [Shigella flexneri 2a str. 2457T] gb|AAN44781.1|AE015342\_8 peptide deformylase [Shigella flexneri 2a str. 301] gb|AAP18590.1| peptide deformylase [Shigella flexneri 2a str. 2457T] Length = 169
- 2193.4 Best-BlastP=> >nrprot 90% Identities = 331/419 (78%), Positives = 379/419 (90%) dbj|BAC95945.1| transcription termination factor [Vibrio vulnificus YJ016] Length = 427
- 2195.1 Best-BlastP=> >nrprot 84% Identities = 356/487 (73%), Positives = 415/487 (85%) ref|NP\_667799.1| putative oxidoreductase [Yersinia pestis KIM] gb|AAM84050.1|AE013646\_10 putative oxidoreductase [Yersinia pestis KIM] Length = 506
- 2196.1 Best-BlastP=> >nrprot 51% Identities = 77/233 (33%), Positives = 122/233 (52%), Gaps = 11/233 (4%) ref|NP\_903454.1| NAD(P)H-flavin reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ61446.1| NAD(P)H-flavin reductase [Chromobacterium violaceum ATCC 12472] Length = 342
- 2197.1 Best-BlastP=> >nrprot No Hits found
- 2198.1 Best-BlastP=> >nrprot 55% Identities = 35/104 (33%), Positives = 58/104 (55%), Gaps = 4/104 (3%) ref|ZP\_00012205.1| COG3785: Uncharacterized conserved protein [Rhodopseudomonas palustris] Length = 110
- 2199.2 Best-BlastP=> >nrprot 97% Identities = 235/238 (98%), Positives = 236/238 (99%) emb|CAC34416.1| putative TatC protein [Legionella pneumophila] Length = 238
- 220.1 Best-BlastP=> >nrprot 65% Identities = 123/228 (53%), Positives = 152/228 (66%) ref|NP\_819791.1| glutamine amidotransferase, class I [Coxiella burnetii RSA 493] gb|AAO90305.1| glutamine amidotransferase, class I [Coxiella burnetii RSA 493] Length = 228
- 2204.2 Best-BlastP=> >nrprot 72% Identities = 279/498 (56%), Positives = 369/498 (74%), Gaps = 3/498 (0%) ref|NP\_841949.1| Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb|CAD85838.1| Sulfate transporter [Nitrosomonas europaea ATCC 19718] Length = 539
- 2207.2 Best-BlastP=> >nrprot 79% Identities = 126/208 (60%), Positives = 167/208 (80%) ref|NP\_841948.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] emb|CAD85837.1| Prokaryotic-type carbonic anhydrase [Nitrosomonas europaea ATCC 19718] Length = 208
- 2208.1 Best-BlastP=> >nrprot No Hits found
- 2209.4 Best-BlastP=> >nrprot 58% Identities = 111/321 (34%), Positives = 189/321 (58%), Gaps = 7/321 (2%) ref|NP\_814373.1| ornithine cyclodeaminase, putative [Enterococcus faecalis V583] gb|AAM75325.1|AF454824\_124 EF0124 [Enterococcus faecalis] gb|AAO80444.1| ornithine cyclodeaminase, putative [Enterococcus faecalis V583] Length = 326

- 221.1 Best-BlastP=> >nrprot 70% Identities = 158/285 (55%), Positives = 212/285 (74%) ref|NP\_00033588.1| COG0329: Dihydrodipicolinate synthase/N-acetylneuraminate lyase [Burkholderia fungorum] Length = 297
- 2212.4 Best-BlastP=> >nrprot 51% Identities = 232/616 (37%), Positives = 344/616 (55%), Gaps = 48/616 (7%) ref|NP\_762611.1| Type IV secretory pathway, VirD4 component [Vibrio vulnificus CMCP6] Length = 697
- 2213.2 Best-BlastP=> >nrprot No Hits found
- 2217.3 Best-BlastP=> >nrprot 66% Identities = 302/609 (49%), Positives = 411/609 (67%), Gaps = 13/609 (2%) sp|P32966|UVR\_C\_PSEFL Excinuclease ABC subunit C gb|AAA98758.1| UVR excinuclease subunit C Length = 607
- 2219.2 Best-BlastP=> >nrprot 34% Identities = 41/91 (45%), Positives = 48/91 (52%) gb|AAA73346.1| Mycobacterium tuberculosis DNA sequence, complete cds., gene products Length = 152
- 222.1 Best-BlastP=> >nrprot 63% Identities = 73/149 (48%), Positives = 102/149 (68%), Gaps = 5/149 (3%) ref|NP\_928633.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE13616.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 149
- 2220.2 Best-BlastP=> >nrprot 71% Identities = 110/213 (51%), Positives = 156/213 (73%) ref|NP\_486035.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AE2055 hypothetical protein all1995 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB73694.1| ORF\_ID:all1995~hypothetical protein [Nostoc sp. PCC 7120] Length = 221
- 2221.3 Best-BlastP=> >nrprot 57% Identities = 58/132 (43%), Positives = 84/132 (63%), Gaps = 4/132 (3%) gb|EAA20351.1| cytosol aminopeptidase [Plasmodium yoelii yoelii] Length = 612
- 2225.2 Best-BlastP=> >nrprot 55% Identities = 116/284 (40%), Positives = 167/284 (58%), Gaps = 6/284 (2%) ref|NP\_902361.1| geranyltransferase [Chromobacterium violaceum ATCC 12472] gb|AAQ60361.1| geranyltransferase [Chromobacterium violaceum ATCC 12472] Length = 298
- 223.1 Best-BlastP=> >nrprot 51% Identities = 97/266 (36%), Positives = 151/266 (56%), Gaps = 9/266 (3%) ref|NP\_00020713.1| hypothetical protein [Chloroflexus aurantiacus] Length = 278
- 2230.2 Best-BlastP=> >nrprot 58% Identities = 68/196 (34%), Positives = 117/196 (59%), Gaps = 2/196 (1%) ref|NP\_767278.1| Maf-like protein [Bradyrhizobium japonicum] dbj|BAC45903.1| Maf-like protein [Bradyrhizobium japonicum USDA 110] Length = 202
- 2231.3 Best-BlastP=> >nrprot 75% Identities = 254/407 (62%), Positives = 318/407 (78%), Gaps = 1/407 (0%) ref|NP\_00079853.1| COG0148: Endolase [Geobacter metallireducens] Length = 429
- 2232.1 Best-BlastP=> >nrprot 32% Identities = 41/123 (33%), Positives = 61/123 (49%), Gaps = 5/123 (4%) ref|NP\_899813.1| 2-dehydro-3-deoxy-phosphogluconate aldolase [Chromobacterium violaceum ATCC 12472] Length = 208
- 2233.3 Best-BlastP=> >nrprot 63% Identities = 64/119 (53%), Positives = 83/119 (69%) ref|NP\_819436.1| lipoprotein signal peptidase [Coxiella burnetii RSA 493] gb|AAO89950.1| lipoprotein signal peptidase [Coxiella burnetii RSA 493] Length = 163
- 2235.2 Best-BlastP=> >nrprot 57% Identities = 220/636 (34%), Positives = 371/636 (58%), Gaps = 29/636 (4%) ref|NP\_819137.1| sulfatase domain protein [Coxiella burnetii RSA 493] gb|AAO89651.1| sulfatase domain protein [Coxiella burnetii RSA 493] Length = 638
- 2239.3 Best-BlastP=> >nrprot 45% Identities = 96/277 (34%), Positives = 149/277 (53%), Gaps = 40/277 (14%) emb|CAA75849.1| hypothetical protein [Coxiella burnetii] Length = 309

- 2240.2 Best-BlastP=> >nrprot 66% Identities = 75/155 (48%), Positives = 105/155 (67%) ref|ZP\_00067293.1| COG1576: Uncharacterized conserved protein [Microbulbifer degradans 2-40] Length = 155
- 2241.2 Best-BlastP=> >nrprot 67% Identities = 51/105 (48%), Positives = 76/105 (72%) ref|ZP\_00090593.1| COG0799: Uncharacterized homolog of plant loiap protein [Azotobacter vinelandii] Length = 117
- 2242.1
- 2244.2 Best-BlastP=> >nrprot 47% Identities = 46/187 (24%), Positives = 89/187 (47%), Gaps = 16/187 (8%) ref|NP\_820065.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90579.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 184
- 2244.2 Best-BlastP=> >nrprot 77% Identities = 129/202 (63%), Positives = 156/202 (77%) gb|AAC33273.1| TnpR [Pseudomonas alcaligenes] Length = 309
- 2245.2 Best-BlastP=> >nrprot 65% Identities = 178/331 (53%), Positives = 236/331 (71%), Gaps = 6/331 (1%) ref|NP\_842305.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD86220.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 346
- 2247.5 Best-BlastP=> >nrprot 61% Identities = 233/551 (42%), Positives = 342/551 (62%), Gaps = 4/551 (0%) ref|NP\_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589
- 2250.2 Best-BlastP=> >nrprot No Hits found
- 2251.3 Best-BlastP=> >nrprot No Hits found
- 2252.1 Best-BlastP=> >nrprot 83% Identities = 254/363 (69%), Positives = 303/363 (83%) ref|NP\_231816.1| GTP-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|D82107 GTP-binding protein VC2185 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95330.1| GTP-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 383
- 2253.2 Best-BlastP=> >nrprot 66% Identities = 96/181 (53%), Positives = 127/181 (70%) ref|NP\_283782.1| putative peptidyl-tRNA hydrolase [Neisseria meningitidis Z2491] sp|Q9JUV42|PTH\_NEIMA Peptidyl-tRNA hydrolase (PTH) pir|B81948 probable aminoacyl-tRNA hydrolase (EC 3.1.1.29) NMA1004 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB84273.1| putative peptidyl-tRNA hydrolase [Neisseria meningitidis Z2491] Length = 192
- 2255.2 Best-BlastP=> >nrprot 67% Identities = 158/294 (53%), Positives = 199/294 (67%), Gaps = 4/294 (1%) ref|NP\_461016.1| ATP phosphoribosyltransferase [Salmonella typhimurium L T2] sp|P00499|HIS1\_SALTY ATP phosphoribosyltransferase pir|XREBT ATP phosphoribosyltransferase (EC 2.4.2.17) [validated] - Salmonella typhimurium emb|CAA31822.1| unnamed protein product [Salmonella typhimurium] gb|AAA27142.1| hisG gb|AAA88614.1| ATP phosphoribosyltransferase gb|AAA80244.1| ATP phosphoribosyltransferase gb|AAA80247.1| ATP phosphoribosyltransferase gb|AAA80249.1| ATP phosphoribosyltransferase gb|AAA80252.1| ATP phosphoribosyltransferase gb|AAA80254.1| ATP phosphoribosyltransferase gb|AAA80257.1| ATP phosphoribosyltransferase gb|AAA80259.1| ATP phosphoribosyltransferase gb|AAA80262.1| ATP phosphoribosyltransferase gb|AAL20975.1| ATP phosphoribosyltransferase [Salmonella typhimurium L T2] Length = 299
- 2258.2 Best-BlastP=> >nrprot No Hits found
- 226.4 Best-BlastP=> >nrprot No Hits found

- 2260.2 Best-BlastP=> >nprot 65% Identities = 115/209 (55%), Positives = 147/209 (70%), Gaps = 1/209 (0%) ref|ZP\_00013996.1| COG2872: Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain [Rhodospirillum rubrum] Length = 214
- 2261.3 Best-BlastP=> >nprot No Hits found
- 2264.2 Best-BlastP=> >nprot 59% Identities = 172/411 (41%), Positives = 247/411 (60%), Gaps = 6/411 (1%) ref|NP\_773878.1| b1r7238 [Bradyrhizobium japonicum] dbj|BAC52503.1| b1r7238 [Bradyrhizobium japonicum USDA 110] Length = 412
- 2266.2 Best-BlastP=> >nprot 76% Identities = 282/410 (68%), Positives = 322/410 (78%), Gaps = 1/410 (0%) ref|ZP\_00021755.1| hypothetical protein [Ralstonia metallidurans] Length = 412
- 2268.2 Best-BlastP=> >nprot 48% Identities = 131/405 (32%), Positives = 197/405 (48%), Gaps = 29/405 (7%) ref|NP\_616925.1| conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb|AAM05405.1| conserved hypothetical protein [Methanosarcina acetivorans str. C2A] Length = 417
- 227.2 Best-BlastP=> >nprot 95% Identities = 281/303 (92%), Positives = 291/303 (96%) gb|AAM00625.1| unknown [Legionella pneumophila] Length = 303
- 2270.2 Best-BlastP=> >nprot 45% Identities = 38/120 (31%), Positives = 58/120 (48%), Gaps = 22/120 (18%) gb|AAA89101.1| protein kinase Length = 379
- 2271.1 Best-BlastP=> >nprot 41% Identities = 25/57 (43%), Positives = 35/57 (61%), Gaps = 4/57 (7%) ref|NP\_012348.1| Delays the onset of mitosis by phosphorylation and inactivation of the cyclin-dependent kinase Cdc28, thereby relaying the morphogenetic signal to the cell cycle. S. pombe wee1+ homolog; Swe1p [Saccharomyces cerevisiae] sp|P32944|SWE1\_YEAST Mitosis inhibitor protein kinase SWE1 pir|S40400 protein kinase SWE1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) emb|CAA52150.1| SWE1 [Saccharomyces cerevisiae] emb|CAA89482.1| SWE1 [Saccharomyces cerevisiae] Length = 819
- 2272.3 Best-BlastP=> >nprot 61% Identities = 228/487 (46%), Positives = 308/487 (63%), Gaps = 8/487 (1%) ref|NP\_744150.1| amidophosphoribosyltransferase [Pseudomonas putida KT2440] gb|AAN67614.1|AE016391\_5 amidophosphoribosyltransferase [Pseudomonas putida KT2440] Length = 501
- 2274.2 Best-BlastP=> >nprot 74% Identities = 194/313 (61%), Positives = 233/313 (74%), Gaps = 5/313 (1%) gb|AAL85973.1| putative phosphoribosylamidimidazole-succinocarboxamide synthase [Arabidopsis thaliana] Length = 374
- 2275.3 Best-BlastP=> >nprot 34% Identities = 75/185 (40%), Positives = 107/185 (57%), Gaps = 19/185 (10%) ref|NP\_437235.1| putative protein, similar to gene related to biosynthesis of peptide antibiotic trifolitin [Sinorhizobium meliloti] pir|G95928 hypothetical protein SMB21116 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC49095.1| putative protein, similar to gene related to biosynthesis of peptide antibiotic trifolitin [Sinorhizobium meliloti] Length = 243
- 2277.2 Best-BlastP=> >nprot 47% Identities = 27/55 (49%), Positives = 41/55 (74%), Gaps = 1/55 (1%) ref|NP\_820051.1| carbon storage regulator [Coxiella burnetii RSA 493] gb|AAO90565.1| carbon storage regulator [Coxiella burnetii RSA 493] Length = 70
- 2279.2 Best-BlastP=> >nprot No Hits found
- 228.1 Best-BlastP=> >nprot No Hits found
- 2282.4 Best-BlastP=> >nprot 98% Identities = 569/577 (98%), Positives = 571/577 (98%), Gaps = 1/577 (0%) sp|P71481|PRIM\_LEGPN DNA primase gb|AAB09542.1| LpdnaG Length = 576

- 2289.2 Best-BlastP=> >nprot 50% Identities = 50/159 (31%), Positives = 81/159 (50%), Gaps = 13/159 (8%) ref|NP\_718655.1| hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56099.1|AE015746\_3 hypothetical protein [Shewanella oneidensis MR-1] Length = 197
- 2290.1 Best-BlastP=> >nprot 53% Identities = 106/293 (36%), Positives = 164/293 (55%), Gaps = 2/293 (0%) ref|NP\_744181.1| conserved hypothetical protein [Pseudomonas putida KT2440] gb|AAN67645.1|AE016394\_6 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 318
- 2291.2 Best-BlastP=> >nprot 81% Identities = 208/316 (65%), Positives = 262/316 (82%), Gaps = 1/316 (0%) ref|ZP\_00067583.1| COG0714: MoxR-like ATPases [Microbulbifer degradans 2-40] Length = 321
- 2292.2 Best-BlastP=> >nprot 28% Identities = 81/371 (21%), Positives = 158/371 (42%), Gaps = 34/371 (9%) prf|2210342A myosin:SUBUNIT=heavy chain Length = 2241
- 2293.5 Best-BlastP=> >nprot 14% Identities = 74/228 (32%), Positives = 119/228 (52%), Gaps = 19/228 (8%) ref|NP\_844638.1| conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP26124.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 324
- 2295.3 Best-BlastP=> >nprot 72% Identities = 93/152 (61%), Positives = 113/152 (74%) ref|NP\_249699.1| bacterioferritin comigratory protein [Pseudomonas aeruginosa PA01] pir|A83520 bacterioferritin comigratory protein PA1008 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG04397.1|AE004533\_8 bacterioferritin comigratory protein [Pseudomonas aeruginosa PA01] Length = 157
- 2297.3 Best-BlastP=> >nprot 79% Identities = 98/156 (62%), Positives = 125/156 (80%), Gaps = 3/156 (1%) ref|NP\_311509.1| small protein B [Escherichia coli O157:H7] ref|NP\_417110.1| small protein B [Escherichia coli K12] ref|NP\_708467.1| small protein B [Shigella flexneri 2a str. 301] ref|NP\_755024.1| SsrA-binding protein [Escherichia coli CFT073] ref|NP\_838189.1| ssrA(tmRNA)-binding protein [Shigella flexneri 2a str. 2457T] sp|P32052|SSRP\_ECOLI SsrA-binding protein (Small protein B) pir|JS0701 small protein B, smpB - Escherichia coli (strain K-12) pir|B91064 small protein B [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) dbj|BAA02062.1| small protein [Escherichia coli] gb|AAA79790.1| smpB gene product gb|AAC75669.1| small protein B [Escherichia coli K12] dbj|BAB36905.1| small protein B [Escherichia coli O157:H7] gb|AAN44174.1|AE015283\_5 small protein B [Shigella flexneri 2a str. 301] gb|AAN81592.1|AE016764\_274 SsrA-binding protein [Escherichia coli CFT073] gb|AAP17999.1| ssrA(tmRNA)-binding protein [Shigella flexneri 2a str. 2457T] Length = 160
- 2298.2 Best-BlastP=> >nprot 16% Identities = 40/142 (28%), Positives = 73/142 (51%), Gaps = 8/142 (5%) ref|NP\_038716.1| t-complex-associated testis expressed 1 [Mus musculus] pir|A45841 T-complex-associated-testes-expressed-1 protein - mouse gb|AAA40406.1| Tcte-1 peptide Length = 506
- 2299.3 Best-BlastP=> >nprot 37% Identities = 22/88 (25%), Positives = 41/88 (46%), Gaps = 5/88 (5%) ref|NP\_819930.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO90444.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 169
- 2301.2 Best-BlastP=> >nprot 70% Identities = 397/715 (55%), Positives = 512/715 (71%), Gaps = 4/715 (0%) ref|NP\_820090.1| ribonuclease R [Coxiella burnetii RSA 493] gb|AAO90604.1| ribonuclease R [Coxiella burnetii RSA 493] Length = 736
- 2302.2 Best-BlastP=> >nprot 72% Identities = 64/108 (59%), Positives = 81/108 (75%) ref|NP\_355166.1| AGR\_C\_4014p [Agrobacterium tumefaciens] ref|NP\_532881.1| secretion chaperone [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|F97624 csaa protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AG2847 secretion chaperone [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK87951.1| AGR\_C\_4014p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43197.1| secretion chaperone [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 113



- 2308.2 Best-BlastP=> >nrprot No Hits found
- 2309.2 Best-BlastP=> >nrprot 45% Identities = 104/406 (25%), Positives = 173/406 (42%), Gaps = 63/406 (15%) sp|Q9MYU4|ENP1\_PIG Ectonucleoside triphosphate diphosphohydrolase 1 (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen) emb|CAB95871.1| ATP-diphosphohydrolase [Sus scrofa] Length = 510
- 2311.4 Best-BlastP=> >nrprot 75% Identities = 490/868 (56%), Positives = 648/868 (74%), Gaps = 13/868 (1%) ref|NP\_928561.1| alanyl-tRNA synthetase (alanine-tRNA ligase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13544.1| alanyl-tRNA synthetase (alanine-tRNA ligase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 876
- 2312.1 Best-BlastP=> >nrprot No Hits found
- 2313.2 Best-BlastP=> >nrprot 19% Identities = 40/156 (25%), Positives = 78/156 (50%), Gaps = 13/156 (8%) ref|NP\_614055.1| Uncharacterized protein [Methanopyrus kandleri AV19] gb|AAM01985.1| Uncharacterized protein [Methanopyrus kandleri AV19] Length = 609
- 2315.3 Best-BlastP=> >nrprot 56% Identities = 93/262 (35%), Positives = 149/262 (56%), Gaps = 2/262 (0%) ref|ZP\_00108734.1| COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Nostoc punctiforme] Length = 270
- 2317.2 Best-BlastP=> >nrprot 71% Identities = 266/484 (54%), Positives = 351/484 (72%), Gaps = 1/484 (0%) ref|NP\_390984.1| glycine betaine aldehyde dehydrogenase [Bacillus subtilis] sp|P71016|DHAB\_BACSU Betaine aldehyde dehydrogenase (BADH) pir|A69629 glycine betaine aldehyde dehydrogenase gbsA - Bacillus subtilis gb|AAC44364.1| GbsA emb|CAB15084.1| glycine betaine aldehyde dehydrogenase [Bacillus subtilis subsp. subtilis str. 168] Length = 490
- 2319.3 Best-BlastP=> >nrprot 72% Identities = 263/462 (56%), Positives = 331/462 (71%), Gaps = 6/462 (1%) ref|NP\_638201.1| L-serine dehydratase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42125.1| L-serine dehydratase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 460
- 2320.3 Best-BlastP=> >nrprot 50% Identities = 163/400 (40%), Positives = 243/400 (60%), Gaps = 17/400 (4%) ref|NP\_865739.1| alginate o-acetyltransferase algI [Pirellula sp.] emb|CAD73424.1| alginate o-acetyltransferase algI [Pirellula sp.] Length = 470
- 2321.3 Best-BlastP=> >nrprot 65% Identities = 90/172 (52%), Positives = 120/172 (69%) ref|NP\_884513.1| putative chromate reductase [Bordetella parapertussis] ref|NP\_888264.1| putative chromate reductase [Bordetella bronchiseptica] emb|CAE32216.1| putative chromate reductase [Bordetella bronchiseptica] emb|CAE37565.1| putative chromate reductase [Bordetella parapertussis] Length = 184
- 2322.2 Best-BlastP=> >nrprot 65% Identities = 113/231 (48%), Positives = 152/231 (65%), Gaps = 3/231 (1%) ref|NP\_820714.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91228.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 237
- 2323.2 Best-BlastP=> >nrprot 34% Identities = 47/220 (21%), Positives = 91/220 (41%), Gaps = 16/220 (7%) ref|NP\_902123.1| hypothetical protein CV2453 [Chromobacterium violaceum ATCC 12472] gb|AAQ60124.1| hypothetical protein CV2453 [Chromobacterium violaceum ATCC 12472] Length = 258
- 2324.4 Best-BlastP=> >nrprot No Hits found
- 2328.2 Best-BlastP=> >nrprot 61% Identities = 376/865 (43%), Positives = 527/865 (60%), Gaps = 23/865 (2%) ref|NP\_778639.1| diaminopimelate decarboxylase; aspartate kinase [Xylella fastidiosa Temecula1] gb|AAO28288.1| diaminopimelate decarboxylase; aspartate kinase [Xylella fastidiosa Temecula1] Length = 868

- 2330.2 Best-BlastP=> >nrprot 72% Identities = 380/665 (57%), Positives = 488/665 (73%), Gaps = 1/665 (0%) ref|NP\_246655.1| Lig [Pasteurella multocida] gb|AAK03800.1| Lig [Pasteurella multocida] Length = 673
- 2333.3 Best-BlastP=> >nrprot 70% Identities = 381/700 (54%), Positives = 501/700 (71%), Gaps = 10/700 (1%) ref|NP\_841209.1| Bacterial extracellular solute-binding protein, family 5 [Nitrosomonas europaea ATCC 19718] emb|CAD85063.1| Bacterial extracellular solute-binding protein, family 5 [Nitrosomonas europaea ATCC 19718] Length = 746
- 2335.2 Best-BlastP=> >nrprot No Hits found
- 2336.2 Best-BlastP=> >nrprot 70% Identities = 353/672 (52%), Positives = 479/672 (71%), Gaps = 4/672 (0%) ref|NP\_796449.1| oligopeptidase A [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC58333.1| oligopeptidase A [Vibrio parahaemolyticus] Length = 680
- 2337.3 Best-BlastP=> >nrprot 76% Identities = 135/215 (62%), Positives = 170/215 (79%) gb|AAK20881.1| AF334761\_2 cell division ATP-binding protein [Aeromonas hydrophila] Length = 222
- 2339.4 Best-BlastP=> >nrprot 74% Identities = 210/345 (60%), Positives = 264/345 (76%), Gaps = 6/345 (1%) ref|ZP\_00126801.1| COG0552: Signal recognition particle GTPase [Pseudomonas syringae pv. syringae B728a] Length = 505
- 234.2 Best-BlastP=> >nrprot 99% Identities = 731/736 (99%), Positives = 734/736 (99%) gb|AAM00624.1| putative copper efflux ATPase [Legionella pneumophila] Length = 736
- 2343.2 Best-BlastP=> >nrprot 33% Identities = 67/259 (25%), Positives = 108/259 (41%), Gaps = 34/259 (13%) ref|NP\_359656.1| cell surface antigen [Rickettsia conorii] pir|C97702 cell surface antigen [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02557.1| cell surface antigen [Rickettsia conorii] Length = 1902
- 2344.4 Best-BlastP=> >nrprot 56% Identities = 270/726 (37%), Positives = 405/726 (55%), Gaps = 16/726 (2%) ref|ZP\_00043557.1| COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1] Length = 734
- 2345.2 Best-BlastP=> >nrprot No Hits found
- 2346.1 Best-BlastP=> >nrprot No Hits found
- 2347.2 Best-BlastP=> >nrprot No Hits found
- 235.2 Best-BlastP=> >nrprot 50% Identities = 145/450 (32%), Positives = 218/450 (48%), Gaps = 60/450 (13%) sp|P42042|AMYG\_ARXAD Glucoamylase precursor (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) emb|CAA86997.1| glucoamylase precursor [Arxula adeninivorans] Length = 624
- 2350.2 Best-BlastP=> >nrprot No Hits found
- 2351.2 Best-BlastP=> >nrprot 59% Identities = 114/258 (44%), Positives = 164/258 (63%) ref|ZP\_00122702.1| COG1043: Acyl-[acyl carrier protein]-UDP-N-acetylglucosamine O-acyltransferase [Haemophilus somnus 129PT] Length = 262
- 2352.2 Best-BlastP=> >nrprot 66% Identities = 160/338 (47%), Positives = 229/338 (67%) ref|ZP\_00052962.1| COG1044: UDP-3-O-[3-hydroxymyristoyl]glucosamine N-acyltransferase [Magnetospirillum magnetotacticum] Length = 339
- 2353.3 Best-BlastP=> >nrprot 65% Identities = 174/375 (46%), Positives = 251/375 (66%), Gaps = 3/375 (0%) ref|NP\_252333.1| lipid A-disaccharide synthase [Pseudomonas aeruginosa PAO1] sp|Q9HXY8|LPXB\_PSEAE Lipid A-disaccharide synthase pir|C83190 lipid A-disaccharide synthase PA3643 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07031.1| AE004784\_4 lipid A-disaccharide synthase [Pseudomonas aeruginosa PAO1] Length = 378

- 2354.2 Best-BlastP=> >nrprot 23% Identities = 27/92 (29%), Positives = 49/92 (53%), Gaps = 2/92 (2%) dbj|BAC97056.1| RTX (repeat in toxin) cytotoxin [Vibrio vulnificus YJ016] Length = 5206
- 2355.2 Best-BlastP=> >nrprot 45% Identities = 83/256 (32%), Positives = 134/256 (52%), Gaps = 18/256 (7%) ref|NP\_832533.1| Probable short-chain type dehydrogenase/reductase vdlC [Bacillus cereus ATCC 14579] gb|AAP09734.1| Probable short-chain type dehydrogenase/reductase vdlC [Bacillus cereus ATCC 14579] Length = 281
- 2356.2 Best-BlastP=> >nrprot 65% Identities = 106/213 (49%), Positives = 141/213 (66%), Gaps = 2/213 (0%) ref|ZP\_00138632.1| COG0259: Pyridoxamine-phosphate oxidase [Pseudomonas aeruginosa UCBPP-PA14] Length = 215
- 2357.4 Best-BlastP=> >nrprot 6% Identities = 26/77 (33%), Positives = 38/77 (49%), Gaps = 2/77 (2%) ref|NP\_752812.1| Putative conserved protein [Escherichia coli CFT073] gb|AAN79355.1|AE016757\_259 Putative conserved protein [Escherichia coli CFT073] Length = 101
- 2358.3 Best-BlastP=> >nrprot 73% Identities = 272/470 (57%), Positives = 346/470 (73%), Gaps = 3/470 (0%) ref|ZP\_00082833.1| COG0773: UDP-N-acetylmuramate-alanine ligase [Pseudomonas fluorescens PfO-1] Length = 486
- 236.1 Best-BlastP=> >nrprot No Hits found
- 2360.2 Best-BlastP=> >nrprot 52% Identities = 115/337 (34%), Positives = 189/337 (56%), Gaps = 40/337 (11%) ref|NP\_486436.1| unknown protein [Nostoc sp. PCC 7120] pir|AE2105 hypothetical protein all2396 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB74095.1| ORF\_ID:all2396-unknown protein [Nostoc sp. PCC 7120] Length = 454
- 2361.4 Best-BlastP=> >nrprot 21% Identities = 193/1010 (19%), Positives = 405/1010 (40%), Gaps = 174/1010 (17%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738
- 2362.3 Best-BlastP=> >nrprot 99% Identities = 302/303 (99%), Positives = 303/303 (100%) gb|AAC38180.1| DotC [Legionella pneumophila] Length = 303
- 2364.1 Best-BlastP=> >nrprot 99% Identities = 376/377 (99%), Positives = 377/377 (100%) gb|AAC38181.1| DotB [Legionella pneumophila] Length = 377
- 2365.2 Best-BlastP=> >nrprot 52% Identities = 197/528 (37%), Positives = 302/528 (57%), Gaps = 37/528 (7%) ref|NP\_658139.1| 5\_nucleotidase, 5'-nucleotidase, catalytic domain [Bacillus anthracis A2012] ref|NP\_846555.1| 5'-nucleotidase family protein [Bacillus anthracis str. Ames] gb|AAP28041.1| 5'-nucleotidase family protein [Bacillus anthracis str. Ames] Length = 529
- 2367.2 Best-BlastP=> >nrprot No Hits found
- 2368.5 Best-BlastP=> >nrprot 46% Identities = 147/450 (32%), Positives = 228/450 (50%), Gaps = 15/450 (3%) ref|NP\_821551.1| putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase [Streptomyces avermitilis MA-4680] dbj|BAC68086.1| putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase [Streptomyces avermitilis MA-4680] Length = 495
- 2369.3 Best-BlastP=> >nrprot 54% Identities = 71/194 (36%), Positives = 111/194 (57%), Gaps = 1/194 (0%) ref|NP\_743077.1| transporter, LysE family [Pseudomonas putida KT2440] gb|AAN66541.1|AE016282\_9 transporter, LysE family [Pseudomonas putida KT2440] Length = 204
- 2371.1 Best-BlastP=> >nrprot 51% Identities = 118/343 (34%), Positives = 175/343 (51%), Gaps = 17/343 (4%) ref|NP\_360212.1| capM protein [Rickettsia conorii] pir|G97771 capM protein [imported] - Rickettsia conorii (strain Malish 7) gb|AAL03113.1| capM protein [Rickettsia conorii] Length = 338

- 2372.3 Best-BlastP=> >nrprot 66% Identities = 53/118 (44%), Positives = 79/118 (66%) ref|ZP\_00111665.1| COG2146: Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases [Nostoc punctiforme] Length = 119
- 2373.2 Best-BlastP=> >nrprot 73% Identities = 185/309 (59%), Positives = 235/309 (76%), Gaps = 2/309 (0%) ref|NP\_819938.1| lytic murein transglycosylase, putative [Coxiella burnetii RSA 493] gb|AAO90452.1| lytic murein transglycosylase, putative [Coxiella burnetii RSA 493] Length = 333
- 2374.2 Best-BlastP=> >nrprot No Hits found
- 2375.3 Best-BlastP=> >nrprot 75% Identities = 115/187 (61%), Positives = 144/187 (77%), Gaps = 2/187 (1%) ref|ZP\_00091537.1| COG0164: Ribonuclease HII [Azotobacter vinelandii] Length = 236
- 2377.2 Best-BlastP=> >nrprot 73% Identities = 181/309 (58%), Positives = 236/309 (76%) ref|NP\_819651.1| oxidoreductase family protein [Coxiella burnetii RSA 493] Length = 327
- 238.1 Best-BlastP=> >nrprot 57% Identities = 185/432 (42%), Positives = 272/432 (62%), Gaps = 10/432 (2%) ref|NP\_391464.1| similar to metabolite transport protein [Bacillus subtilis] pir|E70070 metabolite transport protein homolog ywtG - Bacillus subtilis emb|CAB07473.1| ywtG [Bacillus subtilis] emb|CAB15600.1| ywtG [Bacillus subtilis subsp. subtilis str. 168] Length = 457
- 2381.2 Best-BlastP=> >nrprot 58% Identities = 148/381 (38%), Positives = 225/381 (59%), Gaps = 2/381 (0%) ref|ZP\_00079875.1| COG0763: Lipid A disaccharide synthetase [Geobacter metallireducens] Length = 400
- 2382.2 Best-BlastP=> >nrprot 54% Identities = 39/79 (49%), Positives = 54/79 (68%) ref|NP\_716031.1| DNA-binding protein Fis [Shewanella oneidensis MR-1] gb|AAN53476.1|AE015487\_10 DNA-binding protein Fis [Shewanella oneidensis MR-1] Length = 101
- 2383.4 Best-BlastP=> >nrprot 37% Identities = 21/45 (46%), Positives = 26/45 (57%), Gaps = 2/45 (4%) gb|AAQ17065.1| nucleolin 3 [Cyprinus carpio] gb|AAQ55855.1| nucleolin [Cyprinus carpio] Length = 637
- 2387.3 Best-BlastP=> >nrprot 55% Identities = 130/320 (40%), Positives = 187/320 (58%), Gaps = 4/320 (1%) ref|NP\_768143.1| quinone oxidoreductase [Bradyrhizobium japonicum] db|J|BAC46768.1| quinone oxidoreductase [Bradyrhizobium japonicum USDA 110] Length = 332
- 2388.3 Best-BlastP=> >nrprot 72% Identities = 147/280 (52%), Positives = 212/280 (75%) ref|ZP\_00021514.1| COG1175: ABC-type sugar transport systems, permease components [Ralstonia metallidurans] Length = 293
- 239.1 Best-BlastP=> >nrprot 65% Identities = 106/203 (52%), Positives = 145/203 (71%) ref|NP\_718073.1| 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase [Shewanella oneidensis MR-1] gb|AAN55517.1|AE015690\_5 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase [Shewanella oneidensis MR-1] Length = 213
- 2391.2 Best-BlastP=> >nrprot No Hits found
- 2392.2 Best-BlastP=> >nrprot No Hits found
- 2395.3 Best-BlastP=> >nrprot 63% Identities = 174/360 (48%), Positives = 236/360 (65%), Gaps = 1/360 (0%) ref|NP\_819557.1| phosphoserine aminotransferase [Coxiella burnetii RSA 493] gb|AAO90071.1| phosphoserine aminotransferase [Coxiella burnetii RSA 493] Length = 360
- 24.1 Best-BlastP=> >nrprot 23% Identities = 65/242 (26%), Positives = 117/242 (48%), Gaps = 20/242 (8%) ref|ZP\_00096911.1| COG1738: Uncharacterized conserved protein [Novosphingobium aromaticivorans] Length = 243

- 240.1 Best-BlastP=> >nrprot 57% Identities = 144/316 (45%), Positives = 194/316 (61%), Gaps = 1/316 (0%) ref|NP\_928703.1| Glucokinase (Glucose kinase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 321
- 2400.2 Best-BlastP=> >nrprot 76% Identities = 181/285 (63%), Positives = 226/285 (79%), Gaps = 4/285 (1%) ref|NP\_248803.1| probable cytochrome c oxidase assembly factor [Pseudomonas aeruginosa PAO1] ref|ZP\_00140528.1| COG0109: Polyprenyltransferase (cytochrome oxidase assembly factor) [Pseudomonas aeruginosa UCBPP-PA14] pir|F83632 probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG03503.1|AE004449\_12 probable cytochrome c oxidase assembly factor [Pseudomonas aeruginosa PAO1] Length = 304
- 2401.2 Best-BlastP=> >nrprot 44% Identities = 57/167 (34%), Positives = 96/167 (57%), Gaps = 5/167 (2%) ref|ZP\_00065551.1| COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Microbulbifer degradans 2-40] Length = 219
- 2402.3 Best-BlastP=> >nrprot 81% Identities = 316/450 (70%), Positives = 370/450 (82%), Gaps = 5/450 (1%) ref|NP\_819057.1| chromosomal replication initiator protein DnaA [Coxiella burnetii RSA 493] gb|AAO89571.1| chromosomal replication initiator protein DnaA [Coxiella burnetii RSA 493] Length = 451
- 2404.2 Best-BlastP=> >nrprot 67% Identities = 145/366 (39%), Positives = 247/366 (67%), Gaps = 2/366 (0%) ref|NP\_796391.1| DNA polymerase III, beta chain [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC58275.1| DNA polymerase III, beta chain [Vibrio parahaemolyticus] Length = 366
- 2406.3 Best-BlastP=> >nrprot 57% Identities = 133/360 (36%), Positives = 205/360 (56%), Gaps = 12/360 (3%) ref|NP\_759959.1| Recombinational DNA repair ATPase [Vibrio vulnificus CMCP6] sp|Q8DDJ1|REC\_F\_VIBVU DNA replication and repair protein recF gb|AAO09486.1|AE016800\_91 Recombinational DNA repair ATPase [Vibrio vulnificus CMCP6] Length = 359
- 2407.3 Best-BlastP=> >nrprot 67% Identities = 370/794 (46%), Positives = 536/794 (67%), Gaps = 5/794 (0%) ref|NP\_820311.1| phenylalanyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] gb|AAO90825.1| phenylalanyl-tRNA synthetase, beta subunit [Coxiella burnetii RSA 493] Length = 792
- 2409.3 Best-BlastP=> >nrprot 100% Identities = 233/234 (99%), Positives = 234/234 (100%) emb|CAD42890.1| macrophage infectivity potentiator [Legionella pneumophila serogroup 8] Length = 236
- 241.2 Best-BlastP=> >nrprot 76% Identities = 386/608 (63%), Positives = 470/608 (77%) ref|NP\_718074.1| 6-phosphogluconate dehydratase [Shewanella oneidensis MR-1] gb|AAN55518.1|AE015690\_6 6-phosphogluconate dehydratase [Shewanella oneidensis MR-1] Length = 608
- 2410.2 Best-BlastP=> >nrprot 56% Identities = 157/390 (40%), Positives = 240/390 (61%), Gaps = 7/390 (1%) ref|NP\_668353.1| ampG protein [Yersinia pestis KIM] gb|AAM84604.1|AE013705\_7 ampG protein [Yersinia pestis KIM] Length = 510
- 2412.2 Best-BlastP=> >nrprot 62% Identities = 245/553 (44%), Positives = 350/553 (63%), Gaps = 5/553 (0%) ref|NP\_719011.1| DNA repair protein RecN [Shewanella oneidensis MR-1] gb|AAN56455.1|AE015782\_7 DNA repair protein RecN [Shewanella oneidensis MR-1] Length = 552
- 2413.1 Best-BlastP=> >nrprot 73% Identities = 46/67 (68%), Positives = 51/67 (76%), Gaps = 1/67 (1%) ref|ZP\_00065318.1| COG1278: Cold shock proteins [Microbulbifer degradans 2-40] Length = 69

- 2414.2 Best-BlastP=> >nrprot 46% Identities = 86/333 (25%), Positives = 166/333 (49%), Gaps = 15/333 (4%) ref|NP\_819780.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] gb|AAO90294.1| efflux transporter, RND family, MFP subunit [Coxiella burnetii RSA 493] Length = 348
- 2415.2 Best-BlastP=> >nrprot 37% Identities = 69/273 (25%), Positives = 121/273 (44%), Gaps = 25/273 (9%) ref|ZP\_00087134.1| COG2162: Arylamine N-acetyltransferase [Pseudomonas fluorescens PFO-1] Length = 292
- 2418.2 Best-BlastP=> >nrprot 63% Identities = 106/234 (45%), Positives = 154/234 (65%) ref|NP\_821026.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO91540.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 237
- 2419.3 Best-BlastP=> >nrprot 48% Identities = 74/222 (33%), Positives = 110/222 (49%), Gaps = 10/222 (4%) ref|NP\_626575.1| putative dipeptidase [Streptomyces coelicolor A3(2)] emb|CAB93448.1| putative dipeptidase [Streptomyces coelicolor A3(2)] Length = 218
- 2421.2 Best-BlastP=> >nrprot 68% Identities = 266/502 (52%), Positives = 345/502 (68%), Gaps = 12/502 (2%) ref|NP\_639214.1| competence related protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM43105.1| competence related protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 506
- 2422.3 Best-BlastP=> >nrprot 49% Identities = 31/123 (25%), Positives = 64/123 (52%), Gaps = 3/123 (2%) ref|NP\_703938.1| 6-pyruvoyl tetrahydropterin synthase, putative [Plasmodium falciparum 3D7] emb|CAD50550.1| 6-pyruvoyl tetrahydropterin synthase, putative [Plasmodium falciparum 3D7] Length = 173
- 2423.2 Best-BlastP=> >nrprot 63% Identities = 163/360 (45%), Positives = 237/360 (65%), Gaps = 3/360 (0%) ref|NP\_820807.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91321.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 388
- 2424.3 Best-BlastP=> >nrprot 63% Identities = 92/176 (52%), Positives = 120/176 (68%), Gaps = 1/176 (0%) ref|NP\_407270.1| putative membrane protein [Yersinia pestis] pir|AF0465 probable membrane protein YPO3822 [imported] - Yersinia pestis (strain CO92) emb|CAC93290.1| putative membrane protein [Yersinia pestis CO92] Length = 222
- 2425.2 Best-BlastP=> >nrprot 51% Identities = 72/187 (38%), Positives = 110/187 (58%), Gaps = 1/187 (0%) ref|NP\_419508.1| conserved hypothetical protein [Caulobacter crescentus CB15] pir|H87334 conserved hypothetical protein CC0691 [imported] - Caulobacter crescentus gb|AAK22676.1| conserved hypothetical protein [Caulobacter crescentus CB15] Length = 208
- 2426.2 Best-BlastP=> >nrprot No Hits found
- 2427.4 Best-BlastP=> >nrprot 61% Identities = 37/65 (56%), Positives = 44/65 (67%) ref|ZP\_00091135.1| COG2852: Uncharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 150
- 2428.2 Best-BlastP=> >nrprot 58% Identities = 36/85 (42%), Positives = 55/85 (64%), Gaps = 7/85 (8%) ref|NP\_681031.1| ORF\_ID:tl0240~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP\_681232.1| ORF\_ID:tl0442~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP\_681335.1| ORF\_ID:tl0545~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP\_681541.1| ORF\_ID:tlr0752~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP\_681789.1| ORF\_ID:tlr0999~putative transposase [Thermosynechococcus elongatus BP-1] ref|NP\_682721.1| ORF\_ID:tlr1245~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC07793.1| ORF\_ID:tl0240~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC07994.1| ORF\_ID:tl0442~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC08097.1| ORF\_ID:tl0545~putative transposase [Thermosynechococcus elongatus BP-1] dbj|BAC08303.1| ORF\_ID:tlr0752~p

- 2429.2 Best-BlastP=> >nrprot 69% Identities = 159/294 (54%), Positives = 211/294 (71%), Gaps = 1/294 (0%) ref|NP\_792069.1| moxR protein, putative [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55764.1| moxR protein, putative [Pseudomonas syringae pv. tomato str. DC3000] Length = 305
- 243.2 Best-BlastP=> >nrprot 67% Identities = 163/295 (55%), Positives = 210/295 (71%), Gaps = 1/295 (0%) dbj|BAC95199.1| putative adenine-specific methylase [Vibrio vulnificus YJ016] Length = 310
- 2430.2 Best-BlastP=> >nrprot 63% Identities = 172/365 (47%), Positives = 229/365 (62%), Gaps = 12/365 (3%) ref|NP\_840708.1| Domain of unknown function DUF59 [Nitrosomonas europaea ATCC 19718] emb|CAD84535.1| Domain of unknown function DUF59 [Nitrosomonas europaea ATCC 19718] Length = 361
- 2432.2 Best-BlastP=> >nrprot 70% Identities = 233/378 (61%), Positives = 292/378 (77%) ref|NP\_719320.1| ATP-dependent RNA helicase, DEAD box family [Shewanella oneidensis MR-1] gb|AAN56764.1|AE015812\_3 ATP-dependent RNA helicase, DEAD box family [Shewanella oneidensis MR-1] Length = 535
- 2434.2 Best-BlastP=> >nrprot 70% Identities = 184/388 (47%), Positives = 270/388 (69%), Gaps = 8/388 (2%) ref|NP\_903067.1| probable stearyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] gb|AAQ61061.1| probable stearyl-CoA 9-desaturase [Chromobacterium violaceum ATCC 12472] Length = 405
- 2436.2 Best-BlastP=> >nrprot No Hits found
- 2438.2
- 2439.2 Best-BlastP=> >nrprot 79% Identities = 59/92 (64%), Positives = 75/92 (81%) gb|AAL59720.1| unknown [Vibrio cholerae] Length = 92
- 2439.2 Best-BlastP=> >nrprot 86% Identities = 81/107 (75%), Positives = 93/107 (86%), Gaps = 1/107 (0%) gb|AAL59719.1| unknown [Vibrio cholerae] Length = 107
- 244.1 Best-BlastP=> >nrprot 80% Identities = 230/350 (65%), Positives = 285/350 (81%) dbj|BAC95198.1| chorismate synthase [Vibrio vulnificus YJ016] Length = 377
- 2441.2
- 2442.2 Best-BlastP=> >nrprot 51% Identities = 134/398 (33%), Positives = 209/398 (52%), Gaps = 16/398 (4%) ref|NP\_779202.1| phage-related integrase [Xylella fastidiosa Temecula1] gb|AAO28851.1| phage-related integrase [Xylella fastidiosa Temecula1] Length = 410
- 2442.2 Best-BlastP=> >nrprot 36% Identities = 93/315 (29%), Positives = 158/315 (50%), Gaps = 21/315 (6%) ref|NP\_435846.1| Probable adenylate cyclase [Sinorhizobium meliloti] pir|H95336 probable adenylate cyclase (EC 4.6.1.1) [imported] - Sinorhizobium meliloti (strain 1021) magaplasamid pSymA gb|AAK65258.1| Probable adenylate cyclase [Sinorhizobium meliloti] Length = 584
- 2443.2 Best-BlastP=> >nrprot 36% Identities = 55/232 (23%), Positives = 100/232 (43%), Gaps = 10/232 (4%) ref|ZP\_00068000.1| hypothetical protein [Microbulifer degradans 2-40] Length = 260
- 2445.4 Best-BlastP=> >nrprot 79% Identities = 635/925 (68%), Positives = 746/925 (80%), Gaps = 6/925 (0%) ref|NP\_820536.1| ribonucleoside-diphosphate reductase, alpha subunit [Coxiella burnetii RSA 493] gb|AAO91050.1| ribonucleoside-diphosphate reductase, alpha subunit [Coxiella burnetii RSA 493] Length = 941
- 2447.3 Best-BlastP=> >nrprot 19% Identities = 35/121 (28%), Positives = 62/121 (51%), Gaps = 6/121 (4%) ref|NP\_599246.1| protein associating with small stress protein PASS1 [Rattus norvegicus] gb|AAD48846.1|AF168362\_1 protein associating with small stress protein PASS1 [Rattus norvegicus] Length = 428



- 2448.3 Best-BlastP=> >nrprot 54% Identities = 94/226 (41%), Positives = 142/226 (62%), Gaps = 8/226 (3%) ref|NP\_821052.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91566.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 268
- 245.1 Best-BlastP=> >nrprot 97% Identities = 331/340 (97%), Positives = 332/340 (97%) sp|O31219|DHAS\_LEGPN Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) gb|AAC46292.1| aspartate-B-semialdehyde dehydrogenase [Legionella pneumophila] Length = 347
- 2450.3 Best-BlastP=> >nrprot 67% Identities = 299/616 (48%), Positives = 409/616 (66%), Gaps = 24/616 (3%) ref|NP\_842471.1| ATPase component ABC-type dipeptide/oligopeptide/nickel transport system [Nitrosomonas europaea ATCC 19718] emb|CAD86392.1| ATPase component ABC-type dipeptide/oligopeptide/nickel transport system [Nitrosomonas europaea ATCC 19718] Length = 693
- 2453.4 Best-BlastP=> >nrprot 75% Identities = 554/897 (61%), Positives = 689/897 (76%), Gaps = 3/897 (0%) ref|ZP\_00096570.1| COG0474: Cation transport ATPase [Novosphingobium aromaticivorans] Length = 911
- 2456.2 Best-BlastP=> >nrprot 78% Identities = 201/314 (64%), Positives = 251/314 (79%) ref|NP\_820493.1| acetyl-CoA carboxylase, carboxyl transferase, alpha subunit [Coxiella burnetii RSA 493] gb|AAO91007.1| acetyl-CoA carboxylase, carboxyl transferase, alpha subunit [Coxiella burnetii RSA 493] Length = 316
- 2457.2 Best-BlastP=> >nrprot 46% Identities = 75/215 (34%), Positives = 114/215 (53%), Gaps = 16/215 (7%) ref|ZP\_00107102.1| COG2091: Phosphopantetheinyl transferase [Nostoc punctiforme] Length = 239
- 2458.2 Best-BlastP=> >nrprot 68% Identities = 190/371 (51%), Positives = 259/371 (69%) ref|NP\_819627.1| oxygen-independent coproporphyrinogen III oxidase, putative [Coxiella burnetii RSA 493] gb|AAO90141.1| oxygen-independent coproporphyrinogen III oxidase, putative [Coxiella burnetii RSA 493] Length = 375
- 2459.1 Best-BlastP=> >nrprot 69% Identities = 94/176 (53%), Positives = 131/176 (74%), Gaps = 1/176 (0%) ref|NP\_715832.1| MutT/nudix family protein [Shewanella oneidensis MR-1] gb|AAN53277.1| AE015469\_1 MutT/nudix family protein [Shewanella oneidensis MR-1] Length = 183
- 2460.3 Best-BlastP=> >nrprot 62% Identities = 230/569 (40%), Positives = 358/569 (62%), Gaps = 12/569 (2%) ref|NP\_820129.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] gb|AAO90643.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] Length = 669
- 2461.2 Best-BlastP=> >nrprot 57% Identities = 33/49 (67%), Positives = 41/49 (83%) ref|NP\_051689.1| integrase/recombinase XerD, putative [Deinococcus radiodurans] pir|G75636 probable integrase/recombinase XerD - Deinococcus radiodurans (strain R1) gb|AAF12667.1| AE001827\_5 integrase/recombinase XerD, putative [Deinococcus radiodurans] Length = 236
- 2462.2 Best-BlastP=> >nrprot 33% Identities = 20/38 (52%), Positives = 25/38 (65%) ref|ZP\_00111545.1| COG4644: Transposase and inactivated derivatives, TnpA family [Nostoc punctiforme] Length = 1014
- 2464.2 Best-BlastP=> >nrprot 67% Identities = 61/108 (56%), Positives = 80/108 (74%) ref|NP\_841625.1| transposase [Nitrosomonas europaea ATCC 19718] ref|NP\_842205.1| transposase [Nitrosomonas europaea ATCC 19718] ref|NP\_842439.1| transposase [Nitrosomonas europaea ATCC 19718] emb|CAD85497.1| transposase [Nitrosomonas europaea ATCC 19718] emb|CAD86112.1| transposase [Nitrosomonas europaea ATCC 19718] emb|CAD86359.1| transposase [Nitrosomonas europaea ATCC 19718] Length = 122

- 2466.3 Best-BlastP=> >nrprot 52% Identities = 316/879 (35%), Positives = 473/879 (53%), Gaps = 49/879 (5%) ref|NP\_819380.1| aminopeptidase N [Coxiella burnetii RSA 493] gb|AAO89894.1| aminopeptidase N [Coxiella burnetii RSA 493] Length = 878
- 2468.2 Best-BlastP=> >nrprot 39% Identities = 76/253 (30%), Positives = 122/253 (48%), Gaps = 18/253 (7%) ref|NP\_634577.1| putative hydrolase [Methanosarcina mazei Goe1] gb|AAM32249.1| putative hydrolase [Methanosarcina mazei Goe1] Length = 279
- 2469.2 Best-BlastP=> >nrprot 44% Identities = 138/423 (32%), Positives = 216/423 (51%), Gaps = 7/423 (1%) ref|NP\_798657.1| conserved hypothetical protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60541.1| conserved hypothetical protein [Vibrio parahaemolyticus] Length = 483
- 247.1 Best-BlastP=> >nrprot 29% Identities = 49/120 (40%), Positives = 76/120 (63%) ref|ZP\_00066693.1| COG2840: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 190
- 2471.3
- Best-BlastP=> >nrprot 55% Identities = 129/344 (37%), Positives = 199/344 (57%), Gaps = 6/344 (1%) ref|NP\_819673.1| riboflavin biosynthesis protein RibD [Coxiella burnetii RSA 493] gb|AAO90187.1| riboflavin biosynthesis protein RibD [Coxiella burnetii RSA 493] Length = 354
- 2472.2 Best-BlastP=> >nrprot 61% Identities = 87/219 (39%), Positives = 131/219 (59%), Gaps = 12/219 (5%) ref|NP\_820010.1| dethiobiotin synthetase [Coxiella burnetii RSA 493] gb|AAO90524.1| dethiobiotin synthetase [Coxiella burnetii RSA 493] Length = 242
- 2473.1
- Best-BlastP=> >nrprot 54% Identities = 35/70 (50%), Positives = 48/70 (68%), Gaps = 3/70 (4%) ref|NP\_820541.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91055.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 91
- 2474.1
- Best-BlastP=> >nrprot 72% Identities = 105/192 (54%), Positives = 152/192 (79%), Gaps = 2/192 (1%) ref|NP\_820542.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91056.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 209
- 2477.1
- Best-BlastP=> >nrprot 52% Identities = 68/115 (59%), Positives = 85/115 (73%), Gaps = 2/115 (1%) ref|NP\_819994.1| rare lipoprotein A family protein [Coxiella burnetii RSA 493] gb|AAO90508.1| rare lipoprotein A family protein [Coxiella burnetii RSA 493] Length = 261
- 2479.2 Best-BlastP=> >nrprot No Hits found
- 248.2
- Best-BlastP=> >nrprot 59% Identities = 191/456 (41%), Positives = 278/456 (60%), Gaps = 7/456 (1%) ref|NP\_820284.1| ankyrin repeat domain protein [Coxiella burnetii RSA 493] gb|AAO90798.1| ankyrin repeat domain protein [Coxiella burnetii RSA 493] Length = 465
- 2481.4
- Best-BlastP=> >nrprot 77% Identities = 185/291 (63%), Positives = 231/291 (79%), Gaps = 1/291 (0%) ref|NP\_286072.1| putative phosphonotomutase 2 [Escherichia coli O157:H7 EDL933] ref|NP\_308412.1| putative phosphonotomutase 2 [Escherichia coli O157:H7] pir|A90677 probable phosphonotomutase 2 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir|D85527 probable phosphonotomutase 2 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) gb|AAG54680.1| AE005212\_5 putative phosphonotomutase 2 [Escherichia coli O157:H7 EDL933] dbj|BAB33808.1| putative phosphonotomutase 2 [Escherichia coli O157:H7] Length = 296
- 2482.1
- Best-BlastP=> >nrprot 59% Identities = 75/125 (60%), Positives = 101/125 (80%) ref|NP\_820989.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO91503.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 127
- 2483.2
- Best-BlastP=> >nrprot No Hits found

- 2485.3 Best-BlastP=> >nrprot No Hits found
- 2486.3 Best-BlastP=> >nrprot 55% Identities = 188/514 (36%), Positives = 280/514 (54%), Gaps = 43/514 (8%) ref|ZP\_00087809.1| COG2202: FOG: PAS/PAC domain [Pseudomonas fluorescens PfO-1] Length = 757
- 2488.2 Best-BlastP=> >nrprot No Hits found
- 2489.2 Best-BlastP=> >nrprot No Hits found
- 249.4 Best-BlastP=> >nrprot 97% Identities = 558/575 (97%), Positives = 562/575 (97%), Gaps = 1/575 (0%) gb|AAC12716.1| pilus assembly protein PilB [Legionella pneumophila] Length = 575
- 2490.2 Best-BlastP=> >nrprot No Hits found
- 2492.2 Best-BlastP=> >nrprot No Hits found
- 2493.2 Best-BlastP=> >nrprot 67% Identities = 99/203 (48%), Positives = 135/203 (66%), Gaps = 10/203 (4%) ref|NP\_929371.1| Holliday junction DNA helicase [Photothabdus luminescens subsp. laumondii TTO1] emb|CAE14404.1| Holliday junction DNA helicase [Photothabdus luminescens subsp. laumondii TTO1] Length = 205
- 2495.2 Best-BlastP=> >nrprot 69% Identities = 93/170 (54%), Positives = 121/170 (71%), Gaps = 1/170 (0%) ref|NP\_231481.1| crossover junction endodeoxyribonuclease RuvC [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KR00|RUV\_C\_VIBCH Crossover junction endodeoxyribonuclease ruvC (Holliday junction resolvase ruvC) pir|H82149 crossover junction endodeoxyribonuclease RuvC VC1847 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94995.1| crossover junction endodeoxyribonuclease RuvC [Vibrio cholerae O1 biovar eltor str. N16961] Length = 173
- 25.1 Best-BlastP=> >nrprot 46% Identities = 46/124 (37%), Positives = 72/124 (58%), Gaps = 3/124 (2%) ref|NP\_488674.1| probable cytosine deaminase [Nostoc sp. PCC 7120] pir|AB2385 hypothetical protein alr4634 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB76333.1| ORF\_ID:alr4634~probable cytosine deaminase [Nostoc sp. PCC 7120] Length = 140
- 250.1 Best-BlastP=> >nrprot 98% Identities = 398/406 (98%), Positives = 400/406 (98%) gb|AAC12717.1| pilus assembly protein PilC [Legionella pneumophila] Length = 406
- 2501.2 Best-BlastP=> >nrprot 70% Identities = 213/412 (51%), Positives = 294/412 (71%), Gaps = 12/412 (2%) ref|NP\_819142.1| tolB protein [Coxiella burnetii RSA 493] sp|Q83F59|TOLB\_COXBU TolB protein precursor gb|AAO89656.1| tolB protein [Coxiella burnetii RSA 493] Length = 437
- 2504.4 Best-BlastP=> >nrprot 51% Identities = 106/301 (35%), Positives = 164/301 (54%), Gaps = 34/301 (11%) ref|NP\_718333.1| tolA protein [Shewanella oneidensis MR-1] gb|AAN55777.1|AE015714\_4 tolA protein [Shewanella oneidensis MR-1] Length = 345
- 2506.2 Best-BlastP=> >nrprot 83% Identities = 238/338 (70%), Positives = 282/338 (83%) gb|AAN87043.1| HypE [Thiocapsa roseopersicina] Length = 360
- 2508.3 Best-BlastP=> >nrprot 77% Identities = 234/375 (62%), Positives = 285/375 (76%), Gaps = 6/375 (1%) ref|ZP\_00021585.1| COG0409: Hydrogenase maturation factor [Ralstonia metallidurans] Length = 380
- 2509.3 Best-BlastP=> >nrprot No Hits found
- 251.2 Best-BlastP=> >nrprot 97% Identities = 277/287 (96%), Positives = 281/287 (97%) sp|O68433|LEP4\_LEGPN Type 4 prepilin-like proteins leader peptide processing enzyme [Includes: Leader peptidase (Prepilin peptidase); N-methyltransferase] gb|AAC12718.1| type IV prepilin-like protein specific leader peptidase PilD [Legionella pneumophila] Length = 287

- 2510.2 Best-BlastP=> >nrprot 69% Identities = 310/637 (48%), Positives = 427/637 (67%), Gaps = 19/637 (2%) ref|ZP\_00067611.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Microbulbifer degradans 2-40] Length = 637
- 2514.3 Best-BlastP=> >nrprot 74% Identities = 52/84 (61%), Positives = 67/84 (79%), Gaps = 2/84 (2%) ref|ZP\_00128272.1| COG0851: Septum formation topological specificity factor [Pseudomonas syringae pv. syringae B728a] Length = 84
- 2517.2 Best-BlastP=> >nrprot 65% Identities = 197/336 (58%), Positives = 240/336 (71%), Gaps = 2/336 (0%) ref|NP\_634897.1| L-sorbose dehydrogenase [Methanosarcina mazei Goe1] gb|AAM32569.1| L-sorbose dehydrogenase [Methanosarcina mazei Goe1] Length = 381
- 2518.4 Best-BlastP=> >nrprot 86% Identities = 123/179 (68%), Positives = 156/179 (87%) ref|NP\_250365.1| GTP cyclohydrolase I precursor [Pseudomonas aeruginosa PA01] sp|Q9J351|GC12\_PSEAE GTP cyclohydrolase I 2 (GTP-CH-I.2) pir|C83435 GTP cyclohydrolase I precursor PA1674 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05063.1|AE004595\_2 GTP cyclohydrolase I precursor [Pseudomonas aeruginosa PAO1] Length = 181
- 252.2 Best-BlastP=> >nrprot 40% Identities = 86/303 (28%), Positives = 161/303 (53%), Gaps = 13/303 (4%) ref|NP\_819235.1| CAAX amino terminal protease family protein [Coxiella burnetii RSA 493] gb|AAO89749.1| CAAX amino terminal protease family protein [Coxiella burnetii RSA 493] Length = 297
- 2520.4 Best-BlastP=> >nrprot 73% Identities = 64/111 (57%), Positives = 84/111 (75%), Gaps = 1/111 (0%) ref|NP\_819816.1| HIT family protein [Coxiella burnetii RSA 493] gb|AAO90330.1| HIT family protein [Coxiella burnetii RSA 493] Length = 113
- 2521.4 Best-BlastP=> >nrprot 71% Identities = 205/348 (58%), Positives = 251/348 (72%), Gaps = 1/348 (0%) ref|ZP\_00028857.1| COG1064: Zn-dependent alcohol dehydrogenases [Burkholderia fungorum] Length = 377
- 2522.1 Best-BlastP=> >nrprot No Hits found
- 2523.1 Best-BlastP=> >nrprot 54% Identities = 46/128 (35%), Positives = 73/128 (57%) ref|ZP\_00011417.1| hypothetical protein [Rhodopseudomonas palustris] Length = 135
- 2524.2 Best-BlastP=> >nrprot 51% Identities = 71/192 (36%), Positives = 105/192 (54%), Gaps = 7/192 (3%) sp|Q92J17|DEF2\_RICCN Peptide deformylase 2 (PDF 2) (Polypeptide deformylase 2) Length = 202
- 2526.3 Best-BlastP=> >nrprot 13% Identities = 40/132 (30%), Positives = 59/132 (44%), Gaps = 16/132 (12%) ref|NP\_440029.1| acetyl/polyamine aminohydrolase [Synechocystis sp. PCC 6803] sp|P72702|Y245\_SYNY3 Hypothetical protein slr0245 pir|S74557 acetyl/polyamine aminohydrolase - Synechocystis sp. (strain PCC 6803) dbj|BAA16709.1| acetyl/polyamine aminohydrolase [Synechocystis sp. PCC 6803] Length = 304
- 2528.3 Best-BlastP=> >nrprot 41% Identities = 53/236 (22%), Positives = 105/236 (44%), Gaps = 7/236 (2%) ref|NP\_845027.1| acetyltransferase, GNAT family [Bacillus anthracis str. Ames] gb|AAP26513.1| acetyltransferase, GNAT family [Bacillus anthracis str. Ames] Length = 266
- 2530.3 Best-BlastP=> >nrprot 63% Identities = 266/626 (42%), Positives = 401/626 (64%), Gaps = 8/626 (1%) ref|NP\_900243.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58249.1| potassium uptake protein [Chromobacterium violaceum ATCC 12472] Length = 621

2533.3

Best-BlastP=> >nprot 52% Identities = 88/286 (30%), Positives = 158/286 (55%), Gaps = 4/286 (1%) ref|NP\_763522.1| Transcriptional regulator [Vibrio vulnificus CMCP6] gb|AAO08512.1|AE016813\_264 Transcriptional regulator [Vibrio vulnificus CMCP6] Length = 307

2535.2

Best-BlastP=> >nprot 70% Identities = 200/351 (56%), Positives = 253/351 (72%) ref|NP\_519918.1| PROBABLE PYRUVATE DEHYDROGENASE E1 COMPONENT (ALPHA SUBUNIT) OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum] emb|CAD15499.1| PROBABLE PYRUVATE DEHYDROGENASE E1 COMPONENT (ALPHA SUBUNIT) OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum] Length = 363

2536.2

Best-BlastP=> >nprot 57% Identities = 180/451 (39%), Positives = 255/451 (56%), Gaps = 36/451 (7%) ref|NP\_798254.1| para-aminobenzoate synthase, component I [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60138.1| para-aminobenzoate synthase, component I [Vibrio parahaemolyticus] Length = 454

2538.2

Best-BlastP=> >nprot 78% Identities = 245/394 (62%), Positives = 309/394 (78%) ref|NP\_901758.1| acetyl-CoA C-acetyltransferase [Chromobacterium violaceum ATCC 12472] gb|AAQ59760.1| acetyl-CoA C-acetyltransferase [Chromobacterium violaceum ATCC 12472] Length = 394

254.2

Best-BlastP=> >nprot 49% Identities = 275/851 (32%), Positives = 428/851 (50%), Gaps = 29/851 (3%) ref|NP\_490573.1| ATP-binding protein [Salmonella typhimurium LT2] gb|AAL23492.1| conjugative transfer: assembly [Salmonella typhimurium LT2] Length = 882

2542.2

Best-BlastP=> >nprot 61% Identities = 214/405 (52%), Positives = 282/405 (69%), Gaps = 8/405 (1%) ref|ZP\_00014043.1| COG0260: Leucyl aminopeptidase [Rhodospirillum rubrum] Length = 444

2544.3

Best-BlastP=> >nprot 5% Identities = 36/130 (27%), Positives = 68/130 (52%), Gaps = 7/130 (5%) ref|NP\_711281.1| outer membrane efflux protein [Leptospira interrogans serovar lai str. 56601] gb|AAN48299.1|AE011292\_12 outer membrane efflux protein [Leptospira interrogans serovar lai str. 56601] Length = 533

2545.2

Best-BlastP=> >nprot No Hits found

2546.4

Best-BlastP=> >nprot 47% Identities = 155/432 (35%), Positives = 239/432 (55%), Gaps = 21/432 (4%) emb|CAE02834.1| OSJNBa0043A12.39 [Oryza sativa (japonica cultivar-group)] Length = 487

2549.3

Best-BlastP=> >nprot No Hits found

255.1

Best-BlastP=> >nprot 39% Identities = 23/83 (27%), Positives = 44/83 (53%), Gaps = 1/83 (1%) ref|NP\_762592.1| Unknown [Vibrio vulnificus CMCP6] gb|AAO07582.1|AE016810\_85 Unknown [Vibrio vulnificus CMCP6] Length = 114

2550.2

Best-BlastP=> >nprot 99% Identities = 443/449 (98%), Positives = 446/449 (99%) gb|AAB52239.1| nucleotide binding protein FliI [Legionella pneumophila] Length = 449

2551.2

Best-BlastP=> >nprot 34% Identities = 74/175 (98%), Positives = 74/75 (98%) gb|AAB52238.1| FliH [Legionella pneumophila] Length = 75

2553.3

Best-BlastP=> >nprot 76% Identities = 168/326 (51%), Positives = 251/326 (76%) ref|NP\_791782.1| flagellar motor switch protein FliG [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55477.1| flagellar motor switch protein FliG [Pseudomonas syringae pv. tomato str. DC3000] Length = 333

2555.5

Best-BlastP=> >nprot No Hits found

2557.4

Best-BlastP=> >nprot 61% Identities = 70/135 (51%), Positives = 91/135 (67%) ref|ZP\_00085924.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 141

- 2559.3 Best-BlastP=> >nprot 85% Identities = 243/333 (72%), Positives = 289/333 (86%) ref|NP\_438478.1| Holliday junction DNA helicase [Haemophilus influenzae Rd] sp|P44631|RUVB\_HAEIN Holliday junction DNA helicase ruvB pir|B64061 DNA-binding protein ruvB - Haemophilus influenzae (strain Rd KW20) gb|AAC21975.1| Holliday junction DNA helicase (ruvB) [Haemophilus influenzae Rd] Length = 335
- 256.1 Best-BlastP=> >nprot 52% Identities = 79/194 (40%), Positives = 109/194 (56%), Gaps = 14/194 (7%) ref|NP\_762593.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO07583.1|AE016810\_86 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 226
- 2560.3 Best-BlastP=> >nprot 98% Identities = 186/187 (99%), Positives = 186/187 (99%) gb|AAQ18125.1| RpoE [Legionella pneumophila] Length = 187
- 2562.2 Best-BlastP=> >nprot No Hits found
- 2565.4 Best-BlastP=> >nprot 55% Identities = 88/226 (38%), Positives = 129/226 (57%), Gaps = 17/226 (7%) ref|NP\_651138.1| CG6763-PA [Drosophila melanogaster] gb|AAF56122.1| CG6763-PA [Drosophila melanogaster] gb|AAL68281.1| RE28575p [Drosophila melanogaster] Length = 354
- 2567.2 Best-BlastP=> >nprot 42% Identities = 53/201 (26%), Positives = 92/201 (45%), Gaps = 3/201 (1%) ref|NP\_683243.1| ORF\_ID:tl|2454~unknown protein [Thermosynechococcus elongatus BP-1] dbj|BAC10005.1| ORF\_ID:tl|2454~unknown protein [Thermosynechococcus elongatus BP-1] Length = 253
- 2568.1 Best-BlastP=> >nprot No Hits found
- 2569.3 Best-BlastP=> >nprot 56% Identities = 80/207 (38%), Positives = 122/207 (58%), Gaps = 18/207 (8%) ref|NP\_840655.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD84482.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 253
- 2570.2 Best-BlastP=> >nprot 64% Identities = 144/374 (38%), Positives = 243/374 (64%), Gaps = 4/374 (1%) ref|NP\_518286.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD13693.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 381
- 2571.2 Best-BlastP=> >nprot 64% Identities = 135/292 (46%), Positives = 199/292 (68%), Gaps = 3/292 (1%) ref|ZP\_00056519.1| COG1131: ABC-type multidrug transport system, ATPase component [Magnetospirillum magnetotacticum] Length = 308
- 2573.3 Best-BlastP=> >nprot 98% Identities = 188/192 (97%), Positives = 190/192 (98%) gb|AAK00281.1|AF288536\_3 unknown [Legionella longbeachae] Length = 192
- 2576.2 Best-BlastP=> >nprot 99% Identities = 319/319 (100%), Positives = 319/319 (100%) gb|AAM00641.1| putative Na/Ca antiporter [Legionella pneumophila] Length = 319
- 2578.2 Best-BlastP=> >nprot 99% Identities = 234/234 (100%), Positives = 234/234 (100%) gb|AAM00640.1| unknown [Legionella pneumophila] Length = 234
- 2579.2 Best-BlastP=> >nprot 62% Identities = 54/135 (40%), Positives = 89/135 (65%) ref|NP\_903458.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61450.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 159
- 258.2 Best-BlastP=> >nprot 56% Identities = 161/309 (52%), Positives = 213/309 (68%), Gaps = 4/309 (1%) gb|AAM90716.1| TraU [Salmonella typhi] Length = 331

- 2580.2 Best-BlastP=> >nrprot 78% Identities = 155/249 (62%), Positives = 198/249 (79%) ref|ZP\_00133889.1| COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 258
- 2582.3 Best-BlastP=> >nrprot 47% Identities = 242/883 (27%), Positives = 412/883 (46%), Gaps = 56/883 (6%) ref|NP\_842182.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD86089.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 909
- 2583.3 Best-BlastP=> >nrprot 38% Identities = 40/156 (25%), Positives = 72/156 (46%), Gaps = 23/156 (14%) ref|NP\_764254.1| Na<sup>+</sup>/H<sup>+</sup> antiporter-like protein [Staphylococcus epidermidis ATCC 12228] gb|AAO04296.1|AE016746\_86 Na<sup>+</sup>/H<sup>+</sup> antiporter-like protein [Staphylococcus epidermidis ATCC 12228] Length = 614
- 2585.2 Best-BlastP=> >nrprot 13% Identities = 45/193 (23%), Positives = 77/193 (39%), Gaps = 30/193 (15%) ref|NP\_866179.1| hypothetical protein-transmembrane region and signal peptide prediction [Pirellula sp.] Length = 500
- 2587.2 Best-BlastP=> >nrprot 59% Identities = 114/283 (40%), Positives = 169/283 (59%), Gaps = 4/283 (1%) ref|ZP\_00094776.1| COG0583: Transcriptional regulator [Novosphingobium aromaticivorans] Length = 290
- 2590.3 Best-BlastP=> >nrprot 60% Identities = 125/288 (43%), Positives = 184/288 (63%), Gaps = 3/288 (1%) ref|ZP\_00096382.1| COG0121: Predicted glutamine amidotransferase [Novosphingobium aromaticivorans] Length = 444
- 2591.3 Best-BlastP=> >nrprot 66% Identities = 182/348 (52%), Positives = 234/348 (67%), Gaps = 2/348 (0%) ref|NP\_233382.1| NADH-dependent flavin oxidoreductase, Oye family [Vibrio cholerae O1 biovar eltor str. N16961] pir|JH82391 NADH-dependent flavin oxidoreductase, Oye family VCA0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96894.1| NADH-dependent flavin oxidoreductase, Oye family [Vibrio cholerae O1 biovar eltor str. N16961] Length = 347
- 2592.4 Best-BlastP=> >nrprot No Hits found
- 2593.3
- Best-BlastP=> >nrprot 62% Identities = 98/248 (39%), Positives = 161/248 (64%), Gaps = 7/248 (2%) ref|NP\_250139.1| flagellar biosynthetic protein FlIR [Pseudomonas aeruginosa PA01] pir|B83465 flagellar biosynthetic protein FlIR PA1448 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04837.1|AE004574\_8 flagellar biosynthetic protein FlIR [Pseudomonas aeruginosa PAO1] Length = 258
- 2595.4 Best-BlastP=> >nrprot 77% Identities = 142/241 (58%), Positives = 193/241 (80%), Gaps = 1/241 (0%) ref|NP\_746469.1| flagellar biosynthetic protein FlIP [Pseudomonas putida KT2440] gb|AAD01927.2| FlIP [Pseudomonas putida] gb|AAN69933.1|AE016632\_4 flagellar biosynthetic protein FlIP [Pseudomonas putida KT2440] Length = 251
- 2597.4 Best-BlastP=> >nrprot 99% Identities = 225/226 (99%), Positives = 226/226 (100%) gb|AAM00392.1|AF386079\_2 CcmB [Legionella pneumophila] Length = 226
- 2598.3 Best-BlastP=> >nrprot 59% Identities = 76/216 (35%), Positives = 130/216 (60%), Gaps = 6/216 (2%) ref|NP\_799389.1| conserved hypothetical protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61273.1| conserved hypothetical protein [Vibrio parahaemolyticus] Length = 219
- 2599.4 Best-BlastP=> >nrprot 82% Identities = 380/556 (68%), Positives = 461/556 (82%), Gaps = 2/556 (0%) ref|NP\_927905.1| ATP-binding protein YjyK [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE12850.1| ATP-binding protein YjyK [Photobacterium luminescens subsp. laumondii TTO1] Length = 555



- 26.1 Best-BlastP=> >nrprot 30% Identities = 57/132 (43%), Positives = 81/132 (61%), Gaps = 6/132 (4%) ref|ZP\_00031525.1| hypothetical protein [Burkholderia fungorum] Length = 153
- 2600.4 Best-BlastP=> >nrprot 84% Identities = 239/341 (70%), Positives = 287/341 (84%) ref|NP\_931999.1| threonine 3-dehydrogenase [Photorhabdus laumondii luminescens subsp. laumondii TTO1] emb|CAE17217.1| threonine 3-dehydrogenase [Photorhabdus luminescens subsp. laumondii] Length = 341
- 2602.2 Best-BlastP=> >nrprot 63% Identities = 144/273 (52%), Positives = 188/273 (68%), Gaps = 2/273 (0%) ref|ZP\_00067856.1| COG0061: Predicted sugar kinase [Microbulbifer degradans 2-40] Length = 294
- 2604.3 Best-BlastP=> >nrprot 83% Identities = 437/603 (72%), Positives = 511/603 (84%) ref|ZP\_00043195.1| COG1217: Predicted membrane GTPase involved in stress response [Magnetococcus sp. MC-1] Length = 611
- 2605.3 Best-BlastP=> >nrprot 53% Identities = 300/814 (36%), Positives = 445/814 (54%), Gaps = 23/814 (2%) ref|NP\_111982.1| Type III restriction-modification enzyme, helicase subunit [Thermoplasma volcanium] dbj|BAB60631.1| TVG1539639 [Thermoplasma volcanium] Length = 843
- 2607.2 Best-BlastP=> >nrprot 34% Identities = 87/295 (29%), Positives = 141/295 (47%), Gaps = 10/295 (3%) ref|NP\_827021.1| hypothetical protein [Streptomyces avermitilis MA-4680] dbj|BAC73556.1| hypothetical protein [Streptomyces avermitilis MA-4680] Length = 416
- 2609.2 Best-BlastP=> >nrprot No Hits found
- 2611.1 Best-BlastP=> >nrprot No Hits found
- 2616.1 Best-BlastP=> >nrprot 35% Identities = 58/180 (32%), Positives = 106/180 (58%), Gaps = 1/180 (0%) ref|NP\_624053.1| predicted transposase [Thermoanaerobacter tengcongensis] gb|AAM25657.1| predicted transposase [Thermoanaerobacter tengcongensis] Length = 267
- 2619.1 Best-BlastP=> >nrprot 40% Identities = 37/137 (27%), Positives = 62/137 (45%), Gaps = 39/137 (28%) emb|CAB46580.1| IS1400 transposase B [Yersinia enterocolitica] Length = 294
- 262.3 Best-BlastP=> >nrprot 41% Identities = 123/341 (36%), Positives = 184/341 (53%), Gaps = 21/341 (6%) ref|NP\_827217.1| putative quinolinate synthetase [Streptomyces avermitilis MA-4680] dbj|BAC73752.1| putative quinolinate synthetase [Streptomyces avermitilis MA-4680] Length = 414
- 2620.1 Best-BlastP=> >nrprot 91% Identities = 65/88 (73%), Positives = 81/88 (92%) ref|NP\_395197.1| putative transposase ORFA [Yersinia pestis CO92] ref|NP\_857719.1| low calcium response locus protein S homolog [Yersinia pestis KIM] ref|NP\_857914.1| putative IS element protein [Yersinia pestis KIM] sp|Q00931|L\_CRS\_YERPE Low calcium response locus protein S pir|T43562 probable IS element protein - Yersinia pestis plasmid pCD1 gb|AAA27655.1| lcrS gb|AAC62579.1| low calcium response locus protein S homolog [Yersinia pestis KIM] gb|AAC69827.1| putative IS element protein [Yersinia pestis KIM] emb|CAB54940.1| putative transposase ORFA [Yersinia pestis] Length = 88
- 2622.1 Best-BlastP=> >nrprot 58% Identities = 267/639 (41%), Positives = 378/639 (59%), Gaps = 54/639 (8%) ref|NP\_111983.1| Adenine specific DNA methylase (Mod-related) [Thermoplasma volcanium] dbj|BAB60632.1| modification methylase [Thermoplasma volcanium] Length = 616
- 2624.1 Best-BlastP=> >nrprot 38% Identities = 44/156 (28%), Positives = 71/156 (45%), Gaps = 20/156 (12%) ref|ZP\_00023112.1| hypothetical protein [Ralstonia metallidurans] Length = 348

- 2625.2 Best-BlastP=> >nrrprot 58% Identities = 129/264 (48%), Positives = 170/264 (64%), Gaps = 2/264 (0%) gb|AAM08235.1| LvrA [Legionella pneumophila] Length = 289
- 2626.1 Best-BlastP=> >nrrprot 56% Identities = 80/221 (36%), Positives = 124/221 (56%), Gaps = 16/221 (7%) gb|AAM08234.1| putative phage repressor [Legionella pneumophila] Length = 227
- 2627.1 Best-BlastP=> >nrrprot 79% Identities = 300/397 (75%), Positives = 334/397 (84%), Gaps = 5/397 (1%) gb|AAB05678.1| HeIB Length = 400
- 263.1 Best-BlastP=> >nrrprot 61% Identities = 259/528 (49%), Positives = 339/528 (64%), Gaps = 12/528 (2%) ref|NP\_903600.1| L-aspartate oxidase [Chromobacterium violaceum ATCC 12472] gb|AAQ61592.1| L-aspartate oxidase [Chromobacterium violaceum ATCC 12472] Length = 529
- 2631.4 Best-BlastP=> >nrrprot 94% Identities = 875/974 (89%), Positives = 928/974 (95%) sp|Q48815|HELA\_LEGPN Protein heIA gb|AAB05679.1| HeIA Length = 1052
- 2637.1 Best-BlastP=> >nrrprot No Hits found
- 2639.1
- Best-BlastP=> >nrrprot 53% Identities = 52/149 (34%), Positives = 80/149 (53%), Gaps = 14/149 (9%) ref|NP\_747492.1| hypothetical protein [Pseudomonas putida KT2440] gb|AAN70956.1|AE016739\_9 hypothetical protein [Pseudomonas putida KT2440] Length = 193
- 264.2 Best-BlastP=> >nrrprot 72% Identities = 264/457 (57%), Positives = 333/457 (72%), Gaps = 1/457 (0%) ref|ZP\_00066450.1| COG0015: Adenylosuccinate lyase [Microbulifer degradans 2-40] Length = 459
- 2643.1 Best-BlastP=> >nrrprot 44% Identities = 119/434 (27%), Positives = 193/434 (44%), Gaps = 26/434 (5%) ref|NP\_564271.1| expressed protein [Arabidopsis thaliana] gb|AAF79860.1|AC000348\_13 T7N9.21 [Arabidopsis thaliana] Length = 468
- 2644.1 Best-BlastP=> >nrrprot No Hits found
- 2645.1 Best-BlastP=> >nrrprot 24% Identities = 53/135 (39%), Positives = 80/135 (59%), Gaps = 12/135 (8%) ref|ZP\_00014821.1| hypothetical protein [Rhodospirillum rubrum] Length = 149
- 2646.1 Best-BlastP=> >nrrprot 49% Identities = 45/117 (38%), Positives = 63/117 (53%), Gaps = 1/117 (0%) ref|NP\_386943.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] emb|CAC47416.1| CONSERVED HYPOTHETICAL PROTEIN [Sinorhizobium meliloti] Length = 253
- 2647.2 Best-BlastP=> >nrrprot 72% Identities = 102/185 (55%), Positives = 138/185 (74%), Gaps = 1/185 (0%) ref|NP\_621791.1| 3-Methyladenine DNA glycosylase [Thermoanaerobacter tengcongensis] gb|AAM23395.1| 3-Methyladenine DNA glycosylase [Thermoanaerobacter tengcongensis] Length = 188
- 2648.2 Best-BlastP=> >nrrprot 40% Identities = 98/337 (29%), Positives = 148/337 (43%), Gaps = 67/337 (19%) pir|A42596 major outer membrane protein - Legionella pneumophila gb|AAA25300.1| major outer membrane protein Length = 297
- 2649.1 Best-BlastP=> >nrrprot 45% Identities = 99/375 (26%), Positives = 182/375 (48%), Gaps = 2/375 (0%) ref|ZP\_00026377.1| COG0475: Kef-type K+ transport systems, membrane components [Ralstonia metallidurans] Length = 406
- 2650.1 Best-BlastP=> >nrrprot 64% Identities = 199/424 (46%), Positives = 284/424 (66%), Gaps = 14/424 (3%) ref|ZP\_00031775.1| COG1253: Hemolysins and related proteins containing CBS domains [Burkholderia fungorum] Length = 427
- 2652.2 Best-BlastP=> >nrrprot 46% Identities = 119/354 (33%), Positives = 193/354 (54%), Gaps = 6/354 (1%) gb|AAM00606.1| unknown [Legionella pneumophila] Length = 421

- 2653.1 Best-BlastP=> >nprot No Hits found
- 2654.1 Best-BlastP=> >nprot No Hits found
- 2655.1 Best-BlastP=> >nprot 50% Identities = 35/105 (33%), Positives = 56/105 (53%), Gaps = 6/105 (5%) dbj|BAC93400.1| conserved hypothetical protein [Vibrio vulnificus YJ016] Length = 142
- 2657.3 Best-BlastP=> >nprot 61% Identities = 324/677 (47%), Positives = 455/677 (67%), Gaps = 12/677 (1%) ref|ZP\_00054877.1| COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Magnetospirillum magnetotacticum] Length = 1158
- 2659.2 Best-BlastP=> >nprot 32% Identities = 34/116 (29%), Positives = 54/116 (46%), Gaps = 12/116 (10%) ref|NP\_052947.1| prepropilin [Plasmid R100] sp|P14494|PIL5\_ECOLI\_FIMBRIAL\_PROTEIN\_PRECURSOR (PILIN) pir||YQECR1 fimbrial protein precursor - Escherichia coli plasmid R100-1 gb|AAA92754.1| pilin dbj|BAA78851.1| prepropilin [Plasmid R100] Length = 119
- 2660.1 Best-BlastP=> >nprot 42% Identities = 24/86 (27%), Positives = 41/86 (47%) sp|P12058|TRAL\_SALTI TRAL PROTEIN pir||C25161 traL protein - Salmonella typhimurium plasmid pED208 gb|AAA25608.1| TraL protein [Plasmid pED208] gb|AAM90704.1| TraL [Salmonella typhi] Length = 101
- 2661.2 Best-BlastP=> >nprot 45% Identities = 44/183 (24%), Positives = 85/183 (46%) ref|NP\_932206.1| putative conjugative transfer protein TraE [Vibrio vulnificus YJ016] dbj|BAC97729.1| putative conjugative transfer protein TraE [Vibrio vulnificus YJ016] Length = 200
- 2662.2 Best-BlastP=> >nprot 45% Identities = 72/242 (29%), Positives = 109/242 (45%), Gaps = 19/242 (7%) ref|NP\_762587.1| Unknown [Vibrio vulnificus CMCP6] gb|AAO07577.1| AE016810\_80 Unknown [Vibrio vulnificus CMCP6] Length = 247
- 2665.1 Best-BlastP=> >nprot No Hits found
- 2666.1 Best-BlastP=> >nprot No Hits found
- 2667.1 Best-BlastP=> >nprot No Hits found
- 2669.2 Best-BlastP=> >nprot 20% Identities = 36/154 (23%), Positives = 71/154 (46%), Gaps = 6/154 (3%) ref|XP\_223341.2| similar to KIAA0635 gene product [Rattus norvegicus] Length = 1266
- 267.3 Best-BlastP=> >nprot 68% Identities = 167/307 (54%), Positives = 216/307 (70%), Gaps = 5/307 (1%) ref|NP\_820081.1| tRNA delta(2)-isopentenylpyrophosphate transferase [Coxiella burnetii RSA 493] gb|AAO90595.1| tRNA delta(2)-isopentenylpyrophosphate transferase [Coxiella burnetii RSA 493] Length = 311
- 2670.1 Best-BlastP=> >nprot 16% Identities = 43/143 (30%), Positives = 70/143 (48%), Gaps = 6/143 (4%) ref|NP\_842098.1| possible flagellar hook-length control protein [Nitrosomonas europaea ATCC 19718] emb|CAD85999.1| possible flagellar hook-length control protein [Nitrosomonas europaea ATCC 19718] Length = 381
- 2671.1 Best-BlastP=> >nprot 98% Identities = 203/208 (97%), Positives = 205/208 (98%) sp|P37033|YAC1\_LEGPN Hypothetical 23.7 kDa protein in ACN 5'region pir||A48642 hypothetical protein (acn 5' region) - Legionella pneumophila gb|AAA25294.1| putative Length = 208
- 2674.1 Best-BlastP=> >nprot 99% Identities = 885/891 (99%), Positives = 889/891 (99%) sp|P37032|ACON\_LEGPN Aconitate hydratase (Citrate hydrolyase) (Aconitase) (Major iron-containing protein) (MICP) (IP210) pir||B48642 aconitate hydratase (EC 4.2.1.3) - Legionella pneumophila gb|AAA25295.1| aconitase Length = 891
- 2677.2 Best-BlastP=> >nprot 70% Identities = 231/451 (51%), Positives = 328/451 (72%), Gaps = 1/451 (0%) ref|NP\_820994.1| amino acid antiporter [Coxiella burnetii RSA 493] gb|AAO91508.1| amino acid antiporter [Coxiella burnetii RSA 493] Length = 476

- 268.1 Best-BlastP=> >nrprot 63% Identities = 39/66 (59%), Positives = 45/66 (68%), Gaps = 2/66 (3%) ref|NP\_643775.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38311.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 72
- 2680.1 Best-BlastP=> >nrprot 56% Identities = 93/186 (50%), Positives = 128/186 (68%) ref|NP\_819966.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90480.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 414
- 2682.1 Best-BlastP=> >nrprot 30% Identities = 76/390 (19%), Positives = 169/390 (43%), Gaps = 77/390 (19%) ref|NP\_703923.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD50535.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 947
- 2683.3 Best-BlastP=> >nrprot 64% Identities = 253/483 (52%), Positives = 321/483 (66%), Gaps = 1/483 (0%) ref|NP\_791659.1| succinylglutamic semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55354.1| succinylglutamic semialdehyde dehydrogenase [Pseudomonas syringae pv. tomato str. DC3000] Length = 488
- 2685.2 Best-BlastP=> >nrprot 32% Identities = 47/192 (24%), Positives = 86/192 (44%), Gaps = 4/192 (2%) ref|ZP\_00031024.1| COG0421: Spermidine synthase [Burkholderia fungorum] Length = 252
- 2688.2 Best-BlastP=> >nrprot No Hits found
- 269.1 Best-BlastP=> >nrprot 63% Identities = 159/347 (45%), Positives = 224/347 (64%), Gaps = 2/347 (0%) ref|NP\_820979.1| heptosyl transferase, glycosyltransferase family 9 protein [Coxiella burnetii RSA 493] gb|AAO91493.1| heptosyl transferase, glycosyltransferase family 9 protein [Coxiella burnetii RSA 493] Length = 351
- 2690.2 Best-BlastP=> >nrprot No Hits found
- 2695.2 Best-BlastP=> >nrprot 45% Identities = 55/141 (39%), Positives = 89/141 (63%), Gaps = 6/141 (4%) gb|AAN86353.1| unknown [Listonella pelagia] Length = 195
- 2696.2 Best-BlastP=> >nrprot 70% Identities = 241/483 (49%), Positives = 342/483 (70%), Gaps = 10/483 (2%) ref|ZP\_00117991.1| COG0433: Predicted ATPase [Cytophaga hutchinsonii] Length = 517
- 2698.1 Best-BlastP=> >nrprot 69% Identities = 64/127 (50%), Positives = 89/127 (70%) ref|NP\_522810.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD18400.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 127
- 27.1 Best-BlastP=> >nrprot 37% Identities = 41/149 (27%), Positives = 82/149 (55%), Gaps = 2/149 (1%) ref|NP\_644250.1| hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38786.1| hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 211
- 270.1 Best-BlastP=> >nrprot 61% Identities = 125/278 (44%), Positives = 170/278 (61%), Gaps = 14/278 (5%) gb|AAH53853.1| MGC16638 protein [Homo sapiens] Length = 291
- 2700.2 Best-BlastP=> >nrprot 45% Identities = 112/367 (30%), Positives = 187/367 (50%), Gaps = 6/367 (1%) ref|NP\_907216.1| PUTATIVE EFFLUX PROTEIN [Wolonia succinogenes] emb|CAE10116.1| PUTATIVE EFFLUX PROTEIN [Wolonia succinogenes] Length = 397
- 2702.2 Best-BlastP=> >nrprot 56% Identities = 103/291 (35%), Positives = 165/291 (56%), Gaps = 7/291 (2%) ref|NP\_799583.1| putative transcriptional regulator [Vibrio parahaemolyticus RIMD 2210633] db|BAC61416.1| putative transcriptional regulator [Vibrio parahaemolyticus] Length = 289

- 2704.4 Best-BlastP=> >nprot 45% Identities = 135/395 (34%), Positives = 213/395 (53%), Gaps = 17/395 (4%) ref|NP\_865607.1| probable sensor protein fixL [Pirellula sp.] Length = 651
- 2705.3 Best-BlastP=> >nprot 61% Identities = 173/388 (44%), Positives = 239/388 (61%), Gaps = 16/388 (4%) ref|ZP\_00054896.1| COG3287: Uncharacterized conserved protein [Magnetospirillum magnetotacticum] Length = 376
- 2706.2 Best-BlastP=> >nprot 24% Identities = 72/75 (96%), Positives = 72/75 (96%) gb|AAO61480.1| unknown [Legionella pneumophila] Length = 77
- 2709.1 Best-BlastP=> >nprot 64% Identities = 158/320 (49%), Positives = 212/320 (66%), Gaps = 2/320 (0%) ref|NP\_245036.1| unknown [Pasteurella multocida] gb|AAK02183.1| unknown [Pasteurella multocida] Length = 337
- 271.1 Best-BlastP=> >nprot 29% Identities = 45/133 (33%), Positives = 79/133 (59%), Gaps = 3/133 (2%) ref|NP\_149698.1| 235L [Invertebrate iridescent virus 6] gb|AAK82096.1| AF303741\_235 235L [Chilo iridescent virus] Length = 265
- 2712.1
- Best-BlastP=> >nprot 29% Identities = 57/175 (32%), Positives = 81/175 (46%), Gaps = 13/175 (7%) ref|NP\_231966.1| hypothetical protein VC2335 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 195
- 2713.2
- Best-BlastP=> >nprot 52% Identities = 107/319 (33%), Positives = 178/319 (55%), Gaps = 14/319 (4%) ref|NP\_441143.1| unknown protein [Synechocystis sp. PCC 6803] sp|P73771|YB64\_SYNY3 Hypothetical transport protein sll1164 pir|S74862 hypothetical protein sll1164 - Synechocystis sp. (strain PCC 6803) db|BAA17823.1| ORF\_ID:sll1164~unknown protein [Synechocystis sp. PCC 6803] Length = 349
- 2717.1 Best-BlastP=> >nprot No Hits found
- 2718.1 Best-BlastP=> >nprot 71% Identities = 254/438 (57%), Positives = 324/438 (73%), Gaps = 10/438 (2%) ref|NP\_220059.1| Hexosphosphate Transport [Chlamydia trachomatis] sp|O84548|UHPT\_CHLTR Probable hexose phosphate transport protein pir|A71501 probable hexosphosphate transport - Chlamydia trachomatis (serotype D, strain UW3/Cx) gb|AAC68146.1| Hexosphosphate Transport [Chlamydia trachomatis] Length = 456
- 2721.3 Best-BlastP=> >nprot 67% Identities = 383/736 (52%), Positives = 502/736 (68%), Gaps = 10/736 (1%) ref|ZP\_00095016.1| COG0022: Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, beta subunit [Novosphingobium aromaticivorans] Length = 738
- 2724.3 Best-BlastP=> >nprot 45% Identities = 96/404 (23%), Positives = 177/404 (43%), Gaps = 76/404 (18%) ref|ZP\_00083983.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 524
- 2725.1 Best-BlastP=> >nprot 62% Identities = 39/75 (52%), Positives = 56/75 (74%) ref|NP\_420714.1| flhB-related protein [Caulobacter crescentus CB15] pir|F87485 flhB-related protein [imported] - Caulobacter crescentus gb|AAK23882.1| flhB-related protein [Caulobacter crescentus CB15] Length = 87
- 2726.1 Best-BlastP=> >nprot No Hits found
- 2727.2 Best-BlastP=> >nprot 16% Identities = 70/336 (20%), Positives = 147/336 (43%), Gaps = 50/336 (14%) gb|AAL99918.1| AF432211\_1 CLL-associated antigen KW-11 [Homo sapiens] Length = 460

- 2728.1 Best-BlastP=> >nprot 61% Identities = 49/103 (47%), Positives = 65/103 (63%) ref|NP\_903992.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472]  
Length = 117
- 273.1 Best-BlastP=> >nprot No Hits found
- 2730.1 Best-BlastP=> >nprot No Hits found
- 2732.1 Best-BlastP=> >nprot No Hits found
- 2733.1 Best-BlastP=> >nprot 58% Identities = 133/345 (38%), Positives = 206/345 (59%), Gaps = 12/345 (3%) ref|NP\_437388.1| putative conserved membrane-anchored protein [Sinorhizobium meliloti] pir|H95947 probable conserved membrane-anchored protein Smb21182 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC49248.1| putative conserved membrane-anchored protein [Sinorhizobium meliloti] Length = 394
- 2737.2 Best-BlastP=> >nprot No Hits found
- 2738.2 Best-BlastP=> >nprot 43% Identities = 55/255 (21%), Positives = 112/255 (43%), Gaps = 16/255 (6%) ref|NP\_900118.1| probable ABC transport system permease protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58126.1| probable ABC transport system permease protein [Chromobacterium violaceum ATCC 12472] Length = 257
- 2739.3 Best-BlastP=> >nprot 50% Identities = 67/256 (26%), Positives = 115/256 (44%), Gaps = 51/256 (19%) ref|NP\_518722.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD14131.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 547
- 2741.2 Best-BlastP=> >nprot 52% Identities = 20/40 (50%), Positives = 24/40 (60%) ref|NP\_907600.1| hypothetical protein WS1440 [Wolinella succinogenes] emb|CAE10500.1| hypothetical protein [Wolinella succinogenes] Length = 42
- 2742.2 Best-BlastP=> >nprot 77% Identities = 34/42 (80%), Positives = 34/42 (80%) ref|NP\_759472.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_759895.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_759901.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_760122.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_760328.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_763326.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08316.1|AE016813\_68 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08999.1|AE016798\_159 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09422.1|AE016800\_27 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09428.1|AE016800\_33 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09649.1|AE016800\_254 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 43
- 2743.2 Best-BlastP=> >nprot 82% Identities = 52/66 (78%), Positives = 56/66 (84%) ref|NP\_759471.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_759894.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_759900.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_759939.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_760021.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_760123.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_760329.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_760403.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] ref|NP\_763327.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08317.1|AE016813\_69 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09421.1|AE016800\_26 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09427.1|AE016800\_32 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09466.1|AE016800\_71 Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO09548.1|AE016800\_153 Conserved hypothetical protein [Vibrio vulnificus CMCP6] >nprot No Hits found

- 2747.1 Best-BlastP=> >nprrot 62% Identities = 129/323 (39%), Positives = 203/323 (62%), Gaps = 4/323 (1%) ref|NP\_384238.1| PUTATIVE ADENOSINE DEAMINASE PROTEIN [Sinorhizobium meliloti] sp|Q92T48|ADD\_RHIME Adenosine deaminase (Adenosine aminohydrolase) emb|CAC41519.1| PUTATIVE ADENOSINE DEAMINASE PROTEIN [Sinorhizobium meliloti] Length = 324
- 2748.1 Best-BlastP=> >nprrot No Hits found
- 2749.4 Best-BlastP=> >nprrot 67% Identities = 204/415 (49%), Positives = 283/415 (68%) ref|NP\_819070.1| phosphate transporter family protein [Coxiella burnetii RSA 493] Length = 417
- 2751.1 Best-BlastP=> >nprrot 48% Identities = 83/226 (36%), Positives = 125/226 (55%), Gaps = 5/226 (2%) ref|NP\_212383.1| phosphatidyltransferase [Borrelia burgdorferi] pir|A70131| phosphatidyltransferase homolog - Lyme disease spirochete gb|AAB91497.1| phosphatidyltransferase [Borrelia burgdorferi B31] Length = 234
- 2752.1 Best-BlastP=> >nprrot 49% Identities = 53/167 (31%), Positives = 81/167 (48%), Gaps = 14/167 (8%) ref|NP\_819930.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO90444.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 169
- 2753.1 Best-BlastP=> >nprrot No Hits found
- 2754.2 Best-BlastP=> >nprrot 72% Identities = 109/184 (59%), Positives = 134/184 (72%) ref|NP\_820271.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90785.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 185
- 2755.1 Best-BlastP=> >nprrot 29% Identities = 102/461 (22%), Positives = 198/461 (42%), Gaps = 56/461 (12%) ref|NP\_788908.1| CG33206-PB [Drosophila melanogaster] gb|AAF48467.2| CG33206-PB [Drosophila melanogaster] Length = 1208
- 2757.1 Best-BlastP=> >nprrot 73% Identities = 78/148 (52%), Positives = 110/148 (74%) ref|ZP\_00125250.1| COG0359: Ribosomal protein L9 [Pseudomonas syringae pv. syringae B728a] ref|NP\_794663.1| ribosomal protein L9 [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58358.1| ribosomal protein L9 [Pseudomonas syringae pv. tomato str. DC3000] Length = 148
- 2759.1 Best-BlastP=> >nprrot 40% Identities = 74/283 (26%), Positives = 130/283 (45%), Gaps = 14/283 (4%) ref|NP\_819885.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90399.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 299
- 276.1 Best-BlastP=> >nprrot 25% Identities = 20/25 (80%), Positives = 20/25 (80%), Gaps = 1/25 (4%) ref|NP\_084281.1| RIKEN cDNA A030005K14 [Mus musculus] dbj|BAB32176.1| unnamed protein product [Mus musculus] Length = 122
- 2760.1 Best-BlastP=> >nprrot 85% Identities = 53/75 (70%), Positives = 65/75 (86%) ref|NP\_240367.1| 30S ribosomal protein S18 [Buchnera aphidicola str. APS (Acyrtosiphon pisum)] sp|P57626|RS18\_BUCAI 30S ribosomal protein S18 pir|E84995 30S ribosomal protein S18 [imported] - Buchnera sp. (strain APS) dbj|BAB13253.1| 30S ribosomal protein S18 [Buchnera aphidicola str. APS (Acyrtosiphon pisum)] Length = 75
- 2761.1 Best-BlastP=> >nprrot 75% Identities = 70/107 (65%), Positives = 85/107 (79%) ref|NP\_903310.1| 30S ribosomal protein S6 [Chromobacterium violaceum ATCC 12472] gb|AAQ61302.1| 30S ribosomal protein S6 [Chromobacterium violaceum ATCC 12472] Length = 124
- 2763.2 Best-BlastP=> >nprrot No Hits found
- 2765.2 Best-BlastP=> >nprrot 33% Identities = 48/222 (21%), Positives = 99/222 (44%), Gaps = 21/222 (9%) ref|NP\_106991.1| unknown protein [Mesorhizobium loti] dbj|BAB52777.1| unknown protein [Mesorhizobium loti] Length = 328
- 2767.1 Best-BlastP=> >nprrot No Hits found



2769.2

Best-BlastP=> >nrrprot 53% Identities = 203/594 (34%), Positives = 317/594 (53%), Gaps = 26/594 (4%) ref|NP\_266737.1| hypothetical protein [Lactococcus lactis subsp. lactis] pir|E86697 conserved hypothetical protein yfhG [imported] - Lactococcus lactis subsp. lactis (strain IL1403) gb|AAK04679.1|AE006291\_13 conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 598

277.1

Best-BlastP=> >nrrprot 41% Identities = 60/196 (30%), Positives = 99/196 (50%), Gaps = 18/196 (9%) ref|NP\_436484.1| hypothetical protein [Sinorhizobium meliloti] pir|F95416 hypothetical protein Sma2299 [imported] - Sinorhizobium meliloti (strain 1021) magaplasamid pSymA gb|AAK65896.1| hypothetical protein [Sinorhizobium meliloti] Length = 308

2770.1

Best-BlastP=> >nrrprot 65% Identities = 114/240 (47%), Positives = 153/240 (63%), Gaps = 14/240 (5%) ref|NP\_867184.1| short chain alcohol dehydrogenase-like [Pirellula sp.] emb|CAD74729.1| short chain alcohol dehydrogenase-like [Pirellula sp.] Length = 247

2771.2

Best-BlastP=> >nrrprot 66% Identities = 205/386 (53%), Positives = 260/386 (67%), Gaps = 1/386 (0%) ref|NP\_355900.1| AGR\_L\_236p [Agrobacterium tumefaciens] ref|NP\_535243.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|C98145 hypothetical protein AGR\_L\_236 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AI3142 conserved hypothetical protein Atu4765 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88685.1| AGR\_L\_236p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL45559.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 507

2772.1

Best-BlastP=> >nrrprot 51% Identities = 40/131 (30%), Positives = 71/131 (54%), Gaps = 12/131 (9%) ref|NP\_469941.1| lin0598 [Listeria innocua] pir|IAF1507 hypothetical protein lin0598 [imported] - Listeria innocua (strain Clip11262) emb|CAC95830.1| lin0598 [Listeria innocua] Length = 138

2774.1

Best-BlastP=> >nrrprot 69% Identities = 152/286 (53%), Positives = 204/286 (71%) ref|NP\_697358.1| transcriptional regulator, LysR family [Brucella suis 1330] gb|AAN29273.1|AE014344\_8 transcriptional regulator, LysR family [Brucella suis 1330] Length = 296

2775.1

Best-BlastP=> >nrrprot 50% Identities = 31/52 (59%), Positives = 36/52 (69%), Gaps = 3/52 (5%) ref|ZP\_00021959.1| COG3024:

Uncharacterized protein conserved in bacteria [Ralstonia metallidurans] Length = 63

2777.1

Best-BlastP=> >nrrprot 64% Identities = 174/343 (50%), Positives = 232/343 (67%), Gaps = 5/343 (1%) ref|NP\_780210.1| phosphoribosylaminoimidazole carboxylase, ATPase subunit [Xylella fastidiosa Temecula1] gb|AAO29859.1| phosphoribosylaminoimidazole carboxylase, ATPase subunit [Xylella fastidiosa Temecula1] Length = 394

2778.2

Best-BlastP=> >nrrprot 82% Identities = 113/160 (70%), Positives = 138/160 (86%) ref|ZP\_00066669.1| COG0041:

Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase [Microbulbifer degradans 2-40] Length = 168

278.3

Best-BlastP=> >nrrprot 51% Identities = 218/623 (34%), Positives = 331/623 (53%), Gaps = 47/623 (7%) ref|NP\_070765.1| phosphoribosylformylglycinamide synthase II (purl) [Archaeoglobus fulgidus DSM 4304] sp|O28339|PURL\_ARCFU  
Phosphoribosylformylglycinamide synthase II (FGAM synthase II) pir|C69492 phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component II - Archaeoglobus fulgidus gb|AAB8931.1| phosphoribosylformylglycinamide synthase II (purl) [Archaeoglobus fulgidus DSM 4304] Length = 765

2780.2

Best-BlastP=> >nrrprot 57% Identities = 116/273 (42%), Positives = 162/273 (59%), Gaps = 3/273 (1%) ref|NP\_925031.1| hypothetical protein gir2085 [Gloeobacter violaceus] dbj|BAC90026.1| gir2085 [Gloeobacter violaceus] Length = 288

2781.1

Best-BlastP=> >nrrprot 70% Identities = 49/103 (47%), Positives = 75/103 (72%) ref|NP\_213586.1| putative protein [Aquifex aeolicus] pir|F70374 hypothetical protein aq\_862 - Aquifex aeolicus gb|AAC06993.1| putative protein [Aquifex aeolicus VF5] Length = 109

- 2784.3 Best-BlastP=> >nrprot 49% Identities = 36/80 (45%), Positives = 52/80 (65%) ref|NP\_931069.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16236.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 124
- 2785.1 Best-BlastP=> >nrprot 71% Identities = 153/265 (57%), Positives = 202/265 (76%), Gaps = 1/265 (0%) ref|NP\_819150.1| nicotinate-nucleotide pyrophosphorylase [Coxiella burnetii RSA 493] gb|AAO89664.1| nicotinate-nucleotide pyrophosphorylase [Coxiella burnetii RSA 493] Length = 274
- 2788.1 Best-BlastP=> >nrprot 54% Identities = 158/473 (33%), Positives = 263/473 (55%), Gaps = 39/473 (8%) ref|NP\_485346.1| Na<sup>+</sup>/H<sup>+</sup> antiporter [Nostoc sp. PCC 7120] pir|AD1969 Na<sup>+</sup>/H<sup>+</sup> antiporter [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB73260.1| Na<sup>+</sup>/H<sup>+</sup> antiporter [Nostoc sp. PCC 7120] Length = 470
- 2791.1 Best-BlastP=> >nrprot 82% Identities = 537/779 (68%), Positives = 655/779 (84%), Gaps = 5/779 (0%) ref|NP\_310436.1| phosphoenolpyruvate synthase [Escherichia coli O157:H7] pir|A90930 phosphoenolpyruvate synthase [imported] - Escherichia coli (strain RIMD 0509952) dbj|BAB35832.1| phosphoenolpyruvate synthase [Escherichia coli O157:H7] Length = 792
- 2792.1 Best-BlastP=> >nrprot No Hits found
- 2793.1 Best-BlastP=> >nrprot 50% Identities = 100/343 (29%), Positives = 170/343 (49%), Gaps = 28/343 (8%) ref|NP\_233263.1| hydrolase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir|E82406 probable hydrolase VCA0877 [imported] - Vibrio cholerae (strain serogroup O1) gb|AAF96775.1| hydrolase, putative [Vibrio cholerae O1 biovar eltor str. N16961] Length = 358
- 2794.2 Best-BlastP=> >nrprot 44% Identities = 152/532 (28%), Positives = 250/532 (46%), Gaps = 31/532 (5%) ref|NP\_00029700.1| COG1960: Acyl-CoA dehydrogenases [Burkholderia fungorum] Length = 587
- 2795.1 Best-BlastP=> >nrprot 87% Identities = 60/88 (68%), Positives = 78/88 (88%) ref|NP\_395197.1| putative transposase ORFA [Yersinia pestis CO92] ref|NP\_857719.1| low calcium response locus protein S homolog [Yersinia pestis KIM] ref|NP\_857914.1| putative IS element protein [Yersinia pestis KIM] sp|Q00931|LCRS\_YERPE Low calcium response locus protein S. pir|T43562 probable IS element protein - Yersinia pestis plasmid pCD1 gb|AAA27655.1| lcrS gb|AAC62579.1| low calcium response locus protein S homolog [Yersinia pestis KIM] gb|AAC69827.1| putative IS element protein [Yersinia pestis KIM] emb|CAB54940.1| putative transposase ORFA [Yersinia pestis] Length = 88
- 2799.1 Best-BlastP=> >nrprot 67% Identities = 71/126 (56%), Positives = 91/126 (72%) ref|NP\_867058.1| aspartate 1-decarboxylase [Pirellula sp.] emb|CAD74603.1| aspartate 1-decarboxylase [Pirellula sp.] Length = 156
- 2800.1 Best-BlastP=> >nrprot 66% Identities = 136/258 (52%), Positives = 172/258 (66%), Gaps = 3/258 (1%) ref|NP\_719181.1| dimethyladenosine transferase [Shewanella oneidensis MR-1] sp|Q8EB93|KSGA\_SHEON Dimethyladenosine transferase (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) (16S rRNA dimethylase) (High level kasugamycin resistance protein ksgA) (Kasugamycin dimethyltransferase) gb|AAN56625.1|AE015799\_12 dimethyladenosine transferase [Shewanella oneidensis MR-1] Length = 268
- 2804.1 Best-BlastP=> >nrprot 63% Identities = 232/443 (52%), Positives = 286/443 (64%), Gaps = 2/443 (0%) ref|NP\_629805.1| putative 4-aminobutyrate aminotransferase [Streptomyces coelicolor A3(2)] pir|T35794 probable 4-aminobutyrate aminotransferase - Streptomyces coelicolor emb|CAA20213.1| putative 4-aminobutyrate aminotransferase [Streptomyces coelicolor A3(2)] Length = 444

- 2806.1 Best-BlastP=> >nprot 76% Identities = 118/196 (60%), Positives = 153/196 (78%) ref|NP\_249757.1| probable short-chain dehydrogenase [Pseudomonas aeruginosa PAO1] pir|H83512 probable short-chain dehydrogenase PA1066 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04455.1|AE004538.7 probable short-chain dehydrogenase [Pseudomonas aeruginosa PAO1] Length = 218
- 2807.1 Best-BlastP=> >nprot 71% Identities = 54/113 (47%), Positives = 81/113 (71%), Gaps = 5/113 (4%) ref|NP\_798658.1| arsenate reductase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60542.1| arsenate reductase [Vibrio parahaemolyticus] Length = 116
- 2808.1 Best-BlastP=> >nprot 60% Identities = 39/83 (46%), Positives = 56/83 (67%), Gaps = 1/83 (1%) gb|AAL07519.1| RNA-binding protein precursor [Solanium tuberosum] Length = 339
- 2810.1 Best-BlastP=> >nprot 48% Identities = 130/457 (28%), Positives = 218/457 (47%), Gaps = 24/457 (5%) emb|CAD48863.1| EefC outer membrane protein [Enterobacter aerogenes] Length = 454
- 2811.2 Best-BlastP=> >nprot 25% Identities = 43/179 (24%), Positives = 89/179 (49%), Gaps = 4/179 (2%) ref|NP\_820323.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO90837.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 377
- 2815.2 Best-BlastP=> >nprot 9% Identities = 31/89 (34%), Positives = 54/89 (60%) ref|NP\_819452.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89966.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 262
- 2816.2 Best-BlastP=> >nprot 50% Identities = 191/730 (26%), Positives = 361/730 (49%), Gaps = 43/730 (5%) ref|ZP\_00055987.1| COG0659: Sulfate permease and related transporters (MFS superfamily) [Magnetospirillum magnetotacticum] Length = 733
- 2818.1 Best-BlastP=> >nprot 61% Identities = 155/372 (41%), Positives = 219/372 (58%), Gaps = 37/372 (9%) gb|AAK97454.1|AF388182\_2 alkane-1-monooxygenase [Rhodococcus sp. Q15] Length = 408
- 282.2 Best-BlastP=> >nprot 53% Identities = 58/179 (32%), Positives = 103/179 (57%), Gaps = 12/179 (6%) ref|NP\_900154.1| probable type IV prelin [Chromobacterium violaceum ATCC 12472] gb|AAQ58161.1| probable type IV prelin [Chromobacterium violaceum ATCC 12472] Length = 185
- 2820.1 Best-BlastP=> >nprot 64% Identities = 145/273 (53%), Positives = 183/273 (67%), Gaps = 4/273 (1%) ref|NP\_439796.1| hypothetical protein [Haemophilus influenzae Rd] sp|P45298|YRAL\_HAEIN Hypothetical protein HI1654 pir|A64174 hypothetical protein HI1654 - Haemophilus influenzae (strain Rd KW20) gb|AAC23298.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 283
- 2822.1 Best-BlastP=> >nprot 52% Identities = 202/610 (33%), Positives = 315/610 (51%), Gaps = 29/610 (4%) ref|ZP\_00137912.1| COG3107: Putative lipoprotein [Pseudomonas aeruginosa UCBPP-PA14] Length = 604
- 2824.1 Best-BlastP=> >nprot 72% Identities = 83/138 (60%), Positives = 102/138 (73%) ref|NP\_254240.1| ATP synthase epsilon chain [Pseudomonas aeruginosa PAO1] sp|Q9HT21|ATPE\_PSEAE ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) pir|B82952 ATP synthase epsilon chain PA5553 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08938.1|AE004967\_9 ATP synthase epsilon chain [Pseudomonas aeruginosa PAO1] Length = 141
- 2826.1 Best-BlastP=> >nprot 42% Identities = 110/540 (20%), Positives = 217/540 (40%), Gaps = 94/540 (17%) ref|ZP\_00144200.1| EXONUCLEASE SBCC [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb|EAA24200.1| EXONUCLEASE SBCC [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 921
- 2827.3 Best-BlastP=> >nprot No Hits found

- 2828.3 Best-BlastP=> >nrprot 72% Identities = 29/52 (55%), Positives = 36/52 (69%), Gaps = 2/52 (3%) ref|NP\_885117.1| phosphatidylserine decarboxylase proenzyme [Bordetella parapertussis] emb|CAE38217.1| phosphatidylserine decarboxylase proenzyme [Bordetella parapertussis] Length = 328
- 283.1 Best-BlastP=> >nrprot 47% Identities = 52/142 (36%), Positives = 86/142 (60%), Gaps = 8/142 (5%) ref|NP\_900149.1| probable type-4 fimbrial biogenesis protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58156.1| probable type-4 fimbrial biogenesis protein [Chromobacterium violaceum ATCC 12472] Length = 159
- 2830.3 Best-BlastP=> >nrprot No Hits found
- 2831.1 Best-BlastP=> >nrprot 47% Identities = 71/219 (32%), Positives = 106/219 (48%), Gaps = 10/219 (4%) ref|NP\_801239.1| transcriptional regulator, LuxR family [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC63072.1| transcriptional regulator, LuxR family [Vibrio parahaemolyticus] Length = 251
- 2833.1 Best-BlastP=> >nrprot 56% Identities = 125/332 (37%), Positives = 186/332 (56%), Gaps = 22/332 (6%) sp|Q56686|CPDP\_VIBFI 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE PRECURSOR (PDEASE) (3':5'-CNP) pir|A40602 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - Vibrio fischeri gb|AAA27513.1| cpdP Length = 330
- 2835.1 Best-BlastP=> >nrprot 70% Identities = 151/281 (53%), Positives = 200/281 (71%), Gaps = 1/281 (0%) ref|NP\_754359.1| Putative 3-hydroxyacyl-CoA dehydrogenase [Escherichia coli CFT073] gb|AAN80926.1| AE016762\_179 Putative 3-hydroxyacyl-CoA dehydrogenase [Escherichia coli CFT073] Length = 289
- 2838.1 Best-BlastP=> >nrprot 67% Identities = 176/365 (48%), Positives = 253/365 (69%) ref|ZP\_00110259.1| COG1960: Acyl-CoA dehydrogenases [Nostoc punctiforme] Length = 395
- 284.2 Best-BlastP=> >nrprot 57% Identities = 128/361 (35%), Positives = 203/361 (56%), Gaps = 24/361 (6%) ref|NP\_900150.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58157.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 354
- 2840.1 Best-BlastP=> >nrprot 62% Identities = 225/502 (44%), Positives = 316/502 (62%), Gaps = 9/502 (1%) pir|T44808 mycosubtilin synthetase mycC [imported] - Bacillus subtilis gb|AAF08797.1| AF184956\_4 MycC [Bacillus subtilis] Length = 2609
- 2841.4 Best-BlastP=> >nrprot 58% Identities = 175/439 (39%), Positives = 259/439 (58%), Gaps = 14/439 (3%) ref|ZP\_00111186.1| COG3321: Polyketide synthase modules and related proteins [Nostoc punctiforme] Length = 1853
- 2847.4 Best-BlastP=> >nrprot No Hits found
- 2848.4 Best-BlastP=> >nrprot No Hits found
- 2849.1 Best-BlastP=> >nrprot No Hits found
- 2858.1 Best-BlastP=> >nrprot 28% Identities = 23/33 (69%), Positives = 24/33 (72%) pir|A44803 pG1 protein - human (fragment) Length = 75
- 2859.2 Best-BlastP=> >nrprot 76% Identities = 254/393 (64%), Positives = 308/393 (78%) ref|NP\_716935.1| tyrosyl-tRNA synthetase [Shewanella oneidensis MR-1] gb|AAN54380.1| AE015575\_6 tyrosyl-tRNA synthetase [Shewanella oneidensis MR-1] Length = 398
- 286.2 Best-BlastP=> >nrprot 48% Identities = 48/165 (29%), Positives = 83/165 (50%), Gaps = 18/165 (10%) ref|NP\_900151.1| hypothetical protein CV0481 [Chromobacterium violaceum ATCC 12472] gb|AAQ58158.1| hypothetical protein CV0481 [Chromobacterium violaceum ATCC 12472] Length = 168

- 2861.1 Best-BlastP=> >nrprot 67% Identities = 131/262 (50%), Positives = 185/262 (70%), Gaps = 1/262 (0%) ref|NP\_000680001.1| COG3220: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 290
- 2862.1 Best-BlastP=> >nrprot 52% Identities = 142/396 (35%), Positives = 210/396 (53%), Gaps = 7/396 (1%) ref|NP\_349992.1| Dipeptidyl aminopeptidase/acylaminoacyl-peptidase related protein [Clostridium acetobutylicum] pir|JA97318 dipeptidyl aminopeptidase/acylaminoacyl-peptidase related protein [imported] - Clostridium acetobutylicum gb|AAK81332.1|AE007837\_10 Dipeptidyl aminopeptidase/acylaminoacyl-peptidase related protein [Clostridium acetobutylicum] Length = 400
- 2863.1 Best-BlastP=> >nrprot 35% Identities = 46/117 (39%), Positives = 68/117 (58%), Gaps = 4/117 (3%) ref|NP\_00008611.1| COG0845: Membrane-fusion protein [Rhodospseudomonas palustris] Length = 267
- 2866.1 Best-BlastP=> >nrprot 78% Identities = 276/431 (64%), Positives = 347/431 (80%), Gaps = 1/431 (0%) ref|NP\_901043.1| probable oxidoreductase [Chromobacterium violaceum ATCC 12472] gb|AAQ59048.1| probable oxidoreductase [Chromobacterium violaceum ATCC 12472] Length = 438
- 2868.1 Best-BlastP=> >nrprot 60% Identities = 247/585 (42%), Positives = 357/585 (61%), Gaps = 15/585 (2%) ref|NP\_820704.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] gb|AAO91218.1| thiol:disulfide interchange protein DsbD [Coxiella burnetii RSA 493] Length = 584
- 2869.1 Best-BlastP=> >nrprot 98% Identities = 96/96 (100%), Positives = 96/96 (100%) sp|P26879|CH10\_LEGPN 10 kDa chaperonin (Protein Cpn10) (groES protein) (Heat shock protein A) pir|B41468 heat shock protein groES - Legionella pneumophila gb|AAA25297.1| htpA Length = 96
- 2873.1 Best-BlastP=> >nrprot 40% Identities = 66/274 (24%), Positives = 130/274 (47%), Gaps = 16/274 (5%) ref|NP\_692096.1| hypothetical protein [Oceanobacillus thelyensis HTE831] dbj|BAC13131.1| hypothetical conserved protein [Oceanobacillus thelyensis HTE831] Length = 314
- 2874.1 Best-BlastP=> >nrprot 59% Identities = 111/225 (49%), Positives = 155/225 (68%), Gaps = 1/225 (0%) ref|NP\_662190.1| hypothetical protein [Chlorobium tepidum TLS] gb|AAM72532.1| hypothetical protein [Chlorobium tepidum TLS] Length = 232
- 2877.2 Best-BlastP=> >nrprot 49% Identities = 71/206 (34%), Positives = 109/206 (52%), Gaps = 3/206 (1%) ref|NP\_902629.1| hypothetical protein CV2959 [Chromobacterium violaceum ATCC 12472] gb|AAQ60627.1| hypothetical protein CV2959 [Chromobacterium violaceum ATCC 12472] Length = 214
- 2878.2 Best-BlastP=> >nrprot 98% Identities = 226/230 (98%), Positives = 228/230 (99%) gb|AAK00284.1|AF288536\_6 possible transcriptional regulatory protein [Legionella longbeachae] Length = 230
- 2879.3 Best-BlastP=> >nrprot 96% Identities = 419/444 (94%), Positives = 430/444 (96%), Gaps = 2/444 (0%) gb|AAK00283.1|AF288536\_5 unknown [Legionella longbeachae] Length = 444
- 2881.2 Best-BlastP=> >nrprot 93% Identities = 270/302 (89%), Positives = 281/302 (93%), Gaps = 1/302 (0%) gb|AAK00282.1|AF288536\_4 unknown [Legionella longbeachae] Length = 302
- 2882.2 Best-BlastP=> >nrprot 76% Identities = 146/221 (66%), Positives = 175/221 (79%), Gaps = 1/221 (0%) ref|NP\_249667.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] ref|NP\_00138566.1| COG0603: Predicted PP-loop superfamily ATPase [Pseudomonas aeruginosa UCBPP-PA14] pir|E83522 conserved hypothetical protein PA0976 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04365.1|AE004531\_2 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] gb|AAP82946.1| conserved hypothetical protein [Pseudomonas aeruginosa] Length = 224

- 2884.1 Best-BlastP=> >nrprot No Hits found
- 2889.2 Best-BlastP=> >nrprot 69% Identities = 72/124 (58%), Positives = 90/124 (72%) ref|NP\_719248.1| membrane protein, putative [Shewanella oneidensis MR-1] gb|AAN56692.1|AE015805\_1 membrane protein, putative [Shewanella oneidensis MR-1] Length = 127
- 2891.2 Best-BlastP=> >nrprot 58% Identities = 235/584 (40%), Positives = 358/584 (61%), Gaps = 4/584 (0%) ref|NP\_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589
- 2893.2 Best-BlastP=> >nrprot 51% Identities = 263/741 (35%), Positives = 402/741 (54%), Gaps = 32/741 (4%) ref|ZP\_00080393.1| hypothetical protein [Geobacter metallireducens] Length = 768
- 2898.4 Best-BlastP=> >nrprot 61% Identities = 27/72 (37%), Positives = 47/72 (65%) ref|NP\_660683.1| acyl-carrier protein [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp|Q8K9J4|ACP\_BUCAP Acyl carrier protein (ACP) gb|AAM67894.1| acyl-carrier protein [Buchnera aphidicola str. Sg (Schizaphis graminum)] Length = 79
- 29.1 Best-BlastP=> >nrprot 39% Identities = 26/62 (41%), Positives = 38/62 (61%) gb|AAO43539.1| probable conjugal transfer protein TraD [Rhizobium etli] Length = 71
- 290.2 Best-BlastP=> >nrprot 58% Identities = 501/1050 (47%), Positives = 679/1050 (64%), Gaps = 57/1050 (5%) ref|NP\_900152.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58159.2| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 1040
- 2900.2 Best-BlastP=> >nrprot 50% Identities = 121/308 (39%), Positives = 170/308 (55%), Gaps = 4/308 (1%) ref|NP\_829350.1| 3-oxoacyl-(acyl-carrier-protein) synthase III [Chlamydomophila caviae GPIC] gb|AAP05228.1| 3-oxoacyl-(acyl-carrier-protein) synthase III [Chlamydomophila caviae GPIC] Length = 335
- 2905.2 Best-BlastP=> >nrprot No Hits found
- 2906.2 Best-BlastP=> >nrprot 62% Identities = 95/201 (47%), Positives = 127/201 (63%), Gaps = 1/201 (0%) ref|NP\_929829.1| Glutathione S-transferase [Photorhabdus luminescens subsp. laumondii TTO1] embl|CAE14968.1| Glutathione S-transferase [Photorhabdus luminescens subsp. laumondii TTO1] Length = 201
- 2908.2 Best-BlastP=> >nrprot No Hits found
- 2909.1 Best-BlastP=> >nrprot 54% Identities = 137/387 (35%), Positives = 210/387 (54%), Gaps = 25/387 (6%) ref|NP\_441897.1| D-alanyl-D-alanine carboxypeptidase [Synecocystis sp. PCC 6803] pir|S76446 hypothetical protein - Synecocystis sp. (strain PCC 6803) dbj|BAA18575.1| D-alanyl-D-alanine carboxypeptidase [Synecocystis sp. PCC 6803] Length = 400
- 291.4 Best-BlastP=> >nrprot 79% Identities = 283/419 (67%), Positives = 342/419 (81%) ref|NP\_820426.1| NADH dehydrogenase I, F subunit [Coxiella burnetii RSA 493] gb|AAO90940.1| NADH dehydrogenase I, F subunit [Coxiella burnetii RSA 493] Length = 422
- 2910.1 Best-BlastP=> >nrprot 73% Identities = 272/465 (58%), Positives = 348/465 (74%), Gaps = 1/465 (0%) ref|NP\_928701.1| glutamyl-tRNA synthetase, catalytic subunit [Photorhabdus luminescens subsp. laumondii TTO1] embl|CAE13694.1| glutamyl-tRNA synthetase, catalytic subunit [Photorhabdus luminescens subsp. laumondii TTO1] Length = 472

- 2911.3 Best-BlastP=> >nrprot 58% Identities = 47/95 (49%), Positives = 62/95 (65%) ref|NP\_931076.1| BoA protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE16243.1| BoA protein [Photobacterium luminescens subsp. laumondii TTO1] Length = 104
- 2914.1 Best-BlastP=> >nrprot 60% Identities = 90/225 (40%), Positives = 135/225 (60%), Gaps = 15/225 (6%) ref|NP\_759151.1| Inactive homolog of metal-dependent proteases [Vibrio vulnificus CMCP6] gb|AAO08678.1|AE016797\_133 Inactive homolog of metal-dependent proteases [Vibrio vulnificus CMCP6] Length = 233
- 2915.2 Best-BlastP=> >nrprot 8% Identities = 45/199 (22%), Positives = 77/199 (38%), Gaps = 4/199 (2%) ref|NP\_497967.1| cyclin-like F-box (3F797) [Caenorhabditis elegans] pir|T24435 hypothetical protein T04A8.13 - Caenorhabditis elegans emb|CAA84732.2| Hypothetical protein T04A8.13 [Caenorhabditis elegans] Length = 791
- 2916.1 Best-BlastP=> >nrprot No Hits found
- 2917.1 Best-BlastP=> >nrprot 30% Identities = 44/132 (33%), Positives = 71/132 (53%), Gaps = 11/132 (8%) ref|NP\_707288.1| Activator of ProP osmoprotectant transporter [Shigella flexneri 2a str. 301] gb|AAN42995.1|AE015164\_2 Activator of ProP osmoprotectant transporter [Shigella flexneri 2a str. 301] Length = 232
- 2919.1 Best-BlastP=> >nrprot 55% Identities = 23/55 (41%), Positives = 33/55 (60%), Gaps = 4/55 (7%) ref|NP\_768003.1| bsl1363 [Bradyrhizobium japonicum] dbj|BAC46628.1| bsl1363 [Bradyrhizobium japonicum USDA 110] Length = 73
- 292.1 Best-BlastP=> >nrprot 69% Identities = 75/152 (49%), Positives = 108/152 (71%), Gaps = 1/152 (0%) dbj|BAA25988.1| 24-kDa subunit of complex I [Homo sapiens] Length = 231
- 2920.1 Best-BlastP=> >nrprot No Hits found
- 2921.3 Best-BlastP=> >nrprot 17% Identities = 81/447 (18%), Positives = 193/447 (43%), Gaps = 55/447 (12%) pir|E71606 hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum) Length = 980
- 2924.3 Best-BlastP=> >nrprot No Hits found
- 2925.1 Best-BlastP=> >nrprot 61% Identities = 385/477 (80%), Positives = 412/477 (86%), Gaps = 24/477 (5%) gb|AAD50296.1|AF173009\_1 rep helicase [Legionella pneumophila] Length = 467
- 2926.1 Best-BlastP=> >nrprot No Hits found
- 2928.2 Best-BlastP=> >nrprot 63% Identities = 116/298 (38%), Positives = 178/298 (59%), Gaps = 22/298 (7%) ref|ZP\_00031876.1| COG1281: Disulfide bond chaperones of the HSP33 family [Burkholderia fungorum] Length = 316
- 2929.1 Best-BlastP=> >nrprot 46% Identities = 50/130 (38%), Positives = 77/130 (59%), Gaps = 1/130 (0%) ref|NP\_635963.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM39887.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 171
- 293.2 Best-BlastP=> >nrprot 89% Identities = 326/417 (78%), Positives = 374/417 (89%) ref|NP\_820428.1| NADH dehydrogenase I, D subunit [Coxiella burnetii RSA 493] gb|AAO90942.1| NADH dehydrogenase I, D subunit [Coxiella burnetii RSA 493] Length = 417
- 2932.2 Best-BlastP=> >nrprot 60% Identities = 309/814 (37%), Positives = 491/814 (60%), Gaps = 18/814 (2%) ref|NP\_890811.1| probable membrane protein [Bordetella bronchiseptica] emb|CAE34640.1| probable membrane protein [Bordetella bronchiseptica] Length = 1028



- 2933.2 Best-BlastP=> >nrprot 60% Identities = 122/303 (40%), Positives = 184/303 (60%), Gaps = 14/303 (4%) ref|NP\_603145.1| Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94444.1| Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 310
- 2934.1 Best-BlastP=> >nrprot No Hits found
- 2938.3 Best-BlastP=> >nrprot 41% Identities = 250/1286 (19%), Positives = 507/1286 (39%), Gaps = 229/1286 (17%) ref|NP\_212646.1| B. burgdorferi predicted coding region BB0512 [Borrelia burgdorferi] pir|G70163 hypothetical protein BB0512 - Lyme disease spirochete gb|AAC66876.1| B. burgdorferi predicted coding region BB0512 [Borrelia burgdorferi] B31] Length = 2166
- 294.1
- 2941.1 Best-BlastP=> >nrprot 67% Identities = 121/219 (55%), Positives = 153/219 (69%), Gaps = 1/219 (0%) ref|NP\_820429.1| NADH dehydrogenase I, C subunit [Coxiella burnetii RSA 493] gb|AAO90943.1| NADH dehydrogenase I, C subunit [Coxiella burnetii RSA 493] Length = 227
- 2942.1 Best-BlastP=> >nrprot 49% Identities = 173/480 (36%), Positives = 267/480 (55%), Gaps = 7/480 (1%) ref|NP\_819594.1| apolipoprotein N-acyltransferase [Coxiella burnetii RSA 493] gb|AAO90108.1| apolipoprotein N-acyltransferase [Coxiella burnetii RSA 493] Length = 485
- 2943.1 Best-BlastP=> >nrprot 42% Identities = 48/160 (30%), Positives = 76/160 (47%), Gaps = 4/160 (2%) ref|NP\_252677.1| hypothetical protein [Pseudomonas aeruginosa PA01] ref|ZP\_00137430.1| COG2980: Rare lipoprotein B [Pseudomonas aeruginosa UCBPP-PA14] pir|F83148 hypothetical protein PA3988 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07375.1| AE004816\_11 hypothetical protein PA3988 [Pseudomonas aeruginosa PAO1] Length = 207
- 2949.2 Best-BlastP=> >nrprot 74% Identities = 185/307 (60%), Positives = 238/307 (77%) ref|ZP\_00087322.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 325
- 295.1 Best-BlastP=> >nrprot 88% Identities = 128/152 (84%), Positives = 141/152 (92%) ref|ZP\_00023480.1| COG0377: NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases [Ralstonia metallidurans] Length = 160
- 2951.2
- Best-BlastP=> >nrprot 26% Identities = 100/453 (22%), Positives = 179/453 (39%), Gaps = 86/453 (18%) ref|NP\_703829.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD50441.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1321
- 2952.1 Best-BlastP=> >nrprot 8% Identities = 32/93 (34%), Positives = 53/93 (56%), Gaps = 4/93 (4%) gb|AAL78307.1| AF288617\_4 DotI [Legionella longbeachae] Length = 212
- 2953.2 Best-BlastP=> >nrprot 97% Identities = 161/166 (96%), Positives = 163/166 (98%) pir|S49042 global stress protein gspA - Legionella pneumophila Length = 166
- 2954.3 Best-BlastP=> >nrprot 74% Identities = 198/312 (63%), Positives = 247/312 (79%), Gaps = 5/312 (1%) ref|NP\_903586.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ61577.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 539
- 2955.2 Best-BlastP=> >nrprot 99% Identities = 126/127 (99%), Positives = 127/127 (100%) gb|AAD51393.1| AF117715\_2 unknown [Legionella pneumophila] Length = 127

- 2958.2 Best-BlastP=> >nrprot 98% Identities = 248/252 (98%), Positives = 250/252 (99%), Gaps = 1/252 (0%) sp|Q9S4T3|SURE\_LEGPN Acid phosphatase surE gb|AAD51394.1|AF117715\_3 survival protein homolog [Legionella pneumophila] Length = 251
- 2959.1 Best-BlastP=> >nrprot 97% Identities = 242/247 (97%), Positives = 243/247 (98%) gb|AAD51395.1|AF117715\_4 novel lipoprotein homolog [Legionella pneumophila] Length = 247
- 296.1 Best-BlastP=> >nrprot 78% Identities = 76/118 (64%), Positives = 93/118 (78%) ref|NP\_820431.1| NADH dehydrogenase I, A subunit [Coxiella burnetii RSA 493] gb|AAO90945.1| NADH dehydrogenase I, A subunit [Coxiella burnetii RSA 493] Length = 118
- 2960.1 Best-BlastP=> >nrprot 99% Identities = 337/341 (98%), Positives = 340/341 (99%) gb|AAD51396.1|AF117715\_5 stationary phase specific sigma factor homolog [Legionella pneumophila] Length = 341
- 2961.1 Best-BlastP=> >nrprot 99% Identities = 410/416 (98%), Positives = 414/416 (99%) sp|Q9S4T0|HGD\_LEGPN Homogentisate 1,2-dioxygenase (Homogentisicase) (Homogentisate oxygenase) (Homogentisic acid oxidase) Length = 416
- 2962.1 Best-BlastP=> >nrprot 95% Identities = 235/238 (98%), Positives = 236/238 (99%) gb|AAD51398.1|AF117715\_7 YebC [Legionella pneumophila] Length = 238
- 2963.2 Best-BlastP=> >nrprot 59% Identities = 110/257 (42%), Positives = 151/257 (58%), Gaps = 10/257 (3%) ref|NP\_231867.1| hydroxyacylglutathione hydrolase GloB, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir|A82102 probable hydroxyacylglutathione hydrolase GloB VC2236 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95380.1| hydroxyacylglutathione hydrolase GloB, putative [Vibrio cholerae O1 biovar eltor str. N16961] Length = 252
- 2964.1 Best-BlastP=> >nrprot 62% Identities = 121/275 (44%), Positives = 177/275 (64%), Gaps = 3/275 (1%) ref|NP\_229844.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82353 conserved hypothetical protein VC0187 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93363.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 279
- 2965.1 Best-BlastP=> >nrprot No Hits found
- 2966.1 Best-BlastP=> >nrprot 73% Identities = 164/276 (59%), Positives = 209/276 (75%), Gaps = 1/276 (0%) ref|NP\_438767.1| methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase [Haemophilus influenzae Rd] sp|P44313|FOLD\_HAEIN FOLD bifunctional protein [Includes: Methylenetetrahydrofolate dehydrogenase ; Methylenetetrahydrofolate cyclohydrolase ] pir|A64081 methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) / methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) - Haemophilus influenzae (strain Rd KW20) gb|AAC22268.1| methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate cyclohydrolase (fold) [Haemophilus influenzae Rd] Length = 282
- 2967.1 Best-BlastP=> >nrprot No Hits found
- 2968.3 Best-BlastP=> >nrprot 13% Identities = 115/119 (96%), Positives = 117/119 (98%) gb|AAM21056.1| FimV [Legionella pneumophila] Length = 119
- 2969.1 Best-BlastP=> >nrprot 81% Identities = 50/79 (63%), Positives = 64/79 (81%) ref|NP\_389755.1| similar to transcriptional regulator [Bacillus subtilis] pir|C69931 transcription regulator homolog yozG - Bacillus subtilis emb|CAB13766.1| yozG [Bacillus subtilis subsp. subtilis str. 168] Length = 84
- 297.2 Best-BlastP=> >nrprot 63% Identities = 59/101 (58%), Positives = 69/101 (68%), Gaps = 8/101 (7%) ref|NP\_820432.1| preprotein translocase, SecG subunit [Coxiella burnetii RSA 493] gb|AAO90946.1| preprotein translocase, SecG subunit [Coxiella burnetii RSA 493] Length = 98

- 2970.2 Best-BlastP=> >nrprot 32% Identities = 34/103 (33%), Positives = 56/103 (54%) ref|ZP\_00136103.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 185
- 2972.3 Best-BlastP=> >nrprot 10% Identities = 43/138 (31%), Positives = 63/138 (45%), Gaps = 15/138 (10%) ref|NP\_704193.1| ubiquitin carboxyl-terminal hydrolase, putative [Plasmodium falciparum 3D7] emb|CAD51009.1| ubiquitin carboxyl-terminal hydrolase, putative [Plasmodium falciparum 3D7] Length = 3183
- 2973.2 Best-BlastP=> >nrprot No Hits found
- 2975.2 Best-BlastP=> >nrprot No Hits found
- 2976.1 Best-BlastP=> >nrprot No Hits found
- 2978.1 Best-BlastP=> >nrprot 22% Identities = 41/121 (33%), Positives = 64/121 (52%), Gaps = 11/121 (9%) ref|NP\_818058.1| gp85 [Mycobacteriophage Che9d] gb|AAN08003.1| gp85 [Mycobacteriophage Che9d] Length = 301
- 2982.1 Best-BlastP=> >nrprot 38% Identities = 174/388 (44%), Positives = 236/388 (60%), Gaps = 17/388 (4%) ref|NP\_706610.1| orf, partial conserved hypothetical protein [Shigella flexneri 2a str. 301] ref|NP\_836390.1| putative bacteriophage protein [Shigella flexneri 2a str. 2457T] gb|AAN42317.1| AE015098\_7 orf, partial conserved hypothetical protein [Shigella flexneri 2a str. 301] gb|AAP16196.1| putative bacteriophage protein [Shigella flexneri 2a str. 2457T] Length = 619
- 2983.1 Best-BlastP=> >nrprot 54% Identities = 33/66 (50%), Positives = 47/66 (71%) ref|NP\_478090.1| hypothetical protein [Corynebacterium glutamicum] emb|CAD12221.1| hypothetical protein [Corynebacterium glutamicum] Length = 81
- 2985.1 Best-BlastP=> >nrprot No Hits found
- 2986.1 Best-BlastP=> >nrprot No Hits found
- 2987.1 Best-BlastP=> >nrprot No Hits found
- 2988.1 Best-BlastP=> >nrprot No Hits found
- 2990.1 Best-BlastP=> >nrprot 44% Identities = 34/97 (35%), Positives = 49/97 (50%), Gaps = 1/97 (1%) ref|NP\_771656.1| bl|5016 [Bradyrhizobium japonicum] dbj|BAC50281.1| bl|5016 [Bradyrhizobium japonicum USDA 110] Length = 198
- 2991.1 Best-BlastP=> >nrprot 43% Identities = 90/344 (26%), Positives = 145/344 (42%), Gaps = 68/344 (19%) gb|AAC01562.1| S adenosylhomocysteine hydrolase [Thermotoga maritima] Length = 404
- 2992.2 Best-BlastP=> >nrprot 14% Identities = 38/68 (55%), Positives = 50/68 (73%), Gaps = 1/68 (1%) gb|EAA26507.1| unknown [Rickettsia sibirica] Length = 73
- 2993.2 Best-BlastP=> >nrprot 31% Identities = 40/160 (25%), Positives = 76/160 (47%), Gaps = 11/160 (6%) dbj|BAA00448.1| open reading frame (196 AA) [Mus musculus] Length = 196
- 2994.2 Best-BlastP=> >nrprot 65% Identities = 55/118 (46%), Positives = 82/118 (69%) ref|NP\_353891.1| AGR\_C\_1587p [Agrobacterium tumefaciens] ref|NP\_531567.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|C97465 hypothetical protein AGR\_C\_1587 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AE2683 conserved hypothetical protein Atu0869 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK86676.1| AGR\_C\_1587p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL41883.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 122
- 2995.1 Best-BlastP=> >nrprot 32% Identities = 68/290 (23%), Positives = 135/290 (46%), Gaps = 39/290 (13%) ref|NP\_473345.2| hypothetical protein [Plasmodium falciparum 3D7] emb|CAB39052.2| hypothetical protein [Plasmodium falciparum 3D7] Length = 670

- 2996.1 Best-BlastP=> >nprot No Hits found
- 2998.1 Best-BlastP=> >nprot 51% Identities = 44/134 (32%), Positives = 73/134 (54%), Gaps = 1/134 (0%) ref|NP\_820925.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91439.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 148
- 2999.3 Best-BlastP=> >nprot 24% Identities = 39/156 (25%), Positives = 69/156 (44%), Gaps = 33/156 (21%) ref|ZP\_00047224.1| COG3774: Mannosyltransferase OCH1 and related enzymes [Lactobacillus gasseri] Length = 233
- 3.1 Best-BlastP=> >nprot 49% Identities = 36/79 (45%), Positives = 50/79 (63%) ref|NP\_907749.1| hypothetical protein WS1616 [Wolinella succinogenes] emb|CAE10649.1| hypothetical protein [Wolinella succinogenes] Length = 96
- 30.1 Best-BlastP=> >nprot No Hits found
- 300.2
- Best-BlastP=> >nprot 75% Identities = 346/570 (60%), Positives = 431/570 (75%), Gaps = 3/570 (0%) ref|NP\_752183.1| Prolyl-tRNA synthetase [Escherichia coli CFT073] gb|AAN78727.1|AE016755\_227 Prolyl-tRNA synthetase [Escherichia coli CFT073] Length = 590
- 3000.1 Best-BlastP=> >nprot 58% Identities = 312/711 (43%), Positives = 440/711 (61%), Gaps = 35/711 (4%) ref|ZP\_00090403.1| COG3243: Poly(3-hydroxyalkanoate) synthetase [Azotobacter vinelandii] Length = 824
- 3001.1 Best-BlastP=> >nprot No Hits found
- 3002.1 Best-BlastP=> >nprot 36% Identities = 96/343 (27%), Positives = 152/343 (44%), Gaps = 29/343 (8%) ref|ZP\_00019713.1| hypothetical protein [Chloroflexus aurantiacus] Length = 360
- 3003.1 Best-BlastP=> >nprot 57% Identities = 77/202 (38%), Positives = 119/202 (58%), Gaps = 3/202 (1%) ref|ZP\_00008122.1| COG0500: SAM-dependent methyltransferases [Rhodobacter sphaeroides] Length = 204
- 3005.2 Best-BlastP=> >nprot 69% Identities = 74/164 (45%), Positives = 116/164 (70%), Gaps = 2/164 (1%) ref|NP\_924145.1| hypothetical protein gl11199 [Gloeobacter violaceus] dbj|BAC89140.1| gl11199 [Gloeobacter violaceus] Length = 175
- 3008.1
- Best-BlastP=> >nprot 55% Identities = 65/195 (33%), Positives = 114/195 (58%), Gaps = 1/195 (0%) ref|NP\_820992.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91506.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 203
- 3009.2 Best-BlastP=> >nprot No Hits found
- 3011.2 Best-BlastP=> >nprot 49% Identities = 88/315 (27%), Positives = 164/315 (52%), Gaps = 27/315 (8%) ref|NP\_819925.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90439.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 324
- 3013.2 Best-BlastP=> >nprot 48% Identities = 48/152 (31%), Positives = 75/152 (49%), Gaps = 5/152 (3%) ref|NP\_720010.1| acetyltransferase, GNAT family [Shewanella oneidensis MR-1] gb|AAN57454.1|AE015881\_1 acetyltransferase, GNAT family [Shewanella oneidensis MR-1] Length = 154
- 3014.1 Best-BlastP=> >nprot 48% Identities = 57/192 (29%), Positives = 98/192 (51%), Gaps = 22/192 (11%) ref|NP\_656418.1| APS\_kinase, Adenylylsulfate kinase [Bacillus anthracis A2012] ref|NP\_844924.1| hypothetical protein [Bacillus anthracis str. Ames] gb|AAP26410.1| hypothetical protein BA2556 [Bacillus anthracis str. Ames] Length = 186
- 3015.1 Best-BlastP=> >nprot 50% Identities = 83/250 (33%), Positives = 124/250 (49%), Gaps = 7/250 (2%) ref|NP\_656739.1| Ubie\_methyltran, ubiE/COQ5 methyltransferase family [Bacillus anthracis A2012] ref|NP\_845200.1| conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP26686.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 254
- 3016.1 Best-BlastP=> >nprot No Hits found

- 3017.1 Best-BlastP=> >nrprot No Hits found
- 3018.1 Best-BlastP=> >nrprot No Hits found
- 3022.1 Best-BlastP=> >nrprot No Hits found
- 3023.1 Best-BlastP=> >nrprot 58% Identities = 26/56 (46%), Positives = 41/56 (73%) ref|NP\_832415.1| Glutamate-rich protein grpB [Bacillus cereus ATCC 14579] gb|AAP09616.1| Glutamate-rich protein grpB [Bacillus cereus ATCC 14579] Length = 168
- 3024.1 Best-BlastP=> >nrprot 76% Identities = 253/425 (59%), Positives = 326/425 (76%), Gaps = 2/425 (0%) ref|ZP\_00091804.1| COG0172: Seryl-tRNA synthetase [Azotobacter vinelandii] Length = 607
- 3027.1 Best-BlastP=> >nrprot 68% Identities = 86/149 (57%), Positives = 111/149 (74%) gb|AAM89273.1|AF528189\_2 SecB [Serratia marcescens] Length = 156
- 3028.1 Best-BlastP=> >nrprot 75% Identities = 48/83 (57%), Positives = 64/83 (77%) ref|ZP\_00089760.1| COG0695: Glutaredoxin and related proteins [Azotobacter vinelandii] Length = 84
- 3030.2 Best-BlastP=> >nrprot 63% Identities = 70/163 (42%), Positives = 104/163 (63%), Gaps = 2/163 (1%) ref|ZP\_00021668.1| COG2606: Uncharacterized conserved protein [Ralstonia metallidurans] Length = 165
- 3031.2 Best-BlastP=> >nrprot 42% Identities = 37/136 (27%), Positives = 60/136 (44%), Gaps = 2/136 (1%) ref|NP\_347707.1| Hypothetical protein [Clostridium acetobutylicum] pir|D97032 hypothetical protein CAC1073 [imported] - Clostridium acetobutylicum gb|AAK79047.1|AE007622\_9 Hypothetical protein [Clostridium acetobutylicum] Length = 152
- 3035.2 Best-BlastP=> >nrprot 62% Identities = 89/185 (48%), Positives = 120/185 (64%), Gaps = 9/185 (4%) ref|NP\_753759.1| Hypothetical protein ydcN [Escherichia coli CFT073] gb|AAN80321.1|AE016760\_180 Hypothetical protein ydcN [Escherichia coli CFT073] Length = 178
- 3036.2 Best-BlastP=> >nrprot 46% Identities = 54/146 (36%), Positives = 85/146 (58%), Gaps = 5/146 (3%) ref|NP\_349095.1| Predicted kinase from adenilate kinase family, FLAR-like protein [Clostridium acetobutylicum] pir|H97205 probable kinase from adenilate kinase family, FLAR-like protein [imported] - Clostridium acetobutylicum gb|AAK80435.1|AE007747\_4 Predicted kinase from adenilate kinase family, FLAR-like protein [Clostridium acetobutylicum] Length = 177
- 304.2 Best-BlastP=> >nrprot 21% Identities = 122/500 (24%), Positives = 202/500 (40%), Gaps = 87/500 (17%) gb|AAH16985.2| Unknown (protein for MGC:21968) [Homo sapiens] Length = 579
- 3041.1 Best-BlastP=> >nrprot 16% Identities = 33/146 (22%), Positives = 67/146 (45%), Gaps = 20/146 (13%) gb|AAQ55479.1| hypothetical protein [Methanococcus voltae] Length = 178
- 3042.1 Best-BlastP=> >nrprot No Hits found
- 3045.3 Best-BlastP=> >nrprot 58% Identities = 162/484 (33%), Positives = 261/484 (53%), Gaps = 46/484 (9%) gb|AAP68896.1| putative N5'-nucleotidase [Oryza sativa (japonica cultivar-group)] Length = 569
- 3046.3 Best-BlastP=> >nrprot 26% Identities = 39/103 (37%), Positives = 50/103 (48%), Gaps = 10/103 (9%) pir|F72654 hypothetical protein APE0666 - Aeropyrum pernix (strain K1) dbj|BAA79638.1| 102aa long hypothetical protein [Aeropyrum pernix] Length = 102
- 3047.2 Best-BlastP=> >nrprot 73% Identities = 131/210 (62%), Positives = 159/210 (75%) ref|NP\_716775.1| ribose 5-phosphate isomerase [Shewanella oneidensis MR-1] sp|Q8EHR7|RPIA\_SHEON Ribose 5-phosphate isomerase A (Phosphoriboisomerase A) (PRI) gb|AAN54220.1|AE015559\_4 ribose 5-phosphate isomerase [Shewanella oneidensis MR-1] Length = 219

- 3049.1 Best-BlastP=> >nrprot 69% Identities = 133/239 (55%), Positives = 174/239 (72%), Gaps = 1/239 (0%) ref|NP\_746983.1| RNA methyltransferase, TrmH family, group 3 [Pseudomonas putida KT2440] Length = 248
- 305.2 Best-BlastP=> >nrprot 69% Identities = 124/236 (52%), Positives = 167/236 (70%) ref|NP\_820118.1| dieneolactone hydrolase family protein [Coxiella burnetii RSA 493] Length = 237
- 3053.3 Best-BlastP=> >nrprot 54% Identities = 40/122 (32%), Positives = 80/122 (65%), Gaps = 4/122 (3%) gb|AAA29909.1| ORF 3 Length = 393
- 3054.3 Best-BlastP=> >nrprot 59% Identities = 117/304 (38%), Positives = 170/304 (55%), Gaps = 27/304 (8%) ref|ZP\_00067579.1| COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Microbulbifer degradans 2-40] Length = 658
- 3055.1 Best-BlastP=> >nrprot 52% Identities = 114/330 (34%), Positives = 164/330 (49%), Gaps = 35/330 (10%) ref|NP\_718657.1| TPR domain protein [Shewanella oneidensis MR-1] Length = 679
- 3057.1 Best-BlastP=> >nrprot 61% Identities = 150/319 (47%), Positives = 213/319 (66%), Gaps = 9/319 (2%) ref|ZP\_00087368.1| COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Pseudomonas fluorescens PfO-1] Length = 359
- 3058.1 Best-BlastP=> >nrprot No Hits found
- 3059.2 Best-BlastP=> >nrprot 99% Identities = 258/259 (99%), Positives = 259/259 (100%) emb|CAA06664.1| 29 kDa immunogenic protein [Legionella pneumophila] Length = 259
- 306.1 Best-BlastP=> >nrprot 75% Identities = 290/467 (62%), Positives = 356/467 (76%), Gaps = 1/467 (0%) ref|NP\_254123.1| probable biotin carboxylase subunit of a transcarboxylase [Pseudomonas aeruginosa PA01] pir|G82966 probable biotin carboxylase subunit of a transcarboxylase PA5436 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08821.1|AE004956\_5 probable biotin carboxylase subunit of a transcarboxylase [Pseudomonas aeruginosa PAO1] Length = 471
- 3060.1 Best-BlastP=> >nrprot No Hits found
- 3061.2 Best-BlastP=> >nrprot 72% Identities = 119/204 (58%), Positives = 156/204 (76%), Gaps = 2/204 (0%) ref|ZP\_00084510.1| COG2011: ABC-type metal ion transport system, permease component [Pseudomonas fluorescens PfO-1] Length = 224
- 3063.2 Best-BlastP=> >nrprot 69% Identities = 174/343 (50%), Positives = 238/343 (69%), Gaps = 7/343 (2%) ref|NP\_873575.1| D-methionine transport ATP-binding protein MetN [Haemophilus ducreyi 35000HP] gb|AAP95964.1| D-methionine transport ATP-binding protein MetN [Haemophilus ducreyi 35000HP] Length = 344
- 3065.1 Best-BlastP=> >nrprot 40% Identities = 39/138 (28%), Positives = 63/138 (45%), Gaps = 15/138 (10%) ref|NP\_520406.1| PUTATIVE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] emb|CAD15992.1| PUTATIVE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] Length = 143
- 3067.1 Best-BlastP=> >nrprot 54% Identities = 27/100 (27%), Positives = 59/100 (59%), Gaps = 6/100 (6%) ref|NP\_820531.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91045.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 124

- 3068.1 Best-BlastP=> >nprrot 84% Identities = 290/388 (74%), Positives = 331/388 (85%) ref|NP\_800128.1| putative acyl-CoA dehydrogenase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61961.1| putative acyl-CoA dehydrogenase [Vibrio parahaemolyticus] Length = 389
- 3069.1 Best-BlastP=> >nprrot 55% Identities = 83/222 (37%), Positives = 126/222 (56%), Gaps = 4/222 (1%) ref|NP\_819980.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90494.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 230
- 307.2 Best-BlastP=> >nprrot 47% Identities = 54/168 (32%), Positives = 84/168 (50%), Gaps = 8/168 (4%) ref|NP\_796502.1| hypothetical protein VP0123 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC58386.1| hypothetical protein [Vibrio parahaemolyticus] Length = 180
- 3070.2 Best-BlastP=> >nprrot No Hits found
- 3072.2 Best-BlastP=> >nprrot 67% Identities = 300/598 (50%), Positives = 400/598 (66%), Gaps = 9/598 (1%) ref|NP\_637990.1| ATP-dependent RNA helicase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM41914.1| ATP-dependent RNA helicase [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 642
- 3074.1 Best-BlastP=> >nprrot No Hits found
- 3075.2 Best-BlastP=> >nprrot No Hits found
- 3077.1 Best-BlastP=> >nprrot 42% Identities = 66/214 (30%), Positives = 103/214 (48%), Gaps = 18/214 (8%) ref|NP\_355106.1| AGR\_C\_3887p [Agrobacterium tumefaciens] ref|NP\_532818.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AH2839 conserved hypothetical protein Atu2144 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir|B97617 similar to orf3 gene in methyllobacterium extorquens [imported] - Agrobacterium tumefaciens (strain C58, Cereon) gb|AAK87891.1| AGR\_C\_3887p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43134.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 257
- 3078.2 Best-BlastP=> >nprrot 53% Identities = 128/399 (32%), Positives = 219/399 (54%), Gaps = 38/399 (9%) ref|NP\_071132.1| hypothetical protein [Archaeoglobus fulgidus DSM 4304] sp|O27977|YN07\_ARCFU Hypothetical protein AF2307 pir|C69538 hypothetical protein AF2307 - Archaeoglobus fulgidus gb|AAB88957.1| A. fulgidus predicted coding region AF2307 [Archaeoglobus fulgidus DSM 4304] Length = 365
- 3080.2 Best-BlastP=> >nprrot 64% Identities = 210/490 (42%), Positives = 312/490 (63%), Gaps = 12/490 (2%) ref|ZP\_00139612.1| COG0189: Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase) [Pseudomonas aeruginosa UCBPP-PA14] Length = 495
- 3081.2 Best-BlastP=> >nprrot No Hits found
- 3082.1 Best-BlastP=> >nprrot 67% Identities = 75/157 (47%), Positives = 106/157 (67%) ref|NP\_231147.1| hypothetical protein VC1506 [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82191 hypothetical protein VC1506 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94661.1| hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 158



- 3083.1 Best-BlastP=> >nrprot 48% Identities = 52/171 (30%), Positives = 90/171 (52%), Gaps = 1/171 (0%) ref|NP\_404077.1| osmotically inducible protein Y [Yersinia pestis] ref|NP\_671042.1| hyperosmotically inducible periplasmic protein [Yersinia pestis KIM] pir|AF0053 osmotically inducible protein Y [imported] - Yersinia pestis (strain CO92) emb|CAC89289.1| osmotically inducible protein Y [Yersinia pestis CO92] gb|AAM87293.1| AE013978\_5 hyperosmotically inducible periplasmic protein [Yersinia pestis KIM] Length = 204
- 3085.2 Best-BlastP=> >nrprot 84% Identities = 693/944 (73%), Positives = 805/944 (85%), Gaps = 4/944 (0%) ref|NP\_819318.1| excinuclease ABC, A subunit [Coxiella burnetii RSA 493] gb|AAO89832.1| excinuclease ABC, A subunit [Coxiella burnetii RSA 493] Length = 954
- 3086.1 Best-BlastP=> >nrprot 78% Identities = 133/191 (69%), Positives = 152/191 (79%) ref|NP\_819577.1| lemA protein [Coxiella burnetii RSA 493] gb|AAO90091.1| lemA protein [Coxiella burnetii RSA 493] Length = 192
- 3087.1 Best-BlastP=> >nrprot 77% Identities = 198/344 (57%), Positives = 265/344 (77%), Gaps = 6/344 (1%) ref|NP\_819578.1| heat shock protein HtpX [Coxiella burnetii RSA 493] gb|AAO90092.1| heat shock protein HtpX [Coxiella burnetii RSA 493] Length = 348
- 3088.1 Best-BlastP=> >nrprot 71% Identities = 141/251 (56%), Positives = 185/251 (73%) ref|ZP\_00128291.1| COG0842: ABC-type multidrug transport system, permease component [Pseudomonas syringae pv. syringae B728a] Length = 262
- 309.2 Best-BlastP=> >nrprot 67% Identities = 545/1113 (48%), Positives = 752/1113 (67%), Gaps = 2/1113 (0%) ref|NP\_820221.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90735.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 1619
- 3091.1 Best-BlastP=> >nrprot No Hits found
- 3093.1 Best-BlastP=> >nrprot 73% Identities = 139/243 (57%), Positives = 185/243 (76%), Gaps = 2/243 (0%) ref|NP\_928570.1| tRNA (guanine-N1-)-methyltransferase (M1G-methyltransferase) [Photorhabdus luminescens subsp. laumondii T101] emb|CAE13553.1| tRNA (guanine-N1-)-methyltransferase (M1G-methyltransferase) [Photorhabdus luminescens subsp. laumondii T101] Length = 250
- 3095.1 Best-BlastP=> >nrprot 61% Identities = 65/169 (38%), Positives = 105/169 (62%), Gaps = 7/169 (4%) ref|NP\_716978.1| 16S rRNA processing protein RimM [Shewanella oneidensis MR-1] gb|AAN54423.1| AE015579\_12 16S rRNA processing protein RimM [Shewanella oneidensis MR-1] Length = 177
- 3096.1 Best-BlastP=> >nrprot 74% Identities = 51/85 (60%), Positives = 65/85 (76%) ref|NP\_841705.1| Ribosomal protein S16 [Nitrosomonas europaea ATCC 19718] emb|CAD85582.1| Ribosomal protein S16 [Nitrosomonas europaea ATCC 19718] Length = 89
- 3097.3 Best-BlastP=> >nrprot 79% Identities = 299/447 (66%), Positives = 365/447 (81%), Gaps = 1/447 (0%) ref|NP\_716976.1| signal recognition particle protein Ffh [Shewanella oneidensis MR-1] gb|AAN54421.1| AE015579\_10 signal recognition particle protein Ffh [Shewanella oneidensis MR-1] Length = 457
- 310.1 Best-BlastP=> >nrprot No Hits found
- 3101.1 Best-BlastP=> >nrprot 12% Identities = 46/178 (25%), Positives = 78/178 (43%), Gaps = 12/178 (6%) gb|AAQ73211.1| M protein [Streptococcus pyogenes] Length = 243
- 3102.2 Best-BlastP=> >nrprot 50% Identities = 61/141 (43%), Positives = 80/141 (56%), Gaps = 3/141 (2%) ref|ZP\_00084504.1| COG0735: Fe2+/Zn2+ uptake regulation proteins [Pseudomonas fluorescens PfO-1] Length = 160

- 3104.2 Best-BlastP=> >nrprot 38% Identities = 208/652 (31%), Positives = 329/652 (50%), Gaps = 68/652 (10%) ref|NP\_717300.1| cation transport ATPase, E1-E2 family [Shewanella oneidensis MR-1] gb|AAN54744.1|AE015614\_11 cation transport ATPase, E1-E2 family [Shewanella oneidensis MR-1] Length = 753
- 3105.2 Best-BlastP=> >nrprot 41% Identities = 26/69 (37%), Positives = 42/69 (60%) ref|ZP\_00117353.1| COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] Length = 856
- 3106.2 Best-BlastP=> >nrprot 36% Identities = 149/353 (42%), Positives = 220/353 (62%), Gaps = 3/353 (0%) ref|NP\_442598.1| PleD gene product homologue [Synechocystis sp. PCC 6803] pir|S76977 pleD-4 protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10669.1| sir0302 [Synechocystis sp. PCC 6803] Length = 768
- 3107.2 Best-BlastP=> >nrprot No Hits found
- 3109.2 Best-BlastP=> >nrprot 55% Identities = 39/100 (39%), Positives = 63/100 (63%), Gaps = 1/100 (1%) ref|NP\_455037.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_459436.1| cytochrome o ubiquinol oxidase subunit IV [Salmonella typhimurium LT2] ref|NP\_806150.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|AC0557 cytochrome o ubiquinol oxidase C chain [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL19395.1| cytochrome o ubiquinol oxidase subunit IV [Salmonella typhimurium LT2] emb|CAD08899.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70010.1| cytochrome o ubiquinol oxidase C subunit [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 109
- 3110.1 Best-BlastP=> >nrprot 76% Identities = 128/188 (68%), Positives = 153/188 (81%) ref|NP\_820040.1| cytochrome o ubiquinol oxidase, subunit III [Coxiella burnetii RSA 493] gb|AAO90554.1| cytochrome o ubiquinol oxidase, subunit III [Coxiella burnetii RSA 493] Length = 198
- 3113.1 Best-BlastP=> >nrprot 85% Identities = 482/665 (72%), Positives = 568/665 (85%), Gaps = 3/665 (0%) ref|NP\_820041.1| cytochrome o ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] gb|AAO90555.1| cytochrome o ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] Length = 668
- 3114.2 Best-BlastP=> >nrprot 69% Identities = 173/292 (59%), Positives = 222/292 (76%), Gaps = 10/292 (3%) ref|NP\_820042.1| cytochrome o ubiquinol oxidase, subunit II [Coxiella burnetii RSA 493] gb|AAO90556.1| cytochrome o ubiquinol oxidase, subunit II [Coxiella burnetii RSA 493] Length = 298
- 3116.2 Best-BlastP=> >nrprot 80% Identities = 82/130 (63%), Positives = 106/130 (81%) ref|NP\_820044.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90558.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 133
- 3117.2 Best-BlastP=> >nrprot 68% Identities = 116/211 (54%), Positives = 152/211 (72%), Gaps = 2/211 (0%) ref|ZP\_00085665.1| COG0323: DNA mismatch repair enzyme (predicted ATPase) [Pseudomonas fluorescens PfO-1] Length = 262
- 3118.1 Best-BlastP=> >nrprot No Hits found
- 3119.1 Best-BlastP=> >nrprot 61% Identities = 111/264 (42%), Positives = 162/264 (61%), Gaps = 7/264 (2%) ref|NP\_794780.1| pyrroline-5-carboxylate reductase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58475.1| pyrroline-5-carboxylate reductase [Pseudomonas syringae pv. tomato str. DC3000] Length = 272
- 312.3 Best-BlastP=> >nrprot No Hits found

- 3121.2 Best-BlastP=> >nrprot 67% Identities = 119/225 (52%), Positives = 156/225 (69%) ref|ZP\_00089980.1| COG0325: Predicted enzyme with a TIM-barrel fold [Azotobacter vinelandii] Length = 234
- 3124.2 Best-BlastP=> >nrprot 88% Identities = 258/345 (74%), Positives = 305/345 (88%) ref|NP\_638103.1| twitching motility protein [Xanthomonas campestris pv. campestris str. ATCC 33913] ref|NP\_643233.1| twitching motility protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM37769.1| twitching motility protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM42027.1| twitching motility protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 345
- 3127.1 Best-BlastP=> >nrprot 99% Identities = 235/235 (100%), Positives = 235/235 (100%) sp|Q9X528|RNPH\_LEGPN Ribonuclease PH (RNase PH) (RNA nucleotidyltransferase) gb|AAD28218.1|AF120720\_1 ribonuclease PH [Legionella pneumophila] Length = 235
- 3128.1 Best-BlastP=> >nrprot 57% Identities = 62/172 (36%), Positives = 95/172 (55%), Gaps = 13/172 (7%) ref|NP\_747016.1| conserved hypothetical protein [Pseudomonas putida KT2440] gb|AAN70480.1|AE016689\_8 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 172
- 3129.2 Best-BlastP=> >nrprot 73% Identities = 195/336 (58%), Positives = 247/336 (73%) ref|NP\_252513.1| S-adenosylmethionine:trna ribosyltransferase-isomerase [Pseudomonas aeruginosa PAO1] sp|Q9HXH8|QUEA\_PSEAE S-adenosylmethionine:trna ribosyltransferase isomerase (Queuosine biosynthesis protein queA) pir|A83170 S-adenosylmethionine-trna ribosyltransferase-isomerase (EC 5.4.99.-) queA PA3824 [similarity] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07211.1|AE004799\_17 S-adenosylmethionine:trna ribosyltransferase-isomerase [Pseudomonas aeruginosa PAO1] Length = 347
- 3130.1 Best-BlastP=> >nrprot 18% Identities = 31/100 (31%), Positives = 52/100 (52%), Gaps = 3/100 (3%) ref|NP\_562861.1| queueine tRNA-ribosyltransferase [Clostridium perfringens] sp|Q8XJ16|TGT\_CLOPE Queueine tRNA-ribosyltransferase (tRNA-guanine transglycosylase) (Guanine insertion enzyme) dbj|BAB81651.1| queueine tRNA-ribosyltransferase [Clostridium perfringens str. 13] Length = 380
- 3131.1 Best-BlastP=> >nrprot 68% Identities = 53/111 (47%), Positives = 77/111 (69%) ref|ZP\_00087740.1| COG1862: Preprotein translocase subunit YajC [Pseudomonas fluorescens PfO-1] Length = 111
- 3132.1 Best-BlastP=> >nrprot No Hits found
- 3133.2 Best-BlastP=> >nrprot No Hits found
- 3134.1 Best-BlastP=> >nrprot 57% Identities = 65/150 (43%), Positives = 91/150 (60%), Gaps = 6/150 (4%) ref|NP\_419685.1| hypothetical protein [Caulobacter crescentus CB15] pir|A87357 hypothetical protein CC0868 [imported] - Caulobacter crescentus gb|AAK22853.1| hypothetical protein [Caulobacter crescentus CB15] Length = 196
- 3135.1 Best-BlastP=> >nrprot 69% Identities = 43/63 (68%), Positives = 49/63 (77%) ref|ZP\_00067639.1| COG4728: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40] Length = 93
- 3136.1 Best-BlastP=> >nrprot 54% Identities = 38/105 (36%), Positives = 60/105 (57%), Gaps = 2/105 (1%) gb|AAN62313.1|AF440524\_100 conserved hypothetical protein [Pseudomonas aeruginosa] Length = 130
- 3137.1 Best-BlastP=> >nrprot No Hits found
- 3138.2 Best-BlastP=> >nrprot No Hits found
- 3142.2 Best-BlastP=> >nrprot 53% Identities = 106/281 (37%), Positives = 158/281 (56%), Gaps = 19/281 (6%) ref|ZP\_00065061.1| COG3951: Rod binding protein [Microbulbifer degradans 2-40] Length = 318
- 3145.1 Best-BlastP=> >nrprot No Hits found

- 3146.2 Best-BlastP=> >nrprot 48% Identities = 74/241 (30%), Positives = 122/241 (50%), Gaps = 7/241 (2%) ref|NP\_928923.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13928.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 279
- 3147.1 Best-BlastP=> >nrprot 78% Identities = 107/158 (67%), Positives = 127/158 (80%) ref|NP\_439483.1| transcription elongation factor [Haemophilus influenzae Rd] sp|P43881|GREA\_HAEIN Transcription elongation factor greA (Transcript cleavage factor greA) pir|B64117 transcription elongation factor greA - Haemophilus influenzae (strain Rd KW20) gb|AAC22976.1| transcription elongation factor (greA) [Haemophilus influenzae Rd] Length = 158
- 3148.1 Best-BlastP=> >nrprot 55% Identities = 101/297 (34%), Positives = 150/297 (50%), Gaps = 36/297 (12%) ref|NP\_842462.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD86383.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 304
- 3149.1 Best-BlastP=> >nrprot 36% Identities = 69/341 (20%), Positives = 132/341 (38%), Gaps = 53/341 (15%) ref|NP\_616447.1| hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A] gb|AAM04927.1| hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A] Length = 584
- 315.3 Best-BlastP=> >nrprot 37% Identities = 97/212 (45%), Positives = 127/212 (59%) gb|AAO50865.1| similar to Leishmania major. Ppg3 [Dictyostelium discoideum] Length = 374
- 3150.1 Best-BlastP=> >nrprot 60% Identities = 94/212 (44%), Positives = 138/212 (65%), Gaps = 3/212 (1%) ref|NP\_819377.1| acid phosphatase, class B [Coxiella burnetii RSA 493] gb|AAO89891.1| acid phosphatase, class B [Coxiella burnetii RSA 493] Length = 221
- 3152.1 Best-BlastP=> >nrprot 98% Identities = 174/177 (98%), Positives = 176/177 (99%) gb|AAM00398.1| AF386079\_8 CcmG [Legionella pneumophila] Length = 177
- 3153.3 Best-BlastP=> >nrprot 99% Identities = 643/650 (98%), Positives = 649/650 (99%) gb|AAM00397.1| AF386079\_7 CcmF [Legionella pneumophila] Length = 650
- 3157.1 Best-BlastP=> >nrprot 98% Identities = 142/143 (99%), Positives = 142/143 (99%) gb|AAM00396.1| AF386079\_6 CcmE [Legionella pneumophila] Length = 143
- 3158.1 Best-BlastP=> >nrprot 97% Identities = 72/73 (98%), Positives = 72/73 (98%) gb|AAM00395.1| AF386079\_5 CcmD [Legionella pneumophila] Length = 73
- 3159.2 Best-BlastP=> >nrprot 98% Identities = 247/251 (98%), Positives = 249/251 (99%) gb|AAM00394.1| AF386079\_4 CcmC [Legionella pneumophila] Length = 251
- 3160.1 Best-BlastP=> >nrprot No Hits found
- 3161.1 Best-BlastP=> >nrprot 44% Identities = 60/224 (26%), Positives = 103/224 (45%), Gaps = 13/224 (5%) gb|AAK18828.1| AF327739\_5 Peb1 [Streptococcus thermophilus] Length = 277
- 3163.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1| AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 3165.1 Best-BlastP=> >nrprot No Hits found

- 3166.1 Best-BlastP=> >nrprot 65% Identities = 99/176 (56%), Positives = 127/176 (72%), Gaps = 2/176 (1%) ref|NP\_903124.1| probable DNA-directed DNA polymerase, bacteriophage-type [Chromobacterium violaceum ATCC 12472] gb|AAQ61115.1| probable DNA-directed DNA polymerase, bacteriophage-type [Chromobacterium violaceum ATCC 12472] Length = 280
- 3167.1 Best-BlastP=> >nrprot 63% Identities = 199/415 (47%), Positives = 270/415 (65%), Gaps = 4/415 (0%) ref|NP\_820906.1| transporter, putative [Coxiella burnetii RSA 493] gb|AAO91420.1| transporter, putative [Coxiella burnetii RSA 493] Length = 435
- 3169.1 Best-BlastP=> >nrprot 50% Identities = 90/186 (48%), Positives = 122/186 (65%), Gaps = 3/186 (1%) ref|NP\_926264.1| unknown protein [Gloeobacter violaceus] dbj|BAC91259.1| glr3318 [Gloeobacter violaceus] Length = 228
- 317.1 Best-BlastP=> >nrprot 59% Identities = 142/362 (39%), Positives = 202/362 (55%), Gaps = 33/362 (9%) ref|ZP\_00069313.1| COG0517: FOG: CBS domain [Oenococcus oeni MCW] Length = 382
- 3172.2 Best-BlastP=> >nrprot 68% Identities = 118/270 (43%), Positives = 188/270 (69%), Gaps = 5/270 (1%) ref|ZP\_00014387.1| COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Rhodospirillum rubrum] Length = 369
- 3173.1 Best-BlastP=> >nrprot 63% Identities = 38/88 (43%), Positives = 54/88 (61%), Gaps = 3/88 (3%) ref|ZP\_00068002.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 128
- 3174.1 Best-BlastP=> >nrprot 53% Identities = 100/270 (37%), Positives = 155/270 (57%), Gaps = 1/270 (0%) ref|NP\_903183.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61174.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 276
- 3175.1 Best-BlastP=> >nrprot 35% Identities = 51/201 (25%), Positives = 92/201 (45%), Gaps = 3/201 (1%) ref|NP\_903184.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61175.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 255
- 3177.1 Best-BlastP=> >nrprot 54% Identities = 64/138 (46%), Positives = 84/138 (60%), Gaps = 14/138 (10%) ref|NP\_903185.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61176.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 145
- 3178.1 Best-BlastP=> >nrprot 72% Identities = 124/219 (56%), Positives = 157/219 (71%), Gaps = 4/219 (1%) ref|ZP\_00066950.1| COG0036: Pentose-5-phosphate-3-epimerase [Microbulbifer degradans 2-40] Length = 228
- 3179.1 Best-BlastP=> >nrprot 47% Identities = 179/574 (31%), Positives = 288/574 (50%), Gaps = 25/574 (4%) ref|ZP\_00067610.1| COG0741: Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) [Microbulbifer degradans 2-40] Length = 669
- 318.2 Best-BlastP=> >nrprot 76% Identities = 266/465 (57%), Positives = 361/465 (77%), Gaps = 7/465 (1%) ref|NP\_902486.1| probable PhoH-related protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60484.1| probable PhoH-related protein [Chromobacterium violaceum ATCC 12472] Length = 467
- 3181.2 Best-BlastP=> >nrprot 66% Identities = 154/327 (47%), Positives = 218/327 (66%) ref|ZP\_00016063.1| COG0842: ABC-type multidrug transport system, permease component [Rhodospirillum rubrum] Length = 371
- 3184.3 Best-BlastP=> >nrprot 71% Identities = 221/407 (54%), Positives = 299/407 (73%), Gaps = 7/407 (1%) ref|NP\_820219.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90733.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 445

- 3186.2 Best-BlastP=> >nrprot 71% Identities = 622/1145 (54%), Positives = 830/1145 (72%), Gaps = 9/1145 (0%) ref|NP\_791924.1| transcription-repair coupling factor [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55619.1| transcription-repair coupling factor [Pseudomonas syringae pv. tomato str. DC3000] Length = 1150
- 3190.1 Best-BlastP=> >nrprot 42% Identities = 89/233 (38%), Positives = 127/233 (54%), Gaps = 2/233 (0%) ref|NP\_519922.1| GALA PROTEIN 3 [Ralstonia solanacearum] Length = 522
- 3191.1 Best-BlastP=> >nrprot No Hits found
- 3193.2 Best-BlastP=> >nrprot 50% Identities = 77/223 (34%), Positives = 116/223 (52%), Gaps = 7/223 (3%) sp|P57974|RECO\_PASMU DNA repair protein recO (Recombination protein O) Length = 240
- 3196.3 Best-BlastP=> >nrprot 65% Identities = 225/478 (47%), Positives = 330/478 (69%), Gaps = 2/478 (0%) ref|NP\_462493.1| putative POT family, peptide transport protein [Salmonella typhimurium LT2] gb|AAL22452.1| putative POT family peptide transport protein [Salmonella typhimurium LT2] Length = 489
- 3198.1 Best-BlastP=> >nrprot 54% Identities = 72/174 (41%), Positives = 101/174 (58%), Gaps = 1/174 (0%) ref|ZP\_00081025.1| COG0558: Phosphatidylglycerophosphate synthase [Geobacter metallireducens] Length = 198
- 3199.1 Best-BlastP=> >nrprot 98% Identities = 561/575 (97%), Positives = 566/575 (98%) gb|AAC44717.1| FrgA [Legionella pneumophila] Length = 575
- 3201.1 Best-BlastP=> >nrprot 81% Identities = 451/609 (74%), Positives = 520/609 (85%), Gaps = 3/609 (0%) ref|NP\_820341.1| ATP-dependent metalloprotease FtsH [Coxiella burnetii RSA 493] gb|AAO90855.1| ATP-dependent metalloprotease FtsH [Coxiella burnetii RSA 493] Length = 647
- 3205.3 Best-BlastP=> >nrprot 46% Identities = 466/1207 (38%), Positives = 682/1207 (56%), Gaps = 45/1207 (3%) emb|CAC01603.1| peptide synthetase [Anabaena sp. 90] Length = 2258
- 3207.5 Best-BlastP=> >nrprot 50% Identities = 247/840 (29%), Positives = 419/840 (49%), Gaps = 91/840 (10%) ref|NP\_819809.1| sensory box histidine kinase/response regulator [Coxiella burnetii RSA 493] gb|AAO90323.1| sensory box histidine kinase/response regulator [Coxiella burnetii RSA 493] Length = 808
- 321.3 Best-BlastP=> >nrprot 22% Identities = 44/165 (26%), Positives = 67/165 (40%), Gaps = 22/165 (13%) pir|T18253| probable mitochondrial carrier protein - yeast (Candida albicans) emb|CAA22027.1| putative mitochondrial carrier protein [Candida albicans] Length = 284
- 3212.2 Best-BlastP=> >nrprot 45% Identities = 64/206 (31%), Positives = 105/206 (50%), Gaps = 11/206 (5%) ref|NP\_389092.1| similar to endo-1,4-beta-xylanase [Bacillus subtilis] sp|O34798|YJEA\_BACSU Hypothetical protein yjeA precursor pir|G69849 endo-1,4-beta-xylanase homolog yjeA Bacillus subtilis gb|AAC46306.1| NodB-like protein [Bacillus subtilis] emb|CAB13067.1| yjeA [Bacillus subtilis subsp. subtilis str. 168] Length = 467
- 3217.3 Best-BlastP=> >nrprot 79% Identities = 261/396 (65%), Positives = 314/396 (79%), Gaps = 3/396 (0%) ref|NP\_819161.1| 2-amino-3-ketobutyrate coenzyme A ligase [Coxiella burnetii RSA 493] gb|AAO89675.1| 2-amino-3-ketobutyrate coenzyme A ligase [Coxiella burnetii RSA 493] Length = 396
- 3218.1 Best-BlastP=> >nrprot 59% Identities = 94/211 (44%), Positives = 129/211 (61%) ref|NP\_840138.1| possible pcm; protein-L-isoaspartate o-methyltransferase [Nitrosomonas europaea ATCC 19718] emb|CAD83948.1| possible pcm; protein-L-isoaspartate o-methyltransferase [Nitrosomonas europaea ATCC 19718] Length = 218

- 322.3 Best-BlastP=> >nrprot No Hits found
- 3221.1 Best-BlastP=> >nrprot 62% Identities = 187/450 (41%), Positives = 275/450 (61%), Gaps = 16/450 (3%) ref|NP\_819109.1| outer membrane protein TolC, putative [Coxiella burnetii RSA 493] gb|AAO89623.1| outer membrane protein TolC, putative [Coxiella burnetii RSA 493] Length = 616
- 3223.1 Best-BlastP=> >nrprot 74% Identities = 182/248 (73%), Positives = 212/248 (85%) ref|NP\_820067.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90581.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 256
- 3224.3 Best-BlastP=> >nrprot 62% Identities = 316/713 (44%), Positives = 464/713 (65%), Gaps = 14/713 (1%) ref|NP\_869762.1| probable sulfate transporter [Pirellula sp.] emb|CAD77140.1| probable sulfate transporter [Pirellula sp.] Length = 768
- 3226.2 Best-BlastP=> >nrprot 50% Identities = 28/64 (43%), Positives = 44/64 (68%) gb|AAP78483.1| C.AhdI [Aeromonas hydrophila] Length = 74
- 3228.1 Best-BlastP=> >nrprot 70% Identities = 40/66 (60%), Positives = 49/66 (74%), Gaps = 1/66 (1%) ref|ZP\_00067276.1| COG1278: Cold shock proteins [Microbulbifer degradans 2-40] Length = 71
- 323.2 Best-BlastP=> >nrprot No Hits found
- 3230.1 Best-BlastP=> >nrprot No Hits found
- 3231.1 Best-BlastP=> >nrprot 56% Identities = 25/52 (48%), Positives = 31/52 (59%) ref|NP\_143190.1| hypothetical protein PH1305 [Pyrococcus horikoshii] pir|A71001 hypothetical protein PH1305 - Pyrococcus horikoshii dbj|BAA30409.1| 252aa long hypothetical protein [Pyrococcus horikoshii] Length = 252
- 3232.1 Best-BlastP=> >nrprot No Hits found
- 3233.1 Best-BlastP=> >nrprot No Hits found
- 3234.3 Best-BlastP=> >nrprot 19% Identities = 34/98 (34%), Positives = 52/98 (53%), Gaps = 1/98 (1%) ref|ZP\_00106280.1| COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Nostoc punctiforme] Length = 210
- Best-BlastP=> >nrprot 53% Identities = 71/228 (31%), Positives = 125/228 (54%), Gaps = 1/228 (0%) ref|NP\_928824.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13825.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 231
- 3235.3 Best-BlastP=> >nrprot 66% Identities = 89/162 (54%), Positives = 120/162 (74%) ref|NP\_311228.1| hypothetical protein [Escherichia coli O157:H7] ref|NP\_416820.1| orf, hypothetical protein [Escherichia coli K12] sp|P09548|DEDA\_ECOLI DedA protein (DSG-1 protein) pir|XMECAD dedA protein - Escherichia coli (strain K-12) pir|A98029 hypothetical protein ECs3201 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) gb|AAA23964.1| dedA gb|AAC75377.1| orf, hypothetical protein [Escherichia coli K12] dbj|BAA16174.1| dedA protein [Escherichia coli] dbj|BAB36624.1| hypothetical protein [Escherichia coli O157:H7] Length = 219
- 3236.3 Best-BlastP=> >nrprot No Hits found
- 3238.1 Best-BlastP=> >nrprot 67% Identities = 134/263 (50%), Positives = 195/263 (74%), Gaps = 1/263 (0%) ref|NP\_421700.1| conserved hypothetical protein [Caulobacter crescentus CB15] pir|H87608 conserved hypothetical protein CC2906 [imported] - Caulobacter crescentus gb|AAK24868.1| conserved hypothetical protein [Caulobacter crescentus CB15] Length = 289
- 3239.1 Best-BlastP=> >nrprot 58% Identities = 31/85 (36%), Positives = 57/85 (67%), Gaps = 2/85 (2%) ref|NP\_820572.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91086.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 102



- 324.3 Best-BlastP=> >nrrprot 72% Identities = 106/224 (47%), Positives = 160/224 (71%), Gaps = 5/224 (2%) ref|ZP\_00045186.1| COG2200: FOG: EAL domain [Magnetococcus sp. MC-1] Length = 577
- 3240.3 Best-BlastP=> >nrrprot 52% Identities = 24/64 (37%), Positives = 42/64 (65%) ref|NP\_458973.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_463417.1| hyperosmotically inducible periplasmic protein, RpoS-dependent stationary phase gene [Salmonella typhimurium LT2] ref|NP\_808176.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|AE1072 Putative periplasmic protein [imported] - Salmonella typhimurium LT2] emb|CAD03396.1| Putative periplasmic protein [Salmonella hyperosmotically inducible periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO72036.1| Putative periplasmic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 205
- 3242.3 Best-BlastP=> >nrrprot 14% Identities = 72/325 (22%), Positives = 126/325 (38%), Gaps = 37/325 (11%) gb|AAB96623.1| spheroidin [Heliothis armigera entomopoxvirus] Length = 1007
- 3243.1 Best-BlastP=> >nrrprot No Hits found
- 3244.2 Best-BlastP=> >nrrprot 60% Identities = 102/241 (42%), Positives = 153/241 (63%), Gaps = 2/241 (0%) ref|NP\_465213.1| similar to glucose 1-dehydrogenase [Listeria monocytogenes EGD-e] pir|AH1285 glucose 1-dehydrogenase homolog lmo1688 [imported] - Listeria monocytogenes (strain EGD-e) emb|CAC99766.1| lmo1688 [Listeria monocytogenes] Length = 248
- 3246.2 Best-BlastP=> >nrrprot 24% Identities = 100/360 (27%), Positives = 160/360 (44%), Gaps = 67/360 (18%) ref|NP\_905966.1| conserved hypothetical protein [Porphyromonas gingivalis W83] gb|AAQ66865.1| conserved hypothetical protein [Porphyromonas gingivalis W83] Length = 339
- 3248.1 Best-BlastP=> >nrrprot 38% Identities = 87/154 (56%), Positives = 114/154 (74%) ref|ZP\_00111795.1| COG0784: FOG: CheY-like receiver [Nostoc punctiforme] Length = 557
- 3249.2 Best-BlastP=> >nrrprot 13% Identities = 22/55 (40%), Positives = 29/55 (52%) ref|NP\_798062.1| hypothetical protein VP1683 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC59946.1| hypothetical protein [Vibrio parahaemolyticus] Length = 325
- 325.1 Best-BlastP=> >nrrprot No Hits found
- 3250.1 Best-BlastP=> >nrrprot No Hits found
- 3251.1 Best-BlastP=> >nrrprot 48% Identities = 39/131 (29%), Positives = 65/131 (49%), Gaps = 3/131 (2%) emb|CAC05487.1| YcfB protein [Erwinia amylovora] Length = 132
- 3252.1 Best-BlastP=> >nrrprot No Hits found
- 3257.2 Best-BlastP=> >nrrprot 46% Identities = 40/122 (32%), Positives = 70/122 (57%), Gaps = 4/122 (3%) ref|NP\_755556.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN82129.1|AE016766\_217 Hypothetical protein [Escherichia coli CFT073] Length = 131
- 3258.2 Best-BlastP=> >nrrprot 35% Identities = 70/225 (31%), Positives = 111/225 (49%), Gaps = 27/225 (12%) ref|NP\_755557.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN82130.1|AE016766\_218 Hypothetical protein [Escherichia coli CFT073] Length = 305
- 326.2 Best-BlastP=> >nrrprot No Hits found
- 3260.2 Best-BlastP=> >nrrprot No Hits found
- 3263.2 Best-BlastP=> >nrrprot 61% Identities = 128/368 (34%), Positives = 227/368 (61%), Gaps = 10/368 (2%) ref|NP\_819469.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO89983.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 428

- 3265.1 Best-BlastP=> >nrprot 65% Identities = 140/293 (47%), Positives = 195/293 (66%), Gaps = 2/293 (0%) ref|NP\_820459.1| hydrogen peroxide-inducible genes activator OxyR [Coxiella burnetii] RSA 493] Length = 311
- 3267.1 Best-BlastP=> >nrprot 50% Identities = 57/258 (22%), Positives = 104/258 (40%), Gaps = 75/258 (29%) ref|NP\_797353.1| hypothetical protein VP0974 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC59237.1| hypothetical protein [Vibrio parahaemolyticus] Length = 269
- 3269.1 Best-BlastP=> >nrprot 55% Identities = 400/1113 (35%), Positives = 600/1113 (53%), Gaps = 64/1113 (5%) ref|NP\_820225.1| UvrD/REP helicase family protein [Coxiella burnetii] RSA 493] gb|AAO90739.1| UvrD/REP helicase family protein [Coxiella burnetii] RSA 493] Length = 1110
- 327.2 Best-BlastP=> >nrprot 70% Identities = 364/616 (59%), Positives = 458/616 (74%), Gaps = 7/616 (1%) ref|ZP\_00141174.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 645
- 3271.3 Best-BlastP=> >nrprot 46% Identities = 187/674 (27%), Positives = 308/674 (45%), Gaps = 55/674 (8%) ref|NP\_437090.1| putative membrane-located cell surface saccharide saccharide acetylase protein [Sinorhizobium meliloti] pir|F95910 probable membrane-located cell surface saccharide saccharide acetylase protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb|CAC48950.1| putative membrane-located cell surface saccharide saccharide acetylase protein [Sinorhizobium meliloti] Length = 677
- 3272.1 Best-BlastP=> >nrprot 55% Identities = 49/148 (33%), Positives = 82/148 (55%), Gaps = 14/148 (9%) ref|NP\_820842.1| conserved hypothetical protein [Coxiella burnetii] RSA 493] gb|AAO91356.1| conserved hypothetical protein [Coxiella burnetii] RSA 493] Length = 175
- 3273.1 Best-BlastP=> >nrprot 40% Identities = 34/95 (35%), Positives = 50/95 (52%), Gaps = 4/95 (4%) ref|NP\_930855.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16020.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 175
- 3275.1 Best-BlastP=> >nrprot No Hits found
- 3276.2 Best-BlastP=> >nrprot No Hits found
- 3277.2 Best-BlastP=> >nrprot 61% Identities = 109/264 (41%), Positives = 165/264 (62%), Gaps = 5/264 (1%) ref|ZP\_00055240.1| COG1073: Hydrolases of the alpha/beta superfamily [Magnetospirillum magnetotacticum] Length = 297
- 3278.1 Best-BlastP=> >nrprot 28% Identities = 19/43 (44%), Positives = 28/43 (65%) ref|NP\_523079.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD18671.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 232
- 328.1 Best-BlastP=> >nrprot 68% Identities = 161/292 (55%), Positives = 206/292 (70%), Gaps = 3/292 (1%) ref|NP\_770597.1| 3-hydroxyisobutyrate dehydrogenase [Bradyrhizobium japonicum] dbj|BAC49222.1| 3-hydroxyisobutyrate dehydrogenase [Bradyrhizobium japonicum] USDA 110] Length = 295
- 3280.1 Best-BlastP=> >nrprot 54% Identities = 101/267 (37%), Positives = 156/267 (58%), Gaps = 18/267 (6%) ref|NP\_631554.1| conserved hypothetical protein [Streptomyces coelicolor A3(2)] emb|CAC44686.1| conserved hypothetical protein [Streptomyces coelicolor A3(2)] Length = 277
- 3281.1 Best-BlastP=> >nrprot No Hits found

- 3282.3 Best-BlastP=> >nrprot 82% Identities = 289/413 (69%), Positives = 341/413 (82%), Gaps = 4/413 (0%) ref|NP\_819190.1| cell division protein FtsA [Coxiella burnetii RSA 493] gb|AAO89704.1| cell division protein FtsA [Coxiella burnetii RSA 493] Length = 410
- 3283.1 Best-BlastP=> >nrprot 50% Identities = 72/220 (32%), Positives = 120/220 (54%), Gaps = 1/220 (0%) ref|NP\_253099.1| cell division protein FtsQ [Pseudomonas aeruginosa PA01] pir|B83094 cell division protein FtsQ PA4409 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAF26457.1| FtsQ [Pseudomonas aeruginosa] gb|AAG07797.1|AE004856\_8 cell division protein FtsQ [Pseudomonas aeruginosa PAO1] Length = 287
- 3285.3 Best-BlastP=> >nrprot 48% Identities = 106/303 (34%), Positives = 174/303 (57%), Gaps = 1/303 (0%) ref|ZP\_00032705.1| COG0642: Signal transduction histidine kinase [Burkholderia fungorum] Length = 535
- 3288.3 Best-BlastP=> >nrprot 71% Identities = 120/221 (54%), Positives = 161/221 (72%) ref|ZP\_00080602.1| COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Geobacter metallireducens] Length = 306
- 3290.1 Best-BlastP=> >nrprot No Hits found
- 3291.2 Best-BlastP=> >nrprot No Hits found
- 3295.2 Best-BlastP=> >nrprot 77% Identities = 563/923 (60%), Positives = 715/923 (77%), Gaps = 5/923 (0%) ref|ZP\_00066862.1| COG0525: Valyl-tRNA synthetase [Microbulbifer degradans 2-40] Length = 922
- 3297.3 Best-BlastP=> >nrprot 36% Identities = 75/282 (26%), Positives = 129/282 (45%), Gaps = 11/282 (3%) ref|NP\_603055.1| 3-oxoacyl-[acyl-carrier-protein] synthase III [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94354.1| 3-oxoacyl-[acyl-carrier-protein] synthase III [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 328
- 3299.3 Best-BlastP=> >nrprot 36% Identities = 36/137 (26%), Positives = 51/137 (37%), Gaps = 37/137 (27%) ref|ZP\_00014317.1| hypothetical protein [Rhodospirillum rubrum] Length = 417
- 33.1 Best-BlastP=> >nrprot 87% Identities = 711/878 (80%), Positives = 774/878 (88%), Gaps = 16/878 (1%) gb|AAG45149.1| TraA-like protein [Legionella pneumophila] Length = 883
- 330.2 Best-BlastP=> >nrprot 70% Identities = 267/493 (54%), Positives = 353/493 (71%), Gaps = 1/493 (0%) ref|NP\_819940.1| methylmalonate-semialdehyde dehydrogenase [Coxiella burnetii RSA 493] gb|AAO90454.1| methylmalonate-semialdehyde dehydrogenase [Coxiella burnetii RSA 493] Length = 498
- 3301.2 Best-BlastP=> >nrprot 55% Identities = 160/488 (32%), Positives = 261/488 (53%), Gaps = 38/488 (7%) ref|NP\_787151.1| propionyl-CoA carboxylase beta chain [Tropheryma whipplei str. TW08/27] emb|CAD66717.1| propionyl-CoA carboxylase beta chain [Tropheryma whipplei TW08/27] gb|AAO44120.1| propionyl-CoA carboxylase beta chain [Tropheryma whipplei str. TW08/27] Length = 525
- 3303.2 Best-BlastP=> >nrprot No Hits found
- 3304.2 Best-BlastP=> >nrprot 50% Identities = 133/302 (44%), Positives = 189/302 (62%), Gaps = 7/302 (2%) ref|ZP\_00043253.1| hypothetical protein [Magnetococcus sp. MC-1] Length = 831
- 3306.4 Best-BlastP=> >nrprot 29% Identities = 48/138 (34%), Positives = 71/138 (51%), Gaps = 13/138 (9%) ref|ZP\_00052545.1| COG1020: Non-ribosomal peptide synthetase modules and related proteins [Magnetospirillum magnetotacticum] Length = 676
- 3307.4 Best-BlastP=> >nrprot No Hits found
- 3308.4 Best-BlastP=> >nrprot No Hits found

331.2

Best-BlastP=> >nrprot 69% Identities = 272/538 (50%), Positives = 371/538 (68%), Gaps = 5/538 (0%) ref|NP\_406414.1| putative glutamine-dependent NAD [Yersinia pestis] ref|NP\_668639.1| putative NH3-dependent NAD(+) synthetase [Yersinia pestis KIM] pir|AG0354 NAD synthase (glutamine-hydrolysing) (EC 6.3.5.1) - Yersinia pestis (strain CO92) emb|CAC92162.1| putative glutamine-dependent NAD [Yersinia pestis CO92] gb|AAM84890.1|AE013734\_5 putative NH3-dependent NAD(+) synthetase [Yersinia pestis KIM] Length = 540

3311.1

Best-BlastP=> >nrprot 74% Identities = 275/459 (59%), Positives = 341/459 (74%), Gaps = 9/459 (1%) ref|NP\_250486.1| cysteinyl-tRNA synthetase [Pseudomonas aeruginosa PA01] sp|Q9J2U7|SYC\_PSEAE CysteinyI-tRNA synthetase (Cysteine--tRNA ligase) (CysRS) pir|G83421 cysteinyl-tRNA synthetase PA1795 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05184.1|AE004605\_6 cysteinyl-tRNA synthetase [Pseudomonas aeruginosa PAO1] Length = 460

3312.1

Best-BlastP=> >nrprot 32% Identities = 20/66 (30%), Positives = 34/66 (51%) ref|NP\_759513.1| Unknown [Vibrio vulnificus CMCP6] gb|AAO09040.1|AE016798\_200 Unknown [Vibrio vulnificus CMCP6] db|BAC93437.1| hypothetical protein [Vibrio vulnificus YJ016] Length = 103

3314.2

Best-BlastP=> >nrprot No Hits found

3316.1

Best-BlastP=> >nrprot 26% Identities = 80/363 (22%), Positives = 152/363 (41%), Gaps = 41/363 (11%) ref|NP\_659473.1| hypothetical protein MGC33887 [Homo sapiens] gb|AAM49719.1|AF458591\_1 hypothetical protein [Homo sapiens] Length = 590

3319.1

Best-BlastP=> >nrprot No Hits found

3322.2

Best-BlastP=> >nrprot 98% Identities = 265/269 (98%), Positives = 267/269 (99%) pir|T18335 icmG protein - Legionella pneumophila emb|CAA75166.1| icmG protein [Legionella pneumophila] gb|AAC38187.1| DotF [Legionella pneumophila] emb|CAA75332.1| icmG protein [Legionella pneumophila] Length = 269

3323.1

Best-BlastP=> >nrprot 99% Identities = 194/194 (100%), Positives = 194/194 (100%) pir|T18336 icmC protein - Legionella pneumophila emb|CAA75167.1| icmC protein [Legionella pneumophila] gb|AAC38186.1| DotE [Legionella pneumophila] emb|CAA75333.1| icmC protein [Legionella pneumophila] Length = 194

3324.1

Best-BlastP=> >nrprot 98% Identities = 130/132 (98%), Positives = 131/132 (99%) pir|T18337 icmD protein - Legionella pneumophila emb|CAA75168.1| icmD protein [Legionella pneumophila] emb|CAA75334.1| icmD protein [Legionella pneumophila] Length = 132

3326.2

Best-BlastP=> >nrprot 99% Identities = 261/261 (100%), Positives = 261/261 (100%) gb|AAQ10306.1| DotU [Legionella pneumophila] Length = 261

3327.1

Best-BlastP=> >nrprot 46% Identities = 53/219 (24%), Positives = 99/219 (45%), Gaps = 19/219 (8%) ref|NP\_840938.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD84775.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 343

3328.1

Best-BlastP=> >nrprot 70% Identities = 315/575 (54%), Positives = 407/575 (70%), Gaps = 5/575 (0%) ref|NP\_252414.1| single-stranded-DNA-specific exonuclease RecJ [Pseudomonas aeruginosa PA01] pir|A83181 single-stranded-DNA-specific exonuclease RecJ PA3725 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07112.1|AE004791\_9 single-stranded-DNA-specific exonuclease RecJ [Pseudomonas aeruginosa PAO1] Length = 571

333.3

Best-BlastP=> >nrprot 57% Identities = 426/1088 (39%), Positives = 613/1088 (56%), Gaps = 70/1088 (6%) gb|AAP85938.1| putative helicase, superfamily II [Ralstonia eutropha] Length = 1106

- 3331.1 Best-BlastP=> >nrprot 61% Identities = 145/291 (49%), Positives = 203/291 (69%), Gaps = 1/291 (0%) ref|NP\_719443.1| TIM-barrel protein, yjBN family [Shewanella oneidensis MR-1] gb|AAN56887.1| AE015823\_9 TIM-barrel protein, yjBN family [Shewanella oneidensis MR-1]  
Length = 335
- 3333.1 Best-BlastP=> >nrprot 58% Identities = 52/122 (42%), Positives = 79/122 (64%), Gaps = 1/122 (0%) ref|NP\_930852.1| Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (8-oxo-dGTPase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16017.1| Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (8-oxo-dGTPase) (dGTP pyrophosphohydrolase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 130
- 3334.2 Best-BlastP=> >nrprot No Hits found
- 3336.2 Best-BlastP=> >nrprot No Hits found
- 3337.2 Best-BlastP=> >nrprot No Hits found
- 3338.1 Best-BlastP=> >nrprot No Hits found
- 334.5 Best-BlastP=> >nrprot 42% Identities = 272/697 (39%), Positives = 416/697 (59%), Gaps = 23/697 (3%) ref|NP\_440178.1| regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] dbj|BAA16858.1| regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] Length = 840
- 3341.2 Best-BlastP=> >nrprot No Hits found
- 3343.1 Best-BlastP=> >nrprot No Hits found
- 3345.2 Best-BlastP=> >nrprot 17% Identities = 53/272 (19%), Positives = 137/272 (50%), Gaps = 28/272 (10%) ref|NP\_701067.1| hypothetical protein [Plasmodium falciparum 3D7] gb|AAN35791.1| AE014838\_69 hypothetical protein [Plasmodium falciparum 3D7] Length = 964
- 3346.2 Best-BlastP=> >nrprot 28% Identities = 105/343 (30%), Positives = 168/343 (48%), Gaps = 60/343 (17%) ref|NP\_623492.1| Cell division protein FtsI/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] gb|AAM25096.1| Cell division protein FtsI/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] Length = 553
- 3347.1 Best-BlastP=> >nrprot 94% Identities = 239/266 (89%), Positives = 251/266 (94%) emb|CAC35728.1| OXA-29 [Fluoribacter gormanii] Length = 266
- 3348.2 Best-BlastP=> >nrprot 31% Identities = 115/295 (38%), Positives = 170/295 (57%), Gaps = 15/295 (5%) ref|ZP\_00119503.1| COG0726: Predicted xylanase/chitin deacetylase [Cytophaga hutchinsonii] Length = 314
- 3349.3 Best-BlastP=> >nrprot 45% Identities = 72/238 (30%), Positives = 130/238 (54%), Gaps = 8/238 (3%) ref|NP\_638901.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42825.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 314
- 335.1 Best-BlastP=> >nrprot 67% Identities = 115/207 (55%), Positives = 145/207 (70%), Gaps = 2/207 (0%) ref|NP\_903041.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61035.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 206
- 3350.3 Best-BlastP=> >nrprot 41% Identities = 33/101 (32%), Positives = 50/101 (49%), Gaps = 3/101 (2%) ref|ZP\_00116659.1| COG0346: Lactoylglutathione lyase and related lyases [Cytophaga hutchinsonii] Length = 150

3351.3

Best-BlastP=> >nrprot 30% Identities = 88/194 (45%), Positives = 121/194 (62%), Gaps = 1/194 (0%) ref|NP\_531634.1| methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AH2691 methyltransferase Atu0936 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAL41950.1| methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 202

3352.1

Best-BlastP=> >nrprot 42% Identities = 52/109 (47%), Positives = 67/109 (61%), Gaps = 6/109 (5%) ref|NP\_819444.1| acetyltransferase, GNAT family [Coxiella burnetii RSA 493] gb|AAO89958.1| acetyltransferase, GNAT family [Coxiella burnetii RSA 493] Length = 118

3353.1

Best-BlastP=> >nrprot 48% Identities = 157/467 (33%), Positives = 245/467 (52%), Gaps = 16/467 (3%) ref|NP\_417114.1| hypothetical protein [Escherichia coli K12] sp|P52124|YFJL\_ECOLI Hypothetical protein yfjL pir|T08637 hypothetical protein b2625 - Escherichia coli (strain K-12) gb|AAA79794.1| ORF\_o469 gb|AAC75673.1| orf, hypothetical protein [Escherichia coli K12] Length = 469

3354.1

Best-BlastP=> >nrprot 47% Identities = 58/190 (30%), Positives = 91/190 (47%), Gaps = 2/190 (1%) gb|AAD53919.1|AF179611\_3 pyridoxamine 5'-phosphate oxidase [Zymomonas mobilis] Length = 192

3355.2

Best-BlastP=> >nrprot 72% Identities = 53/94 (56%), Positives = 70/94 (74%), Gaps = 1/94 (1%) gb|AAL55698.1|AF246719\_2 hypothetical protein [Escherichia coli] Length = 95

3356.2

Best-BlastP=> >nrprot 70% Identities = 44/83 (53%), Positives = 59/83 (71%) ref|NP\_232869.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|E82456 conserved hypothetical protein VCA0477 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96381.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 90

3357.2

Best-BlastP=> >nrprot No Hits found

3359.2

Best-BlastP=> >nrprot 48% Identities = 221/706 (31%), Positives = 362/706 (51%), Gaps = 53/706 (7%) ref|NP\_820588.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO91102.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 698

336.1

Best-BlastP=> >nrprot 69% Identities = 186/324 (57%), Positives = 230/324 (70%), Gaps = 2/324 (0%) ref|NP\_384292.1| PHOSPHATE TRANSPORT TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] sp|O30499|PIT\_RHIME Probable low-affinity inorganic phosphate transporter gb|AAB70171.1| phosphate transport protein [Sinorhizobium meliloti] emb|CAC41573.1| PHOSPHATE TRANSPORT TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] Length = 334

3360.1

Best-BlastP=> >nrprot No Hits found

3362.1

Best-BlastP=> >nrprot 43% Identities = 68/209 (32%), Positives = 106/209 (50%), Gaps = 5/209 (2%) ref|NP\_178286.1| membrane protein - related [Arabidopsis thaliana] pir|H84428 probable membrane protein [imported] - Arabidopsis thaliana gb|AAD12695.1| putative membrane protein [Arabidopsis thaliana] Length = 250

3363.2

Best-BlastP=> >nrprot 64% Identities = 148/300 (49%), Positives = 204/300 (68%), Gaps = 11/300 (3%) gb|AAC64375.1| thiamine synthase homolog [Botryotinia fuckeliana] Length = 342

3365.2

Best-BlastP=> >nrprot 66% Identities = 173/347 (49%), Positives = 238/347 (68%), Gaps = 13/347 (3%) ref|NP\_819373.1| thiamine biosynthesis oxidoreductase ThiO, putative [Coxiella burnetii RSA 493] gb|AAO89887.1| thiamine biosynthesis oxidoreductase ThiO, putative [Coxiella burnetii RSA 493] Length = 338

- 3367.1 Best-BlastP=> >nrprot 41% Identities = 81/269 (30%), Positives = 123/269 (45%), Gaps = 20/269 (7%) emb[CAC17409.1] 3'-nucleotidase/nuclease [Leishmania mexicana] Length = 378
- 3368.2 Best-BlastP=> >nrprot No Hits found
- 337.2 Best-BlastP=> >nrprot 67% Identities = 241/457 (52%), Positives = 311/457 (68%), Gaps = 4/457 (0%) ref[NP\_830123.1] Amino acid permease [Bacillus cereus ATCC 14579] gb|AAP07324.1| Amino acid permease [Bacillus cereus ATCC 14579] Length = 471
- 3371.2 Best-BlastP=> >nrprot 83% Identities = 321/438 (73%), Positives = 372/438 (84%) ref[NP\_819599.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90113.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 439
- 3374.1 Best-BlastP=> >nrprot 25% Identities = 60/222 (27%), Positives = 94/222 (42%), Gaps = 21/222 (9%) ref[NP\_774046.1] blI7406 [Bradyrhizobium japonicum] dbj|BAC52671.1| blI7406 [Bradyrhizobium japonicum USDA 110] Length = 300
- 3376.1
- Best-BlastP=> >nrprot 30% Identities = 62/236 (26%), Positives = 106/236 (44%), Gaps = 15/236 (6%) ref[NP\_819950.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90464.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 465
- 3378.2 Best-BlastP=> >nrprot 56% Identities = 210/580 (36%), Positives = 331/580 (57%), Gaps = 9/580 (1%) gb|AAC44717.1| FrgA [Legionella pneumophila] Length = 575
- 3385.1 Best-BlastP=> >nrprot 74% Identities = 252/254 (99%), Positives = 254/254 (100%) gb|AAM00642.1| essential conserved GTPase [Legionella pneumophila] Length = 254
- 3386.1 Best-BlastP=> >nrprot 77% Identities = 62/85 (72%), Positives = 72/85 (84%) ref[NP\_636525.1] 50S ribosomal protein L27 [Xanthomonas campestris pv. campestris str. ATCC 33913] sp|Q8PBH1|RL27\_XANCP 50S ribosomal protein L27 gb|AAM40449.1| 50S ribosomal protein L27 [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 86
- 3388.1 Best-BlastP=> >nrprot 28% Identities = 65/168 (38%), Positives = 105/168 (62%), Gaps = 1/168 (0%) ref[XP\_00125980.1] COG2199: FOG: GGDEF domain [Pseudomonas syringae pv. syringae B728a] Length = 972
- 3389.1 Best-BlastP=> >nrprot 68% Identities = 149/315 (47%), Positives = 222/315 (70%) ref[XP\_00068004.1] COG0142: Geranylgeranyl pyrophosphate synthase [Microbulifer degradans 2-40] Length = 320
- 339.4 Best-BlastP=> >nrprot 89% Identities = 168/194 (86%), Positives = 174/194 (89%), Gaps = 8/194 (4%) gb|AAK52070.1| Rcp [Legionella pneumophila] Length = 186
- 3390.1 Best-BlastP=> >nrprot 37% Identities = 21/61 (34%), Positives = 32/61 (52%) ref[NP\_820745.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91259.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 72
- 3391.2 Best-BlastP=> >nrprot 99% Identities = 748/751 (99%), Positives = 749/751 (99%) gb|AAN17185.1| AF492466\_3 ferrous iron transporter B [Legionella pneumophila] Length = 751
- 3394.1 Best-BlastP=> >nrprot No Hits found
- 3395.2 Best-BlastP=> >nrprot No Hits found
- 3396.1 Best-BlastP=> >nrprot No Hits found
- 3397.1 Best-BlastP=> >nrprot 62% Identities = 72/167 (43%), Positives = 106/167 (63%), Gaps = 6/167 (3%) ref[NP\_840350.1] putative antirestriction protein [Nitrosomonas europaea ATCC 19718] emb|CAD84171.1| putative antirestriction protein [Nitrosomonas europaea ATCC 19718] Length = 171



- 3398.1 Best-BlastP=> >nrprot 61% Identities = 58/145 (40%), Positives = 87/145 (60%), Gaps = 7/145 (4%) ref|NP\_252922.1| single-stranded DNA-binding protein [Pseudomonas aeruginosa PA01] sp|P40947|SSB\_PSEAE Single-strand binding protein (SSB) (Helix-destabilizing protein) pir|S44302 single-stranded DNA-binding protein - Pseudomonas aeruginosa emb|CAA83688.1| single-stranded DNA binding protein [Pseudomonas aeruginosa] gb|AAG07620.1|AE004840\_6 single-stranded DNA-binding protein [Pseudomonas aeruginosa PAO1] Length = 165
- 3399.1 Best-BlastP=> >nrprot No Hits found
- 34.1 Best-BlastP=> >nrprot No Hits found
- 3401.2 Best-BlastP=> >nrprot No Hits found
- 3402.2 Best-BlastP=> >nrprot 53% Identities = 108/298 (36%), Positives = 160/298 (53%), Gaps = 14/298 (4%) ref|NP\_862370.1| unknown [Francisella tularensis subsp. novicida] gb|AAD17308.1| unknown [Francisella tularensis subsp. novicida] Length = 292
- 3404.2 Best-BlastP=> >nrprot 31% Identities = 51/187 (27%), Positives = 86/187 (45%), Gaps = 9/187 (4%) ref|ZP\_00091084.1| COG0582: Integrase [Azotobacter vinelandii] Length = 287
- 3406.2 Best-BlastP=> >nrprot 34% Identities = 46/197 (23%), Positives = 76/197 (38%), Gaps = 13/197 (6%) ref|NP\_466297.1| hypothetical membrane protein [Listeria monocytogenes EGD-e] pir|AF1421 hypothetical membrane protein lmo2775 [imported] - Listeria monocytogenes (strain EGD-e) emb|CAD00988.1| lmo2775 [Listeria monocytogenes] Length = 722
- 341.6 Best-BlastP=> >nrprot 99% Identities = 141/141 (100%), Positives = 141/141 (100%) gb|AAC44222.1| hemin binding protein Hbp [Legionella pneumophila] Length = 141
- 3411.2 Best-BlastP=> >nrprot 20% Identities = 42/162 (25%), Positives = 75/162 (46%), Gaps = 10/162 (6%) ref|NP\_871522.1| rplA [Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis] sp|Q8D236|RL1\_WIGBR 50S ribosomal protein L1 dbj|BAC24665.1| rplA [Wigglesworthia brevipalpis] Length = 242
- 3413.2 Best-BlastP=> >nrprot 49% Identities = 76/296 (25%), Positives = 150/296 (50%), Gaps = 16/296 (5%) ref|NP\_832129.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] gb|AAP09330.1| Transcriptional regulators, LysR family [Bacillus cereus ATCC 14579] Length = 300
- 3414.3 Best-BlastP=> >nrprot 33% Identities = 115/406 (28%), Positives = 184/406 (45%), Gaps = 47/406 (11%) ref|ZP\_00112010.1| COG0666: FOG: Ankyrin repeat [Nostoc punctiforme] Length = 427
- 3415.2 Best-BlastP=> >nrprot 38% Identities = 48/154 (31%), Positives = 69/154 (44%), Gaps = 14/154 (9%) ref|NP\_740808.1| dot1l Histone Methyltransferase (1C952) [Caenorhabditis elegans] gb|AAK39620.2| Hypothetical protein Y39G10AR.18a [Caenorhabditis elegans] Length = 1015
- 3416.1 Best-BlastP=> >nrprot 73% Identities = 65/99 (65%), Positives = 76/99 (76%) ref|NP\_820718.1| integration host factor, beta subunit [Coxiella burnetii RSA 493] gb|AAO91232.1| integration host factor, beta subunit [Coxiella burnetii RSA 493] Length = 112
- 3417.1 Best-BlastP=> >nrprot 91% Identities = 155/191 (81%), Positives = 172/191 (90%), Gaps = 3/191 (1%) ref|NP\_780077.1| deoxycytidine triphosphate deaminase [Xylella fastidiosa Temecula1] sp|Q87AD1|DCD\_XYLFT Deoxycytidine triphosphate deaminase (dCTP deaminase) gb|AAO29726.1| deoxycytidine triphosphate deaminase [Xylella fastidiosa Temecula1] Length = 191
- 3418.1 Best-BlastP=> >nrprot 99% Identities = 283/283 (100%), Positives = 283/283 (100%) gb|AAC83338.1| major outer membrane protein precursor [Legionella pneumophila] gb|AAC83342.1| major outer membrane protein precursor [Legionella pneumophila] Length = 289

- 3419.3 Best-BlastP=> >nrprot 36% Identities = 47/225 (20%), Positives = 93/225 (41%), Gaps = 37/225 (16%) ref|NP\_703974.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7] emb|CAD50587.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7] Length = 2879
- 342.2 Best-BlastP=> >nrprot 74% Identities = 237/407 (58%), Positives = 310/407 (76%) ref|NP\_924319.1| probable aminotransferase [Gloeobacter violaceus] dbj|BAC89314.1| gir1373 [Gloeobacter violaceus] Length = 417
- 3421.2 Best-BlastP=> >nrprot 27% Identities = 56/257 (21%), Positives = 108/257 (42%), Gaps = 32/257 (12%) ref|NP\_705457.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD52694.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1179
- 3423.3 Best-BlastP=> >nrprot 86% Identities = 335/366 (91%), Positives = 346/366 (94%) gb|AAL23711.1| RalF [Legionella pneumophila] Length = 374
- 3426.1 Best-BlastP=> >nrprot 33% Identities = 56/142 (39%), Positives = 78/142 (54%), Gaps = 2/142 (1%) ref|NP\_108258.1| hypothetical protein [Mesorhizobium loti] dbj|BAB53719.1| hypothetical protein [Mesorhizobium loti] Length = 285
- 3428.1 Best-BlastP=> >nrprot 47% Identities = 72/233 (30%), Positives = 129/233 (55%), Gaps = 2/233 (0%) ref|ZP\_00006345.1| COG1409: Predicted phosphohydrolases [Rhodobacter sphaeroides] Length = 273
- 3429.1 Best-BlastP=> >nrprot 33% Identities = 126/638 (19%), Positives = 247/638 (38%), Gaps = 85/638 (13%) gb|EAA15312.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 1527
- 343.1 Best-BlastP=> >nrprot 70% Identities = 78/139 (56%), Positives = 106/139 (76%) ref|NP\_924320.1| hypothetical protein gir1374 [Gloeobacter violaceus] dbj|BAC93315.1| gir1374 [Gloeobacter violaceus] Length = 148
- 3431.3 Best-BlastP=> >nrprot 39% Identities = 109/279 (39%), Positives = 169/279 (60%), Gaps = 8/279 (2%) ref|ZP\_00023400.1| COG2056: Predicted permease [Ralstonia metallidurans] Length = 325
- 3432.2 Best-BlastP=> >nrprot 63% Identities = 161/334 (48%), Positives = 218/334 (65%) ref|NP\_346834.1| Similar to chloromuconate cycloisomerase [Clostridium acetobutylicum] pir|C96923 similar to chloromuconate cycloisomerase [imported] - Clostridium acetobutylicum gb|AAK78174.1|AE007532\_7 Similar to chloromuconate cycloisomerase [Clostridium acetobutylicum] Length = 358
- 3437.1 Best-BlastP=> >nrprot 32% Identities = 79/336 (23%), Positives = 125/336 (37%), Gaps = 58/336 (17%) ref|NP\_523168.1| PROBABLE ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD18760.1| PROBABLE ACID SPHINGOMYELINASE-LIKE PHOSPHODIESTERASE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 476
- 344.1 Best-BlastP=> >nrprot 67% Identities = 58/107 (54%), Positives = 76/107 (71%) ref|ZP\_00096500.1| COG2151: Predicted metal-sulfur cluster biosynthetic enzyme [Novosphingobium aromaticivorans] Length = 160
- 3442.3 Best-BlastP=> >nrprot 41% Identities = 160/450 (35%), Positives = 247/450 (54%), Gaps = 6/450 (1%) ref|NP\_819065.1| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Coxiella burnetii RSA 493] gb|AAO89579.1| D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Coxiella burnetii RSA 493] Length = 477
- 3443.1 Best-BlastP=> >nrprot 64% Identities = 112/252 (44%), Positives = 170/252 (67%) ref|ZP\_00091089.1| COG1475: Predicted transcriptional regulators [Azotobacter vinelandii] Length = 294
- 3444.1 Best-BlastP=> >nrprot No Hits found

- 3445.3 Best-BlastP=> >nrprot 53% Identities = 141/332 (42%), Positives = 185/332 (55%), Gaps = 16/332 (4%) ref|ZP\_00140422.1| COG1652: Uncharacterized protein containing LysM domain [Pseudomonas aeruginosa UCBPP-PA14] Length = 371
- 3446.1 Best-BlastP=> >nrprot 56% Identities = 158/291 (54%), Positives = 205/291 (70%), Gaps = 3/291 (1%) ref|NP\_820973.1| DNA processing protein DprA, putative [Coxiella burnetii RSA 493] gb|AAO91487.1| DNA processing protein DprA, putative [Coxiella burnetii RSA 493] Length = 308
- 3447.1 Best-BlastP=> >nrprot 43% Identities = 30/121 (24%), Positives = 64/121 (52%), Gaps = 5/121 (4%) ref|NP\_484103.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AC1814 hypothetical protein all0059 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB77583.1| ORF\_ID:all0059-hypothetical protein [Nostoc sp. PCC 7120] Length = 727
- 3450.2 Best-BlastP=> >nrprot 73% Identities = 202/344 (58%), Positives = 264/344 (76%), Gaps = 1/344 (0%) ref|NP\_469414.1| similar to E. coli Ada protein (O6-methylguanine-DNA methyltransferase) [Listeria innocua] pir|AE1441 E. coli Ada protein (O6-methylguanine-DNA methyltransferase) homolog lin0068 [imported] - Listeria innocua (strain Clp11262) emb|CAC95301.1| lin0068 [Listeria innocua] Length = 350
- 3451.1 Best-BlastP=> >nrprot No Hits found
- 3453.1 Best-BlastP=> >nrprot 10% Identities = 40/127 (31%), Positives = 53/127 (41%), Gaps = 19/127 (14%) ref|NP\_356305.1| AGR\_L\_1030p [Agrobacterium tumefaciens] ref|NP\_534828.1| hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AB3091 hypothetical protein Atu4350 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir|H98195 hypothetical protein AGR\_L\_1030 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) gb|AAK89090.1| AGR\_L\_1030p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL45144.1| hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 278
- 3454.1 Best-BlastP=> >nrprot 42% Identities = 31/137 (22%), Positives = 62/137 (45%), Gaps = 21/137 (15%) ref|NP\_832446.1| Acetyltransferase [Bacillus cereus ATCC 14579] gb|AAP09647.1| Acetyltransferase [Bacillus cereus ATCC 14579] Length = 141
- 3455.3 Best-BlastP=> >nrprot No Hits found
- 3456.4 Best-BlastP=> >nrprot 70% Identities = 83/166 (50%), Positives = 119/166 (71%), Gaps = 7/166 (4%) ref|ZP\_00012554.1| COG3158: K+ transporter [Rhodopseudomonas palustris] Length = 620
- 3459.3 Best-BlastP=> >nrprot 57% Identities = 189/475 (39%), Positives = 283/475 (59%), Gaps = 7/475 (1%) gb|AAP85869.1| putative potassium uptake protein [Ralstonia eutropha] Length = 632
- 346.2 Best-BlastP=> >nrprot 67% Identities = 160/326 (49%), Positives = 216/326 (66%), Gaps = 11/326 (3%) sp|Q9KNS6|SYK3\_VIBCH Putative lysyl-tRNA synthetase (Lysine--tRNA ligase) (LysRS) (GX) Length = 324
- 3461.4 Best-BlastP=> >nrprot 18% Identities = 67/286 (23%), Positives = 116/286 (40%), Gaps = 45/286 (15%) gb|EAA19312.1| heat shock protein hsp70 homologue Pfhs70-3 [Plasmodium yoelii] Length = 663
- 3463.1 Best-BlastP=> >nrprot 84% Identities = 199/269 (73%), Positives = 233/269 (86%) ref|ZP\_00103515.1| COG2877: 3-deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase [Desulfitobacterium hafniense] Length = 277
- 3465.2 Best-BlastP=> >nrprot 84% Identities = 371/544 (68%), Positives = 460/544 (84%), Gaps = 1/544 (0%) ref|ZP\_00067534.1| COG0504: CTP synthase (UTP-ammonia lyase) [Microbulbifer degradans] Length = 543

- 3466.1 Best-BlastP=> >nrprot 61% Identities = 28/60 (46%), Positives = 41/60 (68%), Gaps = 2/60 (3%) ref|NP\_908035.1| HYPOTHETICAL PROTEIN-Putative Site-specific recombinaase [Wolinella succinogenes] Length = 207
- 3468.2 Best-BlastP=> >nrprot 78% Identities = 236/412 (57%), Positives = 320/412 (77%), Gaps = 14/412 (3%) pir|S42875 dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Coxiella burnetii emb|CAA54875.1| putative dihydrolipoamide succinyltransferase [Coxiella burnetii] Length = 405
- 347.1 Best-BlastP=> >nrprot 60% Identities = 119/292 (40%), Positives = 182/292 (62%), Gaps = 1/292 (0%) ref|ZP\_00055839.1| COG2933: Predicted SAM-dependent methyltransferase [Magnetospirillum magnetotacticum] Length = 324
- 3472.1 Best-BlastP=> >nrprot 27% Identities = 26/50 (52%), Positives = 28/50 (56%), Gaps = 10/50 (20%) ref|NP\_773097.1| bl6457 [Bradyrhizobium japonicum] dbj|BAC51722.1| bl6457 [Bradyrhizobium japonicum USDA 110] Length = 254
- 3473.1 Best-BlastP=> >nrprot No Hits found
- 3476.1 Best-BlastP=> >nrprot 63% Identities = 160/356 (44%), Positives = 238/356 (66%) ref|NP\_819753.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 377
- 3477.2 Best-BlastP=> >nrprot 76% Identities = 140/241 (58%), Positives = 187/241 (77%) ref|NP\_819754.1| ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] gb|AAO90268.1| ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] Length = 268
- 3480.4 Best-BlastP=> >nrprot 56% Identities = 185/551 (33%), Positives = 314/551 (56%), Gaps = 12/551 (2%) ref|NP\_441242.1| hypothetical protein [Synechocystis sp. PCC 6803] pir|S75060 conserved hypothetical protein sl1595 - Synechocystis sp. (strain PCC 6803) dbj|BAA17922.1| ORF\_ID:sl1595-hypothetical protein [Synechocystis sp. PCC 6803] Length = 568
- 3481.2 Best-BlastP=> >nrprot 67% Identities = 38/89 (42%), Positives = 61/89 (68%), Gaps = 1/89 (1%) ref|NP\_442504.1| PCC7942 clock gene...ORFE [Synechocystis sp. PCC 6803] pir|S76630 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj|BAA10574.1| sl0486 [Synechocystis sp. PCC 6803] Length = 102
- 3483.3 Best-BlastP=> >nrprot 52% Identities = 71/196 (36%), Positives = 106/196 (54%), Gaps = 7/196 (3%) ref|NP\_216630.1| hypothetical protein Rv2114 [Mycobacterium tuberculosis H37Rv] ref|NP\_855787.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pir|E70512 hypothetical protein Rv2114 - Mycobacterium tuberculosis (strain H37RV) emb|CAB10705.1| hypothetical protein Rv2114 [Mycobacterium tuberculosis H37Rv] emb|CAD96991.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 207
- 3484.1 Best-BlastP=> >nrprot No Hits found
- 3485.1 Best-BlastP=> >nrprot No Hits found
- 3486.1 Best-BlastP=> >nrprot No Hits found
- 3488.1 Best-BlastP=> >nrprot 16% Identities = 52/260 (20%), Positives = 116/260 (44%), Gaps = 26/260 (10%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738
- 3489.2 Best-BlastP=> >nrprot 22% Identities = 37/178 (20%), Positives = 74/178 (41%), Gaps = 13/178 (7%) ref|NP\_624872.1| hypothetical protein SCF73.06c [Streptomyces coelicolor A3(2)] emb|CAB57411.1| hypothetical protein SCF73.06c [Streptomyces coelicolor A3(2)] Length = 333

- 349.2 Best-BlastP=> >nprot 66% Identities = 109/211 (51%), Positives = 143/211 (67%), Gaps = 1/211 (0%) ref|ZP\_00013996.1| COG2872: Predicted metal-dependent hydrolases related to alanyl-tRNA synthetase HxxxH domain [Rhodospirillum rubrum] Length = 214
- 3494.2 Best-BlastP=> >nprot 55% Identities = 41/85 (48%), Positives = 58/85 (68%) ref|ZP\_00015213.1| COG2823: Predicted periplasmic or secreted lipoprotein [Rhodospirillum rubrum] Length = 104
- 3496.2 Best-BlastP=> >nprot 30% Identities = 37/120 (30%), Positives = 50/120 (41%), Gaps = 24/120 (20%) ref|NP\_827755.1| hypothetical protein [Streptomyces avermitilis MA-4680] dbj|BAC74290.1| hypothetical protein [Streptomyces avermitilis MA-4680] Length = 574
- 3498.1 Best-BlastP=> >nprot No Hits found
- 3499.1 Best-BlastP=> >nprot No Hits found
- 35.1 Best-BlastP=> >nprot 98% Identities = 262/265 (98%), Positives = 262/265 (98%) emb|CAB60063.1| lvrE [Legionella pneumophila] Length = 265
- 350.3 Best-BlastP=> >nprot 25% Identities = 29/124 (23%), Positives = 50/124 (40%), Gaps = 12/124 (9%) gb|AAD40638.1| AF128842\_1 extracellular calcium-sensing receptor [Mus musculus] Length = 1079
- 3500.3 Best-BlastP=> >nprot 30% Identities = 61/283 (21%), Positives = 120/283 (42%), Gaps = 16/283 (5%) ref|NP\_928738.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13733.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 417
- 3502.3 Best-BlastP=> >nprot 55% Identities = 57/145 (39%), Positives = 91/145 (62%), Gaps = 5/145 (3%) pir|JQ0144 probable protein-disulfide oxidoreductase (EC 1.8.4.-) - Pseudomonas aeruginosa Length = 163
- 3503.2 Best-BlastP=> >nprot 74% Identities = 229/383 (59%), Positives = 287/383 (74%) ref|NP\_820071.1| queueine tRNA-ribosyltransferase [Coxiella burnetii RSA 493] gb|AAO90585.1| queueine tRNA-ribosyltransferase [Coxiella burnetii RSA 493] Length = 385
- 3504.1 Best-BlastP=> >nprot 98% Identities = 163/164 (99%), Positives = 163/164 (99%) pir|S49314 peptidylprolyl isomerase (EC 5.2.1.8) - Legionella pneumophila emb|CAA58722.1| cyclophilin [Legionella pneumophila] Length = 164
- 3506.1 Best-BlastP=> >nprot 69% Identities = 116/212 (54%), Positives = 146/212 (68%), Gaps = 4/212 (1%) ref|NP\_245872.1| unknown [Pasteurella multocida] gb|AAK03019.1| unknown [Pasteurella multocida] Length = 226
- 3507.1 Best-BlastP=> >nprot 52% Identities = 29/123 (23%), Positives = 60/123 (48%), Gaps = 8/123 (6%) gb|EAA21917.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 296
- 3508.2 Best-BlastP=> >nprot 61% Identities = 43/94 (45%), Positives = 61/94 (64%) ref|ZP\_00088933.1| COG0640: Predicted transcriptional regulators [Azotobacter vinelandii] Length = 107
- 3509.2 Best-BlastP=> >nprot 15% Identities = 31/117 (26%), Positives = 55/117 (47%) ref|XP\_306772.1| ENSANGP00000000282 [Anopheles gambiae] gb|EAA02010.2| ENSANGP00000000282 [Anopheles gambiae str. PEST] Length = 210
- 351.1 Best-BlastP=> >nprot 59% Identities = 52/141 (36%), Positives = 89/141 (63%), Gaps = 6/141 (4%) ref|NP\_562901.1| conserved hypothetical protein [Clostridium perfringens] dbj|BAB81691.1| conserved hypothetical protein [Clostridium perfringens str. 13] Length = 168

- 3511.2 Best-BlastP=> >nprot 61% Identities = 160/368 (43%), Positives = 237/368 (64%) ref[NP\_902574.1] conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60572.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 377
- 3512.1 Best-BlastP=> >nprot 13% Identities = 37/145 (25%), Positives = 72/145 (49%), Gaps = 9/145 (6%) dbj|BAB62990.1| hypothetical protein [Macaca fascicularis] Length = 533
- 3514.1 Best-BlastP=> >nprot No Hits found
- 3515.2 Best-BlastP=> >nprot 25% Identities = 28/85 (32%), Positives = 42/85 (49%), Gaps = 4/85 (4%) ref[NP\_745177.1] pyocin R2\_PP, transcriptional repressor, C1/C2 family [Pseudomonas putida KT2440] gb|AAN6864.1|AE016494\_1 pyocin R2\_PP, transcriptional repressor, C1/C2 family [Pseudomonas putida KT2440] Length = 243
- 3516.2 Best-BlastP=> >nprot 53% Identities = 25/56 (44%), Positives = 38/56 (67%) ref[NP\_246251.1] unknown [Pasteurella multocida] sp|Q9CLC6|YD13\_PASMU Hypothetical UPF0235 protein PM1313 gb|AAK03397.1| unknown [Pasteurella multocida] Length = 99
- 3517.3 Best-BlastP=> >nprot 56% Identities = 135/383 (35%), Positives = 219/383 (57%), Gaps = 2/383 (0%) ref[NP\_820467.1] major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO90981.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 428
- 3519.1 Best-BlastP=> >nprot 31% Identities = 80/231 (34%), Positives = 124/231 (53%), Gaps = 7/231 (3%) ref[NP\_828099.1] putative glycosyl transferase [Streptomyces avermitilis MA-4680] dbj|BAC74634.1| putative glycosyl transferase [Streptomyces avermitilis MA-4680] Length = 265
- 3520.1 Best-BlastP=> >nprot 33% Identities = 90/291 (30%), Positives = 153/291 (52%), Gaps = 5/291 (1%) ref[ZP\_00056311.1] COG1807: 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family [Magnetospirillum magnetotacticum] Length = 500
- 3521.2 Best-BlastP=> >nprot 38% Identities = 88/281 (31%), Positives = 147/281 (52%), Gaps = 16/281 (5%) ref[NP\_561543.1] probable choline kinase [Clostridium perfringens] dbj|BAB80333.1| probable choline kinase [Clostridium perfringens str. 13] Length = 622
- 3522.1 Best-BlastP=> >nprot 70% Identities = 143/261 (54%), Positives = 180/261 (68%), Gaps = 11/261 (4%) ref[ZP\_00022284.1] COG3298: Predicted 3'-5' exonuclease related to the exonuclease domain of PolB [Ralstonia metallidurans] Length = 278
- 3524.1 Best-BlastP=> >nprot 67% Identities = 76/142 (53%), Positives = 97/142 (68%) ref[ZP\_00065344.1] COG4764: Uncharacterized protein conserved in bacteria [Microbulifer degradans 2-40] Length = 204
- 3525.1 Best-BlastP=> >nprot 78% Identities = 137/218 (62%), Positives = 171/218 (78%) ref[NP\_888550.1] adenylate kinase [Bordetella bronchiseptica] emb|CAE32502.1| adenylate kinase [Bordetella bronchiseptica] Length = 218
- 3527.1 Best-BlastP=> >nprot 63% Identities = 50/115 (43%), Positives = 77/115 (66%) ref[ZP\_00042420.1] COG0526: Thiol-disulfide isomerase and thioredoxins [Magnetococcus sp. MC-1] Length = 124
- 3530.1 Best-BlastP=> >nprot No Hits found
- 3532.1 Best-BlastP=> >nprot 25% Identities = 141/689 (20%), Positives = 276/689 (40%), Gaps = 124/689 (17%) ref[NP\_048227.1] ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] pir|T28317 ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus gb|AAC97677.1| ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] Length = 1127

- 3533.1 Best-BlastP=> >nrprot 81% Identities = 155/205 (75%), Positives = 173/205 (84%) ref|NP\_819890.1| uridine kinase [Coxiella burnetii RSA 493]  
gb|AAO90404.1| uridine kinase [Coxiella burnetii RSA 493] Length = 215
- 3534.2 Best-BlastP=> >nrprot 79% Identities = 353/540 (65%), Positives = 435/540 (80%), Gaps = 1/540 (0%) emb|CAD23197.1| alkaline  
phosphomonoesterase [Fluoribacter gormanii] Length = 540
- 3535.5 Best-BlastP=> >nrprot No Hits found
- 3536.2 Best-BlastP=> >nrprot 58% Identities = 38/91 (41%), Positives = 58/91 (63%) ref|NP\_819118.1| rhodanese domain protein [Coxiella burnetii RSA  
493] gb|AAO89632.1| rhodanese domain protein [Coxiella burnetii RSA 493] Length = 124
- 3538.1 Best-BlastP=> >nrprot 47% Identities = 107/257 (41%), Positives = 151/257 (58%), Gaps = 2/257 (0%) ref|ZP\_00025602.1| COG1052: Lactate  
dehydrogenase and related dehydrogenases [Ralstonia metallidurans] Length = 312
- 354.1 Best-BlastP=> >nrprot 67% Identities = 239/471 (50%), Positives = 320/471 (67%), Gaps = 19/471 (4%) ref|NP\_820171.1| deoxyribodipyrimidine  
photolyase - class I [Coxiella burnetii RSA 493] gb|AAO90685.1| deoxyribodipyrimidine photolyase - class I [Coxiella burnetii RSA  
493] Length = 472
- 3540.2 Best-BlastP=> >nrprot 95% Identities = 574/614 (93%), Positives = 591/614 (96%) sp|Q48806|DLPA\_LEGPN Protein dlpA pir|S61390 dlpA  
protein - Legionella pneumophila gb|AAA79904.1| DlpA Length = 615
- 3541.1
- 3542.1 Best-BlastP=> >nrprot 67% Identities = 127/248 (51%), Positives = 172/248 (69%), Gaps = 2/248 (0%) ref|NP\_819461.1| pantoate-beta-alanine  
ligase [Coxiella burnetii RSA 493] gb|AAO89975.1| pantoate-beta-alanine ligase [Coxiella burnetii RSA 493] Length = 257
- Best-BlastP=> >nrprot 70% Identities = 134/256 (52%), Positives = 186/256 (72%) ref|NP\_819462.1| 3-methyl-2-oxobutanoate  
hydroxymethyltransferase [Coxiella burnetii RSA 493] gb|AAO89976.1| 3-methyl-2-oxobutanoate hydroxymethyltransferase [Coxiella  
burnetii RSA 493] Length = 266
- 3543.1 Best-BlastP=> >nrprot 57% Identities = 87/197 (44%), Positives = 127/197 (64%) ref|NP\_820749.1| conserved hypothetical protein [Coxiella  
burnetii RSA 493] gb|AAO91263.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 205
- 3544.2 Best-BlastP=> >nrprot 99% Identities = 355/360 (98%), Positives = 359/360 (99%) gb|AAN17183.1|AF492466\_1 hypothetical protein [Legionella  
pneumophila] Length = 360
- 3545.1 Best-BlastP=> >nrprot 64% Identities = 153/310 (49%), Positives = 211/310 (68%), Gaps = 3/310 (0%) ref|ZP\_00123394.1| COG0196: FAD  
synthase [Haemophilus somnus 129PT] ref|ZP\_00133316.1| hypothetical protein [Haemophilus somnus 2336] Length = 314
- 3547.1
- Best-BlastP=> >nrprot 62% Identities = 64/141 (45%), Positives = 90/141 (63%), Gaps = 2/141 (1%) ref|NP\_820893.1| universal stress protein A,  
putative [Coxiella burnetii RSA 493] sp|P45680|YJ16\_COXBU Hypothetical protein CBU1916 pir||40650 hypothetical protein 146 - Coxiella  
burnetii gb|AAA56915.1| unknown gb|AAO91407.1| universal stress protein A, putative [Coxiella burnetii RSA 493] Length = 146
- 3548.2 Best-BlastP=> >nrprot 41% Identities = 104/503 (20%), Positives = 202/503 (40%), Gaps = 80/503 (15%) ref|ZP\_00084271.1| COG3266:  
Uncharacterized protein conserved in bacteria [Pseudomonas fluorescens PfO-1] Length = 533
- 3550.1 Best-BlastP=> >nrprot 51% Identities = 189/192 (98%), Positives = 190/192 (98%) gb|AAF05326.1| 3-dehydroquinate synthetase homolog  
[Legionella pneumophila] Length = 192
- 3551.1 Best-BlastP=> >nrprot 75% Identities = 103/165 (62%), Positives = 133/165 (80%) ref|ZP\_00134627.1| COG0703: Shikimate kinase  
[Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 173



- 3554.4 Best-BlastP=> >nrprot 64% Identities = 92/193 (47%), Positives = 129/193 (66%), Gaps = 5/193 (2%) ref|NP\_794862.1| type IV pilus biogenesis protein PilO [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58557.1| type IV pilus biogenesis protein PilO [Pseudomonas syringae pv. tomato str. DC3000] Length = 207
- 3555.2 Best-BlastP=> >nrprot 60% Identities = 72/175 (41%), Positives = 111/175 (63%) gb|AAA93087.1| membrane protein Length = 199
- 3556.2 Best-BlastP=> >nrprot 44% Identities = 35/118 (29%), Positives = 63/118 (53%), Gaps = 1/118 (0%) ref|NP\_820127.1| NifU family protein [Coxiella burnetii RSA 493] gb|AAO90641.1| NifU family protein [Coxiella burnetii RSA 493] Length = 119
- 3557.1 Best-BlastP=> >nrprot 78% Identities = 236/383 (61%), Positives = 303/383 (79%) ref|NP\_717860.1| cysteine desulfurase [Shewanella oneidensis MR-1] gb|AAN55304.1|AE015668\_5 cysteine desulfurase [Shewanella oneidensis MR-1] Length = 404
- 3558.1 Best-BlastP=> >nrprot No Hits found
- 3559.2 Best-BlastP=> >nrprot No Hits found
- 3561.2 Best-BlastP=> >nrprot 99% Identities = 782/783 (99%), Positives = 783/783 (100%) pir|T18329| icmO protein - Legionella pneumophila emb|CAAT3241.1| icmO protein [Legionella pneumophila] gb|AAC38193.1| DotL [Legionella pneumophila] emb|CAA75326.1| icmO protein [Legionella pneumophila] Length = 783
- 3562.3 Best-BlastP=> >nrprot 99% Identities = 374/376 (99%), Positives = 376/376 (100%) pir|T18328| icmP protein - Legionella pneumophila emb|CAAT3240.1| icmP protein [Legionella pneumophila] gb|AAC38194.1| DotM [Legionella pneumophila] emb|CAA75325.1| icmP protein [Legionella pneumophila] Length = 376
- 3563.2 Best-BlastP=> >nrprot 47% Identities = 35/90 (38%), Positives = 55/90 (61%), Gaps = 5/90 (5%) dbj|BAC94688.1| hypothetical protein [Vibrio vulnificus YJ016] Length = 343
- 3564.2 Best-BlastP=> >nrprot No Hits found
- 3566.1 Best-BlastP=> >nrprot 76% Identities = 246/389 (63%), Positives = 305/389 (78%) ref|NP\_716561.1| phosphoglycerate kinase [Shewanella oneidensis MR-1] sp|Q8EIB1|PGK\_SHEON Phosphoglycerate kinase gb|AAN54006.1|AE015538\_3 phosphoglycerate kinase [Shewanella oneidensis MR-1] Length = 391
- 3568.3 Best-BlastP=> >nrprot 66% Identities = 231/477 (48%), Positives = 318/477 (66%), Gaps = 6/477 (1%) ref|NP\_743521.1| pyruvate kinase II [Pseudomonas putida KT2440] gb|AAN66985.1|AE016326\_11 pyruvate kinase II [Pseudomonas putida KT2440] Length = 484
- 357.2 Best-BlastP=> >nrprot 75% Identities = 138/234 (58%), Positives = 177/234 (75%) ref|NP\_540513.1| LrgB protein [Brucella melitensis] pir|AF3451|lrgB protein [imported] - Brucella melitensis (strain 16M) gb|AAL52777.1| murein hydrolase export regulator [Brucella melitensis 16M] Length = 235
- 3570.2 Best-BlastP=> >nrprot 67% Identities = 33/70 (47%), Positives = 48/70 (68%) ref|NP\_902003.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60005.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 75
- 3572.1 Best-BlastP=> >nrprot 88% Identities = 109/139 (78%), Positives = 124/139 (89%) ref|ZP\_00012735.1| COG0432: Uncharacterized conserved protein [Rhodopseudomonas palustris] Length = 139

- 3574.1 Best-BlastP=> >nrprot 40% Identities = 83/316 (26%), Positives = 130/316 (41%), Gaps = 44/316 (13%) ref|NP\_790689.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54384.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 312
- 3575.2 Best-BlastP=> >nrprot 42% Identities = 112/408 (27%), Positives = 192/408 (47%), Gaps = 20/408 (4%) ref|NP\_638463.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42387.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 414
- 3578.2 Best-BlastP=> >nrprot 91% Identities = 465/524 (88%), Positives = 480/524 (91%), Gaps = 6/524 (1%) gb|AAC35592.1| LphB [Legionella pneumophila] Length = 518
- 3581.1 Best-BlastP=> >nrprot 64% Identities = 148/160 (92%), Positives = 153/160 (95%) pir|S61389 small basic protein sbpA - Legionella pneumophila gb|AAA79903.1| SbpA Length = 161
- 3582.2 Best-BlastP=> >nrprot 64% Identities = 134/282 (47%), Positives = 186/282 (65%), Gaps = 1/282 (0%) ref|ZP\_00127817.1| hypothetical protein [Pseudomonas syringae pv. syringae B728a] Length = 288
- 3584.1 Best-BlastP=> >nrprot 60% Identities = 26/60 (43%), Positives = 39/60 (65%), Gaps = 2/60 (3%) ref|NP\_840361.1| possible transposase [Nitrosomonas europaea ATCC 19718] ref|NP\_841665.1| possible transposase [Nitrosomonas europaea ATCC 19718] emb|CAD84183.1| possible transposase [Nitrosomonas europaea ATCC 19718] emb|CAD85541.1| possible transposase [Nitrosomonas europaea ATCC 19718] Length = 135
- 3586.2 Best-BlastP=> >nrprot 67% Identities = 186/367 (50%), Positives = 251/367 (68%) ref|ZP\_00012935.1| COG3177: Uncharacterized conserved protein [Rhodopseudomonas palustris] Length = 367
- 3588.2 Best-BlastP=> >nrprot 69% Identities = 83/161 (51%), Positives = 115/161 (71%) ref|NP\_531634.1| methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|AH2691 methyltransferase Atu0936 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAL41950.1| methyltransferase [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 202
- 359.2 Best-BlastP=> >nrprot 41% Identities = 67/120 (55%), Positives = 85/120 (70%) ref|NP\_697359.1| conserved hypothetical protein [Brucella suis 1330] gb|AAN29274.1| AE014344\_9 conserved hypothetical protein [Brucella suis 1330] Length = 139
- 3591.2 Best-BlastP=> >nrprot 65% Identities = 83/182 (45%), Positives = 124/182 (68%), Gaps = 1/182 (0%) ref|ZP\_00067204.1| COG1678: Putative transcriptional regulator [Microbulifer degradans 2-40] Length = 203
- 3592.1 Best-BlastP=> >nrprot 65% Identities = 73/134 (54%), Positives = 94/134 (70%) gb|AAA69116.1| ORF\_o180; was also ORF\_o62p before splice Length = 180
- 3593.1 Best-BlastP=> >nrprot 62% Identities = 133/297 (44%), Positives = 193/297 (64%), Gaps = 10/297 (3%) ref|NP\_821065.1| aspartate carbamoyltransferase [Coxiella burnetii RSA 493] gb|AAO91579.1| aspartate carbamoyltransferase [Coxiella burnetii RSA 493] Length = 310
- 3594.1 Best-BlastP=> >nrprot No Hits found
- 3595.1 Best-BlastP=> >nrprot 64% Identities = 39/75 (52%), Positives = 56/75 (74%) ref|NP\_820996.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91510.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 81
- 3596.1 Best-BlastP=> >nrprot 79% Identities = 82/112 (73%), Positives = 99/112 (88%) ref|ZP\_00025955.1| COG0347: Nitrogen regulatory protein PII [Ralstonia metallidurans] Length = 112

- 3597.3 Best-BlastP=> >nrprot 56% Identities = 73/189 (38%), Positives = 109/189 (57%), Gaps = 7/189 (3%) ref|NP\_819119.1| 5-formyltetrahydrofolate  
cyclo-ligase family protein [Coxiella  
burnetii RSA 493] Length = 197
- 3598.3 Best-BlastP=> >nrprot No Hits found
- 3599.4 Best-BlastP=> >nrprot 48% Identities = 78/229 (34%), Positives = 131/229 (57%), Gaps = 3/229 (1%) ref|NP\_819456.1| 4-amino-4-  
deoxychorismate lyase, putative [Coxiella burnetii RSA  
493] Length = 281
- 36.1 Best-BlastP=> >nrprot 98% Identities = 606/613 (98%), Positives = 607/613 (99%) emb|CAB60062.1| lvhD4 [Legionella pneumophila]  
Length = 691
- 360.3 Best-BlastP=> >nrprot 7% Identities = 39/94 (41%), Positives = 47/94 (50%), Gaps = 1/94 (1%) ref|NP\_900714.1| hypothetical protein CV1044  
[Chromobacterium violaceum ATCC 12472] gb|AAQ58719.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472].  
Length = 499
- 3600.2 Best-BlastP=> >nrprot 66% Identities = 147/311 (47%), Positives = 207/311 (66%), Gaps = 1/311 (0%) ref|NP\_232559.1| conserved hypothetical  
protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|H82491 conserved hypothetical protein VCA0159 [imported] - Vibrio cholerae  
(strain N16961 serogroup O1) gb|AAF96072.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length =  
313
- 3601.1 Best-BlastP=> >nrprot 68% Identities = 183/385 (47%), Positives = 262/385 (68%), Gaps = 8/385 (2%) ref|ZP\_00065865.1| COG3004: Na+/H+  
antiporter [Microbulifer degradans 2-40] Length = 401
- 3602.2 Best-BlastP=> >nrprot 20% Identities = 73/282 (25%), Positives = 120/282 (42%), Gaps = 50/282 (17%) gb|EAA19568.1| hypothetical protein  
[Plasmodium yoelii yoelii] Length = 5074
- 3607.2 Best-BlastP=> >nrprot 56% Identities = 158/379 (41%), Positives = 224/379 (59%), Gaps = 12/379 (3%) ref|ZP\_00128328.1| COG2850:  
Uncharacterized conserved protein [Pseudomonas syringae pv. syringae B728a] Length = 388
- 3608.1 Best-BlastP=> >nrprot No Hits found
- 3609.1
- 3610.1 Best-BlastP=> >nrprot 99% Identities = 191/192 (99%), Positives = 192/192 (100%) sp|P31108|SODF\_LEGPN Superoxide dismutase [Fe]  
pir|J50749 superoxide dismutase (EC 1.15.1.1) (Fe) - Legionella pneumophila dbj|BAA02306.1| iron superoxide dismutase (Fe-SOD) [Legionella  
pneumophila] gb|AAM00603.1| superoxide dismutase [Legionella pneumophila] prf|2014300A Fe superoxide dismutase Length = 192
- Best-BlastP=> >nrprot 72% Identities = 202/384 (52%), Positives = 284/384 (73%) ref|NP\_841480.1| argD; acetylornithine aminotransferase  
[Nitrosomonas europaea ATCC 19718] emb|CAD85350.1| argD; acetylornithine aminotransferase [Nitrosomonas europaea ATCC  
19718] Length = 393
- 3611.2 Best-BlastP=> >nrprot 66% Identities = 119/254 (46%), Positives = 169/254 (66%), Gaps = 2/254 (0%) ref|NP\_440288.1| unknown protein  
[Synechocystis sp. PCC 6803] pir|S74928 hypothetical protein sl0647 - Synechocystis sp. (strain PCC 6803) dbj|BAA16968.1|  
ORF\_ID:sl0647~unknown protein [Synechocystis sp. PCC 6803] Length = 256
- 3612.2 Best-BlastP=> >nrprot 40% Identities = 68/222 (30%), Positives = 106/222 (47%), Gaps = 16/222 (7%) ref|NP\_229421.1| hypothetical protein  
[Thermotoga maritima] pir|G72232 hypothetical protein - Thermotoga maritima (strain MSB8) gb|AAD36688.1|AE001805\_13 hypothetical protein  
[Thermotoga maritima] Length = 222

- 3613.3 Best-BlastP=> >nrprot 75% Identities = 245/422 (58%), Positives = 326/422 (77%), Gaps = 2/422 (0%) ref|NP\_405097.1| NAD-dependent malic enzyme [Yersinia pestis] ref|NP\_669960.1| NAD-linked malate dehydrogenase (malic enzyme) [Yersinia pestis KIM] pir|AC0184 malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38) [imported] - Yersinia pestis (strain CO92) emb|CAC90334.1| NAD-dependent malic enzyme [Yersinia pestis CO92] gb|AAM86211.1|AE013868\_5 NAD-linked malate dehydrogenase (malic enzyme) [Yersinia pestis KIM] Length = 565
- 3614.3 Best-BlastP=> >nrprot 99% Identities = 353/354 (99%), Positives = 354/354 (100%) gb|AAM00637.1| putative cobalt/magnesium uptake transporter [Legionella pneumophila] Length = 354
- 3617.2 Best-BlastP=> >nrprot 83% Identities = 68/101 (67%), Positives = 85/101 (84%) ref|NP\_820421.1| NADH dehydrogenase I, K subunit [Coxiella burnetii RSA 493] gb|AAO90935.1| NADH dehydrogenase I, K subunit [Coxiella burnetii RSA 493] Length = 101
- 3618.2
- 3619.1 Best-BlastP=> >nrprot 70% Identities = 63/137 (45%), Positives = 100/137 (72%) ref|NP\_253434.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9HV53|YBE6\_PSEAE Hypothetical UPF0090 protein PA4746 pir|A83053 conserved hypothetical protein PA4746 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08132.1|AE004888\_7 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 152
- 3621.2 Best-BlastP=> >nrprot 78% Identities = 307/491 (62%), Positives = 385/491 (78%), Gaps = 2/491 (0%) ref|ZP\_000666603.1| COG0195: Transcription elongation factor [Microbulbifer degradans 2-40] Length = 493
- 3622.3 Best-BlastP=> >nrprot 71% Identities = 168/313 (53%), Positives = 226/313 (72%), Gaps = 1/313 (0%) ref|ZP\_00092328.1| hypothetical protein [Azotobacter vinelandii] Length = 379
- 3623.2 Best-BlastP=> >nrprot 73% Identities = 74/123 (60%), Positives = 92/123 (74%), Gaps = 1/123 (0%) ref|NP\_716411.1| glycine cleavage system H protein [Shewanella oneidensis MR-1] gb|AAN53856.1|AE015522\_11 glycine cleavage system H protein [Shewanella oneidensis MR-1] Length = 129
- 3625.2 Best-BlastP=> >nrprot 73% Identities = 270/452 (59%), Positives = 338/452 (74%), Gaps = 2/452 (0%) ref|NP\_840693.1| Glycine cleavage system P-protein [Nitrosomonas europaea ATCC 19718] emb|CAD84520.1| Glycine cleavage system P-protein [Nitrosomonas europaea ATCC 19718] Length = 453
- 3626.1 Best-BlastP=> >nrprot 59% Identities = 44/90 (48%), Positives = 61/90 (67%) ref|NP\_713147.1| conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb|AAN50165.1|AE011460\_7 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] Length = 104
- 3629.2 Best-BlastP=> >nrprot 75% Identities = 170/291 (58%), Positives = 223/291 (76%) ref|ZP\_00065024.1| COG1159: GTPase [Microbulbifer degradans 2-40] Length = 298
- 3631.4 Best-BlastP=> >nrprot No Hits found
- 3632.3 Best-BlastP=> >nrprot 49% Identities = 273/1022 (26%), Positives = 507/1022 (49%), Gaps = 42/1022 (4%) gb|AAP44228.1| transposase TnpA [Pseudomonas sp. ND6] Length = 1009
- 3633.3 Best-BlastP=> >nrprot 63% Identities = 122/307 (39%), Positives = 196/307 (63%) ref|NP\_819755.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90269.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 308

- 3634.1 Best-BlastP=> >nrprot 55% Identities = 103/103 (100%), Positives = 103/103 (100%) sp|P26880|YPA1\_LEGPN Hypothetical protein in PAL 5'region (ORFU) Length = 103
- 3636.1 Best-BlastP=> >nrprot 99% Identities = 176/176 (100%), Positives = 176/176 (100%) sp|P26493|PAL\_LEGPN Peptidoglycan-associated lipoprotein precursor (19 kDa surface antigen) (PPL) pir|A60337 outer membrane protein ppiA, peptidoglycan-associated, precursor - Legionella pneumophila emb|CAA43033.1| lipoprotein antigen [Legionella pneumophila] Length = 176
- 3637.1 Best-BlastP=> >nrprot 59% Identities = 188/201 (93%), Positives = 193/201 (96%), Gaps = 4/201 (1%) sp|P26881|YPA2\_LEGPN Hypothetical protein in PAL 3'region (ORFD) Length = 201
- 3638.2 Best-BlastP=> >nrprot 78% Identities = 141/217 (64%), Positives = 171/217 (78%), Gaps = 1/217 (0%) ref|ZP\_00083811.1| COG0602: Organic radical activating enzymes [Pseudomonas fluorescens PfO-1] Length = 218
- 364.2 Best-BlastP=> >nrprot 5% Identities = 31/70 (44%), Positives = 38/70 (54%), Gaps = 3/70 (4%) ref|NP\_900714.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472] gb|AAQ58719.1| hypothetical protein CV1044 [Chromobacterium violaceum ATCC 12472] Length = 499
- 3640.2 Best-BlastP=> >nrprot 51% Identities = 94/313 (30%), Positives = 162/313 (51%), Gaps = 21/313 (6%) emb|CAC51371.1| mevalonate diphosphate decarboxylase [Lactobacillus helveticus] Length = 320
- 3641.1 Best-BlastP=> >nrprot 42% Identities = 65/228 (28%), Positives = 108/228 (47%), Gaps = 12/228 (5%) ref|NP\_820494.1| transporter, ZIP family [Coxiella burnetii RSA 493] gb|AAO91008.1| transporter, ZIP family [Coxiella burnetii RSA 493] Length = 261
- 3642.2 Best-BlastP=> >nrprot 57% Identities = 154/329 (46%), Positives = 220/329 (66%), Gaps = 3/329 (0%) ref|NP\_820351.1| cation-efflux family protein [Coxiella burnetii RSA 493] gb|AAO90865.1| cation-efflux family protein [Coxiella burnetii RSA 493] Length = 378
- 3645.3 Best-BlastP=> >nrprot 67% Identities = 132/255 (51%), Positives = 171/255 (67%), Gaps = 15/255 (5%) ref|ZP\_00016164.1| COG0378: Ni2+-binding GTPase involved in regulation of expression and maturation of urease and hydrogenase [Rhodospirillum rubrum] Length = 268
- 3647.2 Best-BlastP=> >nrprot 71% Identities = 37/67 (55%), Positives = 54/67 (80%) ref|ZP\_00021586.1| COG0298: Hydrogenase maturation factor [Ralstonia metallidurans] Length = 103
- 365.4 Best-BlastP=> >nrprot 49% Identities = 88/327 (26%), Positives = 165/327 (50%), Gaps = 15/327 (4%) ref|NP\_819818.1| multidrug resistance protein [Coxiella burnetii RSA 493] gb|AAO90332.1| multidrug resistance protein [Coxiella burnetii RSA 493] Length = 331
- 3650.1 Best-BlastP=> >nrprot 52% Identities = 171/363 (47%), Positives = 221/363 (60%), Gaps = 8/363 (2%) ref|ZP\_00089787.1| COG1145: Ferredoxin [Azotobacter vinelandii] Length = 382
- 3651.1 Best-BlastP=> >nrprot 56% Identities = 114/269 (42%), Positives = 158/269 (58%), Gaps = 3/269 (1%) ref|ZP\_00089785.1| COG0543: 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases [Azotobacter vinelandii] Length = 283
- 3652.2 Best-BlastP=> >nrprot 64% Identities = 132/249 (53%), Positives = 169/249 (67%), Gaps = 1/249 (0%) ref|ZP\_00089784.1| COG1941: Coenzyme F420-reducing hydrogenase, gamma subunit [Azotobacter vinelandii] Length = 256
- 3653.3 Best-BlastP=> >nrprot 56% Identities = 26/40 (65%), Positives = 33/40 (82%), Gaps = 3/40 (7%) gb|AAG45149.1| TraA-like protein [Legionella pneumophila] Length = 883
- 3655.1 Best-BlastP=> >nrprot No Hits found

- 3657.1 Best-BlastP=> >nrprot 48% Identities = 65/171 (38%), Positives = 103/171 (60%), Gaps = 2/171 (1%) ref|NP\_174343.2| expressed protein [Arabidopsis thaliana] Length = 391
- 3658.1 Best-BlastP=> >nrprot No Hits found
- 3659.2 Best-BlastP=> >nrprot No Hits found
- 366.2 Best-BlastP=> >nrprot No Hits found
- 3661.4 Best-BlastP=> >nrprot 32% Identities = 71/191 (37%), Positives = 108/191 (56%), Gaps = 22/191 (11%) ref|NP\_901795.1| hypothetical protein CV2125 [Chromobacterium violaceum ATCC 12472] gb|AAQ59798.1| hypothetical protein CV2125 [Chromobacterium violaceum ATCC 12472] Length = 202
- 3663.1 Best-BlastP=> >nrprot No Hits found
- 3664.1 Best-BlastP=> >nrprot 52% Identities = 142/332 (42%), Positives = 203/332 (61%), Gaps = 5/332 (1%) gb|AAK49795.1| WcbB [Burkholderia pseudomallei] Length = 365
- 3665.1 Best-BlastP=> >nrprot 52% Identities = 109/243 (44%), Positives = 162/243 (66%) ref|ZP\_00125435.1| COG0500: SAM-dependent methyltransferases [Pseudomonas syringae pv. syringae B728a] Length = 646
- 3666.2 Best-BlastP=> >nrprot 44% Identities = 121/287 (42%), Positives = 173/287 (60%), Gaps = 2/287 (0%) gb|AAK49795.1| WcbB [Burkholderia pseudomallei] Length = 365
- 3667.1 Best-BlastP=> >nrprot No Hits found
- 3669.1 Best-BlastP=> >nrprot 83% Identities = 227/316 (71%), Positives = 264/316 (83%) ref|NP\_820997.1| cystathionine beta-synthase, putative [Coxiella burnetii RSA 493] gb|AAO91511.1| cystathionine beta-synthase, putative [Coxiella burnetii RSA 493] Length = 316
- 3670.2 Best-BlastP=> >nrprot No Hits found
- 3671.2 Best-BlastP=> >nrprot 24% Identities = 34/134 (25%), Positives = 59/134 (44%), Gaps = 7/134 (5%) ref|XP\_283791.1| RIKEN cDNA B230210E21 gene [Mus musculus] Length = 484
- 3673.2 Best-BlastP=> >nrprot 51% Identities = 137/403 (33%), Positives = 211/403 (52%), Gaps = 9/403 (2%) ref|NP\_793575.1| major facilitator family transporter [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57270.1| major facilitator family transporter [Pseudomonas syringae pv. tomato str. DC3000] Length = 445
- 3674.2 Best-BlastP=> >nrprot 63% Identities = 123/273 (45%), Positives = 173/273 (63%), Gaps = 17/273 (6%) ref|ZP\_00084952.1| COG1766: Flagellar biosynthesis/type III secretory pathway lipoprotein [Pseudomonas fluorescens PfO-1] Length = 595
- 3675.1 Best-BlastP=> >nrprot 60% Identities = 45/87 (51%), Positives = 64/87 (73%), Gaps = 5/87 (5%) dbj|BAC95246.1| flagellar hook-basal body protein FlIE [Vibrio vulnificus YJ016] Length = 122
- 3676.2 Best-BlastP=> >nrprot 60% Identities = 261/267 (97%), Positives = 263/267 (98%) gb|AAG45148.1| putative response regulator [Legionella pneumophila] Length = 267
- 3679.3 Best-BlastP=> >nrprot 56% Identities = 129/324 (39%), Positives = 194/324 (59%), Gaps = 5/324 (1%) ref|NP\_746486.1| sensory box histidine kinase FleS [Pseudomonas putida KT2440] gb|AAN69950.1| AE016633\_8 sensory box histidine kinase FleS [Pseudomonas putida KT2440] Length = 405
- 368.2 Best-BlastP=> >nrprot 22% Identities = 123/487 (25%), Positives = 188/487 (38%), Gaps = 62/487 (12%) emb|CAD27470.1| SPAPB18E9.04c [Schizosaccharomyces pombe] Length = 800

- 3680.1 Best-BlastP=> >nrprot 84% Identities = 230/314 (73%), Positives = 268/314 (85%) ref|ZP\_00135925.1| COG0492: Thioredoxin reductase [Pseudomonas aeruginosa UCBPP-PA14] Length = 316
- 3681.1 Best-BlastP=> >nrprot 63% Identities = 110/221 (49%), Positives = 142/221 (64%), Gaps = 3/221 (1%) ref|NP\_842221.1| Leucyl/phenylalanyl-tRNA--protein transferase [Nitrosomonas europaea ATCC 19718] sp|Q82ST5|LFTR NITEU Leucyl/phenylalanyl-tRNA--protein transferase (L/F-transferase) (Leucyltransferase) (Phenylalanyltransferase) emb|CAD86131.1| Leucyl/phenylalanyl-tRNA--protein transferase [Nitrosomonas europaea ATCC 19718] Length = 236
- 3682.1 Best-BlastP=> >nrprot 66% Identities = 58/122 (47%), Positives = 83/122 (68%) ref|NP\_819118.1| rhodanese domain protein [Coxiella burnetii] RSA 493 gb|AAO89632.1| rhodanese domain protein [Coxiella burnetii] RSA 493 Length = 124
- 3683.2 Best-BlastP=> >nrprot 93% Identities = 63/72 (87%), Positives = 69/72 (95%) ref|NP\_404963.1| translation initiation factor IF-1 [Yersinia pestis] ref|NP\_670107.1| protein chain initiation factor IF-1 [Yersinia pestis KIM] ref|NP\_928886.1| translation initiation factor IF-1 [Phototribadus luminescens subsp. laumondii TTO1] sp|Q8ZGD3|IF1\_YERPE Translation initiation factor IF-1 pir|AD0167 translation initiation factor IF-1 [imported] - Yersinia pestis (strain CO92) emb|CAC90199.1| translation initiation factor IF-1 [Yersinia pestis CO92] gb|AAM86358.1|AE013884\_5 protein chain initiation factor IF-1 [Yersinia pestis KIM] emb|CAE13888.1| translation initiation factor IF-1 [Phototribadus luminescens subsp. laumondii TTO1] Length = 72
- 3684.2 Best-BlastP=> >nrprot 30% Identities = 27/117 (23%), Positives = 61/117 (52%), Gaps = 2/117 (1%) ref|NP\_716604.1| hypothetical protein [Shewanella oneidensis MR-1] gb|AAN54049.1|AE015542\_5 hypothetical protein [Shewanella oneidensis MR-1] Length = 474
- 3685.1 Best-BlastP=> >nrprot 47% Identities = 41/88 (46%), Positives = 52/88 (59%), Gaps = 2/88 (2%) ref|NP\_800276.1| putative glutamate synthetase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62109.1| putative glutamate synthetase [Vibrio parahaemolyticus] Length = 513
- 3686.1 Best-BlastP=> >nrprot 39% Identities = 118/353 (33%), Positives = 206/353 (58%), Gaps = 1/353 (0%) ref|ZP\_00084494.1| COG2199: FOG: GGDEF domain [Pseudomonas fluorescens PfO-1] Length = 696
- 3687.1 Best-BlastP=> >nrprot 70% Identities = 182/294 (61%), Positives = 232/294 (78%) ref|NP\_294489.1| lipoic acid synthase [Deinococcus radiodurans] sp|Q9RWA4|LIPA\_DEIRA Lipoic acid synthetase (Lip-syn) (Lipoate synthase) pir|A75480 lipoic acid synthase - Deinococcus radiodurans (strain R1) gb|AAF10341.1|AE001931\_12 lipoic acid synthase [Deinococcus radiodurans] Length = 331
- 3688.1 Best-BlastP=> >nrprot 59% Identities = 42/90 (46%), Positives = 56/90 (62%), Gaps = 2/90 (2%) ref|NP\_773278.1| bir6638 [Bradyrhizobium japonicum] dbj|BAC51903.1| bir6638 [Bradyrhizobium japonicum USDA 110] Length = 112
- 3694.2 Best-BlastP=> >nrprot 81% Identities = 246/361 (68%), Positives = 294/361 (81%) ref|NP\_819175.1| phospho-N-acetylmuramoyl-pentapeptide-transferase [Coxiella burnetii] RSA 493 gb|AAO89689.1| phospho-N-acetylmuramoyl-pentapeptide-transferase [Coxiella burnetii] RSA 493 Length = 361
- 3697.4 Best-BlastP=> >nrprot 61% Identities = 456/1174 (38%), Positives = 715/1174 (60%), Gaps = 26/1174 (2%) ref|ZP\_00065347.1| COG1196: Chromosome segregation ATPases [Microbulbifer degradans 2-40] Length = 1168
- 3699.3 Best-BlastP=> >nrprot No Hits found
- 37.1 Best-BlastP=> >nrprot 98% Identities = 322/334 (96%), Positives = 330/334 (98%) gb|AAM08248.1| putative component of the type IV secretion system [Legionella pneumophila] Length = 334



- 3701.1 Best-BlastP=> >nrprot 31% Identities = 57/156 (36%), Positives = 84/156 (53%), Gaps = 8/156 (5%) ref|NP\_522544.1| PROBABLE TRANSCRIPTION REGULATOR PROTEIN [Ralstonia solanacearum] Length = 227
- 3702.1 Best-BlastP=> >nrprot 69% Identities = 131/242 (54%), Positives = 172/242 (71%), Gaps = 4/242 (1%) ref|NP\_284288.1| putative pseudouridine synthase [Neisseria meningitidis Z2491] pir|H81849 probable pseudouridine synthase NMA1573 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB84800.1| putative pseudouridine synthase [Neisseria meningitidis Z2491] Length = 256
- 3703.1 Best-BlastP=> >nrprot 67% Identities = 90/173 (52%), Positives = 130/173 (75%) ref|ZP\_00127917.1| COG1386: Predicted transcriptional regulator containing the HTH domain [Pseudomonas syringae pv. syringae B728a] Length = 255
- 3705.1 Best-BlastP=> >nrprot 70% Identities = 140/250 (56%), Positives = 186/250 (74%) ref|NP\_642633.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM37169.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 279
- 3706.2 Best-BlastP=> >nrprot 77% Identities = 254/396 (64%), Positives = 314/396 (79%) ref|NP\_519264.1| PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE (SYW PROTEIN) [Ralstonia solanacearum] sp|Q8Y0A1|SYW\_RALSO Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) emb|CAD14845.1| PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE (SYW PROTEIN) [Ralstonia solanacearum] Length = 400
- 3708.1 Best-BlastP=> >nrprot 75% Identities = 130/205 (63%), Positives = 167/205 (81%) ref|ZP\_00067870.1| COG0009: Putative translation factor (SUA5) [Microbulbifer degradans 2-40] Length = 207
- 3709.1 Best-BlastP=> >nrprot 58% Identities = 119/275 (43%), Positives = 165/275 (60%), Gaps = 2/275 (0%) ref|NP\_841756.1| PHP domain N-terminal region:PHP domain C-terminal region [Nitrosomonas europaea ATCC 19718] emb|CAD85635.1| PHP domain N-terminal region:PHP domain C-terminal region [Nitrosomonas europaea ATCC 19718] Length = 316
- 371.1 Best-BlastP=> >nrprot No Hits found
- 3710.1 Best-BlastP=> >nrprot 67% Identities = 152/329 (46%), Positives = 214/329 (65%), Gaps = 25/329 (7%) ref|NP\_245983.1| PhoH [Pasteurella multocida] gb|AAK03130.1| PhoH [Pasteurella multocida] Length = 372
- 3711.1 Best-BlastP=> >nrprot 66% Identities = 78/152 (51%), Positives = 105/152 (69%), Gaps = 2/152 (1%) ref|NP\_746893.1| conserved hypothetical protein TIGR00043 [Pseudomonas putida KT2440] gb|AAN70357.1|AE016677\_8 conserved hypothetical protein TIGR00043 [Pseudomonas putida KT2440] Length = 157
- 3712.2 Best-BlastP=> >nrprot 65% Identities = 139/261 (53%), Positives = 189/261 (72%) dbj|BAC93678.1| putative hemolysin [Vibrio vulnificus YJ016] Length = 306
- 3714.3 Best-BlastP=> >nrprot No Hits found
- 3720.2 Best-BlastP=> >nrprot 86% Identities = 192/264 (72%), Positives = 228/264 (86%) ref|ZP\_00024661.1| COG0207: Thymidylate synthase [Ralstonia metallidurans] Length = 264
- 3721.1 Best-BlastP=> >nrprot 64% Identities = 79/143 (55%), Positives = 101/143 (70%) ref|NP\_819678.1| riboflavin synthase, beta subunit [Coxiella burnetii RSA 493] gb|AAO90192.1| riboflavin synthase, beta subunit [Coxiella burnetii RSA 493] Length = 151

- 3729.1 Best-BlastP=> >nrprot 53% Identities = 70/188 (37%), Positives = 101/188 (53%), Gaps = 14/188 (7%) ref|NP\_636438.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM40362.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 176
- 3730.1 Best-BlastP=> >nrprot No Hits found
- 3731.1 Best-BlastP=> >nrprot 63% Identities = 56/114 (49%), Positives = 77/114 (67%), Gaps = 1/114 (0%) ref|NP\_890078.1| phage integrase [Bordetella bronchiseptica] emb|CAE34037.1| phage integrase [Bordetella bronchiseptica] Length = 407
- 3732.1 Best-BlastP=> >nrprot 36% Identities = 58/180 (32%), Positives = 107/180 (59%), Gaps = 1/180 (0%) ref|NP\_624053.1| predicted transposase [Thermoanaerobacter tengcongensis] gb|AAM25657.1| predicted transposase [Thermoanaerobacter tengcongensis] Length = 267
- 3734.1 Best-BlastP=> >nrprot 37% Identities = 86/323 (26%), Positives = 140/323 (43%), Gaps = 53/323 (16%) ref|NP\_563745.1| expressed protein [Arabidopsis thaliana] gb|AAM65464.1| unknown [Arabidopsis thaliana] gb|AAN72060.1| expressed protein [Arabidopsis thaliana] gb|AAP42733.1| At1g05620 [Arabidopsis thaliana] Length = 322
- 3735.2 Best-BlastP=> >nrprot 36% Identities = 106/496 (21%), Positives = 199/496 (40%), Gaps = 61/496 (12%) gb|EAA16521.1| 235 kDa rhostry protein [Plasmodium yoelii yoelii] Length = 2740
- 3737.1 Best-BlastP=> >nrprot No Hits found
- 3739.3 Best-BlastP=> >nrprot 79% Identities = 100/146 (68%), Positives = 117/146 (80%) ref|NP\_539647.1| LACTOYLGLUTATHIONE LYASE [Brucella melitensis] pir|AD3343 lactoylglutathione lyase (EC 4.4.1.5) [imported] - Brucella melitensis (strain 16M) gb|AAL51911.1| LACTOYLGLUTATHIONE LYASE [Brucella melitensis 16M] Length = 173
- 374.2 Best-BlastP=> >nrprot 66% Identities = 302/595 (50%), Positives = 393/595 (66%), Gaps = 13/595 (2%) ref|ZP\_00029131.1| COG3243: Poly(3-hydroxyalkanoate) synthetase [Burkholderia fungorum] Length = 642
- 3740.3 Best-BlastP=> >nrprot 72% Identities = 95/159 (59%), Positives = 128/159 (80%) ref|ZP\_00021733.1| COG2862: Predicted membrane protein [Ralstonia metallidurans] Length = 206
- 3741.1 Best-BlastP=> >nrprot 32% Identities = 61/271 (22%), Positives = 133/271 (49%), Gaps = 18/271 (6%) ref|XP\_230851.2| similar to hypothetical protein [Rattus norvegicus] Length = 396
- 3742.1 Best-BlastP=> >nrprot No Hits found
- 3743.1 Best-BlastP=> >nrprot No Hits found
- 3744.2 Best-BlastP=> >nrprot No Hits found
- 3747.2 Best-BlastP=> >nrprot 49% Identities = 99/264 (37%), Positives = 149/264 (56%), Gaps = 7/264 (2%) ref|NP\_743187.1| peptidase, M23/M37 family [Pseudomonas putida KT2440] gb|AAN66651.1|AE016293\_1 peptidase, M23/M37 family [Pseudomonas putida KT2440] Length = 275
- 3748.1 Best-BlastP=> >nrprot 63% Identities = 192/445 (43%), Positives = 280/445 (62%), Gaps = 5/445 (1%) ref|NP\_461447.1| exonuclease VII, large subunit [Salmonella typhimurium LT2] sp|Q8ZN58|EXTL\_SAL Ty Probable exodeoxyribonuclease VII large subunit (Exonuclease VII large subunit) gb|AAL21406.1| exonuclease VII, large subunit [Salmonella typhimurium LT2] Length = 449
- 3750.2 Best-BlastP=> >nrprot 42% Identities = 156/424 (36%), Positives = 245/424 (57%), Gaps = 2/424 (0%) pir|S27611 agglutination protein - Pseudomonas putida gb|AAA25695.1| agglutination protein Length = 452

- 3752.2 Best-BlastP=> >nrprot 54% Identities = 82/187 (43%), Positives = 116/187 (62%), Gaps = 2/187 (1%) ref|ZP\_00065146.1| COG3672: Predicted periplasmic protein [Microbulbifer degradans 2-40] Length = 241
- 3753.2 Best-BlastP=> >nrprot 55% Identities = 197/655 (30%), Positives = 352/655 (53%), Gaps = 41/655 (6%) ref|ZP\_00086698.1| COG2200: FOG: EAL domain [Pseudomonas fluorescens PfO-1] Length = 648
- 3754.2 Best-BlastP=> >nrprot 36% Identities = 48/170 (28%), Positives = 88/170 (51%), Gaps = 11/170 (6%) ref|NP\_773217.1| bl6577 [Bradyrhizobium japonicum] dbj|BAC51842.1| bl6577 [Bradyrhizobium japonicum USDA 110] Length = 237
- 3756.2 Best-BlastP=> >nrprot 67% Identities = 234/439 (53%), Positives = 301/439 (68%), Gaps = 7/439 (1%) ref|NP\_713336.1| putative flavin-containing monooxygenase [Leptospira interrogans serovar lai str. 56601] gb|AA50354.1| AE011478\_5 putative flavin-containing monooxygenase [Leptospira interrogans serovar lai str. 56601] Length = 468
- 376.3 Best-BlastP=> >nrprot 69% Identities = 155/329 (47%), Positives = 230/329 (69%), Gaps = 4/329 (1%) ref|NP\_931992.1| glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE17210.1| glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 340
- 3760.3 Best-BlastP=> >nrprot 69% Identities = 292/614 (47%), Positives = 418/614 (68%), Gaps = 13/614 (2%) ref|NP\_924289.1| glutathione-regulated potassium efflux system protein KefC homolog [Gloeobacter violaceus] dbj|BAC89284.1| gir1343 [Gloeobacter violaceus] Length = 634
- 3761.1 Best-BlastP=> >nrprot No Hits found
- 3763.1 Best-BlastP=> >nrprot 44% Identities = 59/195 (30%), Positives = 90/195 (46%), Gaps = 34/195 (17%) ref|NP\_052362.1| unnamed protein product [Coxiella burnetii] ref|NP\_819025.1| hypothetical protein [Coxiella burnetii RSA 493] pir|S38244 hypothetical protein - Coxiella burnetii emb|CAA53132.1| unnamed protein product [Coxiella burnetii] gb|AAO91585.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 361
- 3764.3 Best-BlastP=> >nrprot No Hits found
- 3765.1 Best-BlastP=> >nrprot 46% Identities = 80/315 (25%), Positives = 147/315 (46%), Gaps = 20/315 (6%) ref|ZP\_00124222.1| COG1721: Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) [Pseudomonas syringae pv. syringae B728a] Length = 327
- 377.1 Best-BlastP=> >nrprot 66% Identities = 137/265 (51%), Positives = 185/265 (69%), Gaps = 6/265 (2%) ref|NP\_819341.1| glutamate racemase [Coxiella burnetii RSA 493] gb|AAO89855.1| glutamate racemase [Coxiella burnetii RSA 493] Length = 280
- 3771.2 Best-BlastP=> >nrprot 66% Identities = 105/197 (53%), Positives = 138/197 (70%), Gaps = 2/197 (1%) ref|NP\_717670.1| phosphoribosyl-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase [Shewanella oneidensis MR-1] gb|AA55114.1| AE015648\_7 phosphoribosyl-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase [Shewanella oneidensis MR-1] Length = 211

- 3772.2 Best-BlastP=> >nrprot 69% Identities = 185/353 (52%), Positives = 245/353 (69%), Gaps = 2/353 (0%) ref|NP\_405132.1| histidinol-phosphatase and imidazoleglycerol-phosphate dehydratase [Yersinia pestis] ref|NP\_669926.1| imidazoleglycerol-phosphate dehydratase; histidinol-phosphate phosphatase [Yersinia pestis KIM] sp|Q8ZFX7|HIS7\_YERPE Histidine biosynthesis bifunctional protein hisB [Includes: Histidinol-phosphatase; Imidazoleglycerol-phosphate dehydratase (IGPD)] pir|AF0188 imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) [imported] - Yersinia pestis (strain CO92) emb|CAC90369.1| histidinol-phosphatase and imidazoleglycerol-phosphate dehydratase [Yersinia pestis KIM] gb|AAM86177.1|AE013864\_4 imidazoleglycerol-phosphate dehydratase; histidinol-phosphate phosphatase [Yersinia pestis KIM] Length = 355
- 3778.2 Best-BlastP=> >nrprot 62% Identities = 50/84 (59%), Positives = 62/84 (73%) ref|ZP\_00038938.1| COG4496: Uncharacterized protein conserved in bacteria [Xylella fastidiosa Dixon] Length = 112
- 3780.2 Best-BlastP=> >nrprot 23% Identities = 30/60 (50%), Positives = 37/60 (61%), Gaps = 5/60 (8%) ref|NP\_700818.1| merozoite surface protein 3 [Plasmodium falciparum 3D7] gb|AAC09377.1| antigen [Plasmodium falciparum] gb|AAN35542.1|AE014834\_39 merozoite surface protein 3 [Plasmodium falciparum 3D7] Length = 354
- 3783.1 Best-BlastP=> >nrprot 75% Identities = 55/95 (57%), Positives = 74/95 (77%) ref|ZP\_00096296.1| COG2827: Predicted endonuclease containing a URI domain [Novosphingobium aromaticivorans] Length = 111
- 3784.2 Best-BlastP=> >nrprot 72% Identities = 190/364 (52%), Positives = 266/364 (73%), Gaps = 3/364 (0%) ref|ZP\_00122463.1| COG3842: ABC-type spermidine/putrescine transport systems, ATPase components [Haemophilus somnus 129PT] Length = 372
- 3785.2 Best-BlastP=> >nrprot 71% Identities = 124/276 (44%), Positives = 203/276 (73%), Gaps = 2/276 (0%) ref|NP\_439497.1| spermidine/putrescine ABC transporter permease protein [Haemophilus influenzae Rd] sp|P45170|POTB\_HAEIN Spermidine/putrescine transport system permease protein potB pir|A64118 spermidine/putrescine transport system permease potB - Haemophilus influenzae (strain Rd KW20) gb|AAC22990.1| spermidine/putrescine ABC transporter, permease protein (potB) [Haemophilus influenzae Rd] Length = 286
- 3788.1 Best-BlastP=> >nrprot 68% Identities = 115/251 (45%), Positives = 176/251 (70%) ref|ZP\_00128580.1| COG1177: ABC-type spermidine/putrescine transport system, permease component II [Desulfovibrio desulfuricans G20] Length = 257
- 3789.2 Best-BlastP=> >nrprot 65% Identities = 122/283 (43%), Positives = 187/283 (66%), Gaps = 3/283 (1%) ref|NP\_231067.1| spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82201 spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein VC1424 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94581.1| spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 345
- 3791.1 Best-BlastP=> >nrprot No Hits found
- 3792.1 Best-BlastP=> >nrprot No Hits found
- 3793.3 Best-BlastP=> >nrprot 43% Identities = 78/264 (29%), Positives = 132/264 (50%), Gaps = 10/264 (3%) ref|ZP\_00018971.1| hypothetical protein [Chloroflexus aurantiacus] Length = 303
- 3796.3 Best-BlastP=> >nrprot 58% Identities = 87/178 (48%), Positives = 120/178 (67%) ref|NP\_840387.1| Bacterial regulatory proteins, TetR family [Nitrosomonas europaea ATCC 19718] emb|CAD84211.1| Bacterial regulatory proteins, TetR family [Nitrosomonas europaea ATCC 19718] Length = 213

- 3797.1 Best-BlastP=> >nprot 68% Identities = 167/346 (48%), Positives = 239/346 (69%), Gaps = 6/346 (1%) ref|NP\_831149.1| Nitropropane dioxygenase / Trans-enoyl-CoA reductase family [Bacillus cereus ATCC 14579] gb|AAP08350.1| Nitropropane dioxygenase / Trans-enoyl-CoA reductase family [Bacillus cereus ATCC 14579] Length = 363
- 3798.1 Best-BlastP=> >nprot No Hits found
- 3800.4 Best-BlastP=> >nprot No Hits found
- 3801.2 Best-BlastP=> >nprot 99% Identities = 477/483 (98%), Positives = 481/483 (99%) gb|AAM00644.1| adenylate cyclase [Legionella pneumophila] Length = 483
- 3802.2 Best-BlastP=> >nprot 63% Identities = 189/413 (45%), Positives = 270/413 (65%), Gaps = 2/413 (0%) ref|NP\_742893.1| glutamyl-tRNA reductase [Pseudomonas putida KT2440] gb|AAN66357.1|AE016264\_1 glutamyl-tRNA reductase [Pseudomonas putida KT2440] Length = 425
- 3803.1 Best-BlastP=> >nprot 84% Identities = 235/358 (65%), Positives = 306/358 (85%) ref|NP\_820940.1| peptide chain release factor 1 [Coxiella burnetii RSA 493] sp|P47849|RF1\_COXBU Peptide chain release factor 1 (RF-1) gb|AAO91454.1| peptide chain release factor 1 [Coxiella burnetii RSA 493] Length = 361
- 3804.2 Best-BlastP=> >nprot 66% Identities = 134/281 (47%), Positives = 192/281 (68%), Gaps = 6/281 (2%) ref|ZP\_00066170.1| COG2890: Methylase of polypeptide chain release factors [Microbulbifer degradans 2-40] Length = 288
- 3807.2 Best-BlastP=> >nprot 84% Identities = 97/133 (72%), Positives = 115/133 (86%) ref|NP\_706093.1| dnaK suppressor protein [Shigella flexneri 2a str. 301] ref|NP\_752128.1| DnaK suppressor protein [Escherichia coli CFT073] gb|AAN41800.1|AE015050\_16 dnaK suppressor protein [Shigella flexneri 2a str. 301] gb|AAN78672.1|AE016755\_172 DnaK suppressor protein [Escherichia coli CFT073] Length = 157
- 381.6 Best-BlastP=> >nprot 24% Identities = 141/721 (19%), Positives = 282/721 (39%), Gaps = 94/721 (13%) ref|NP\_010225.1| involved intracellular protein transport, coiled-coil protein necessary for protein transport from ER to Golgi; Uso1p [Saccharomyces cerevisiae] Length = 1790
- 3810.1 Best-BlastP=> >nprot 53% Identities = 78/237 (32%), Positives = 123/237 (51%), Gaps = 22/237 (9%) ref|NP\_721557.1| conserved hypothetical protein [Streptococcus mutans UA159] gb|AAN58863.1|AE014954\_2 conserved hypothetical protein [Streptococcus mutans UA159] Length = 246
- 3811.1 Best-BlastP=> >nprot 48% Identities = 43/154 (27%), Positives = 73/154 (47%), Gaps = 35/154 (22%) ref|ZP\_00074907.1| COG0534: Na+-driven multidrug efflux pump [Trichodesmium erythraeum IMS101] Length = 931
- 3814.1 Best-BlastP=> >nprot 98% Identities = 278/282 (98%), Positives = 280/282 (99%) gb|AAM73852.1|AF454863\_1 putative lipase LipA [Legionella pneumophila] Length = 282
- 3815.2 Best-BlastP=> >nprot 65% Identities = 41/81 (50%), Positives = 62/81 (76%), Gaps = 2/81 (2%) ref|NP\_901660.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ59662.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 104
- 3816.2 Best-BlastP=> >nprot 69% Identities = 121/232 (52%), Positives = 170/232 (73%) ref|NP\_719120.1| CDP-diacylglycerol--serine O-phosphatidyltransferase, putative [Shewanella oneidensis MR-1] gb|AAN56564.1|AE015794\_2 CDP-diacylglycerol--serine O-phosphatidyltransferase, putative [Shewanella oneidensis MR-1] Length = 269

- 3818.1 Best-BlastP=> >nrprot 81% Identities = 50/89 (56%), Positives = 73/89 (82%) ref|NP\_900485.1| sugar transport PTS system phosphocarrier protein HPR [Chromobacterium violaceum ATCC 12472] gb|AAQ58490.1| sugar transport PTS system phosphocarrier protein HPR [Chromobacterium violaceum ATCC 12472] Length = 89
- 3819.2 Best-BlastP=> >nrprot 76% Identities = 61/95 (64%), Positives = 76/95 (80%) db|BAC93211.1| putative sigma-54 modulation protein [Vibrio vulnificus YJ016] Length = 95
- 3821.1 Best-BlastP=> >nrprot No Hits found
- 3822.2 Best-BlastP=> >nrprot 41% Identities = 44/157 (28%), Positives = 74/157 (47%), Gaps = 16/157 (10%) ref|NP\_863847.1| hypothetical protein [Pirellula sp.] emb|CAD71520.1| hypothetical protein [Pirellula sp.] Length = 171
- 3824.2 Best-BlastP=> >nrprot 56% Identities = 166/428 (38%), Positives = 244/428 (57%), Gaps = 12/428 (2%) ref|NP\_820492.1| mesJ protein [Coxiella burnetii RSA 493] gb|AAO91006.1| mesJ protein [Coxiella burnetii RSA 493] Length = 449
- 3826.1 Best-BlastP=> >nrprot 57% Identities = 129/323 (39%), Positives = 190/323 (58%), Gaps = 9/323 (2%) ref|NP\_820009.1| birA bifunctional protein [Coxiella burnetii RSA 493] gb|AAO90523.1| birA bifunctional protein [Coxiella burnetii RSA 493] Length = 323
- 3827.2 Best-BlastP=> >nrprot 49% Identities = 224/663 (33%), Positives = 330/663 (49%), Gaps = 66/663 (9%) ref|NP\_106287.1| O-antigen acetylase [Mesorhizobium loti] db|BAB52073.1| O-antigen acetylase [Mesorhizobium loti] Length = 628
- 3830.2 Best-BlastP=> >nrprot No Hits found
- 3832.1 Best-BlastP=> >nrprot 41% Identities = 107/294 (36%), Positives = 168/294 (57%), Gaps = 16/294 (5%) ref|NP\_899726.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] gb|AAQ57736.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] Length = 415
- 3834.1 Best-BlastP=> >nrprot No Hits found
- 3835.2 Best-BlastP=> >nrprot 47% Identities = 66/245 (26%), Positives = 118/245 (48%), Gaps = 10/245 (4%) emb|CAA60105.1| artJ [Escherichia coli] Length = 243
- 3837.3 Best-BlastP=> >nrprot 12% Identities = 45/120 (37%), Positives = 61/120 (50%), Gaps = 8/120 (6%) gb|AAH52346.1| 4921520G13Rik protein [Mus musculus] Length = 379
- 3838.3 Best-BlastP=> >nrprot 99% Identities = 710/718 (98%), Positives = 716/718 (99%) emb|CAD90951.1| LssB protein [Legionella pneumophila] Length = 718
- 384.3 Best-BlastP=> >nrprot 30% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180
- 3840.1 Best-BlastP=> >nrprot 99% Identities = 352/355 (99%), Positives = 355/355 (100%) emb|CAD90958.1| LssD protein [Legionella pneumophila] Length = 378
- 3841.2 Best-BlastP=> >nrprot 91% Identities = 719/842 (85%), Positives = 774/842 (91%) emb|CAD90957.1| LssE protein [Legionella pneumophila] Length = 842
- 3846.2 Best-BlastP=> >nrprot 41% Identities = 205/677 (30%), Positives = 350/677 (51%), Gaps = 31/677 (4%) gb|AAM82673.1| PacS [Synechococcus sp. PCC 7942] Length = 747
- 3849.1 Best-BlastP=> >nrprot 69% Identities = 117/228 (51%), Positives = 169/228 (74%), Gaps = 2/228 (0%) ref|ZP\_00067594.1| COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Microbulbifer degradans 2-40] Length = 244

- 3850.1 Best-BlastP=> >nrprot 72% Identities = 82/139 (58%), Positives = 102/139 (73%) ref|ZP\_00086776.1| COG1981: Predicted membrane protein [Pseudomonas fluorescens PfO-1] Length = 142
- 3851.1 Best-BlastP=> >nrprot 83% Identities = 43/56 (76%), Positives = 49/56 (87%) ref|NP\_841467.1| Rubredoxin:Rubredoxin-type Fe(Cys)<sub>4</sub> protein [Nitrosomonas europaea ATCC 19718] emb|CAD85337.1| Rubredoxin:Rubredoxin-type Fe(Cys)<sub>4</sub> protein [Nitrosomonas europaea ATCC 19718] Length = 62
- 3853.2 Best-BlastP=> >nrprot 74% Identities = 264/426 (61%), Positives = 318/426 (74%) ref|ZP\_00133736.1| COG0001: Glutamate-1-semialdehyde aminotransferase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 426
- 3855.1 Best-BlastP=> >nrprot 59% Identities = 115/256 (44%), Positives = 157/256 (61%), Gaps = 1/256 (0%) ref|NP\_251460.1| hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9I073|YR70\_PSEAE Hypothetical protein PA2770 pir|A83301 hypothetical protein PA2770 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06158.1|AE004704\_12 hypothetical protein PA2770 [Pseudomonas aeruginosa PAO1] Length = 259
- 3857.3 Best-BlastP=> >nrprot 99% Identities = 367/372 (98%), Positives = 371/372 (99%) gb|AAD42885.1|AF157018\_1 PrpC [Legionella pneumophila] Length = 372
- 3859.2 Best-BlastP=> >nrprot 84% Identities = 308/442 (69%), Positives = 374/442 (84%), Gaps = 5/442 (1%) ref|NP\_756738.1| ATP-dependent hsl protease ATP-binding subunit hslU [Escherichia coli CFT073] sp|Q8FBC0|HSLU\_ECOL6 ATP-dependent hsl protease ATP-binding subunit hslU gb|AAN83312.1|AE016770\_112 ATP-dependent hsl protease ATP-binding subunit hslU [Escherichia coli CFT073] Length = 443
- 3860.2 Best-BlastP=> >nrprot 89% Identities = 146/180 (81%), Positives = 164/180 (91%) ref|NP\_820986.1| protease HslVU, subunit HslV [Coxiella burnetii RSA 493] gb|AAO91500.1| protease HslVU, subunit HslV [Coxiella burnetii RSA 493] Length = 181
- 3863.2 Best-BlastP=> >nrprot 99% Identities = 196/199 (98%), Positives = 198/199 (99%) sp|O32481|GRPE\_LEGPN GRPE PROTEIN (HSP-70 COFACTOR) db|BAA22782.1| GrpE [Legionella pneumophila] Length = 199
- 3867.2 Best-BlastP=> >nrprot 72% Identities = 242/435 (55%), Positives = 325/435 (74%), Gaps = 1/435 (0%) gb|AAK14074.1|AF303107\_1 family II 2-keto-3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Xanthomonas campestris] Length = 478
- 3871.1 Best-BlastP=> >nrprot No Hits found
- 3872.1 Best-BlastP=> >nrprot No Hits found
- 3874.1 Best-BlastP=> >nrprot No Hits found
- 3876.1 Best-BlastP=> >nrprot 42% Identities = 49/160 (30%), Positives = 71/160 (44%), Gaps = 29/160 (18%) ref|ZP\_00079746.1| COG3034: Uncharacterized protein conserved in bacteria [Geobacter metallireducens] Length = 175
- 3878.1 Best-BlastP=> >nrprot 23% Identities = 112/536 (20%), Positives = 244/536 (45%), Gaps = 42/536 (7%) gb|AAO52540.1| similar to Entamoeba histolytica. Myosin heavy chain [Dictyostelium discoideum] Length = 915
- 3884.2 Best-BlastP=> >nrprot No Hits found
- 3887.1 Best-BlastP=> >nrprot 37% Identities = 87/397 (21%), Positives = 155/397 (39%), Gaps = 28/397 (7%) ref|NP\_764987.1| multidrug resistance protein-like protein [Staphylococcus epidermidis ATCC 12228] gb|AAO05031.1|AE016748\_265 multidrug resistance protein-like protein [Staphylococcus epidermidis ATCC 12228] Length = 404
- 3888.1 Best-BlastP=> >nrprot No Hits found



- 3889.1 Best-BlastP=> >nrprot 48% Identities = 75/257 (29%), Positives = 126/257 (49%), Gaps = 23/257 (8%) ref|NP\_922978.1| hypothetical protein glI0032 [Gloeobacter violaceus] dbj|BAC87973.1| glI0032 [Gloeobacter violaceus] Length = 267
- 389.3 Best-BlastP=> >nrprot 61% Identities = 283/637 (44%), Positives = 401/637 (62%), Gaps = 10/637 (1%) ref|NP\_840954.1| probable ATP-dependent DNA helicase-related protein [Nitrosomonas europaea ATCC 19718] emb|CAD84791.1| probable ATP-dependent DNA helicase-related protein [Nitrosomonas europaea ATCC 19718] Length = 646
- 3890.2 Best-BlastP=> >nrprot No Hits found
- 3891.2 Best-BlastP=> >nrprot 56% Identities = 85/194 (43%), Positives = 120/194 (61%), Gaps = 7/194 (3%) ref|NP\_698073.1| conserved hypothetical protein [Brucella suis 1330] gb|AAN29988.1|AE014408.2 conserved hypothetical protein [Brucella suis 1330] Length = 203
- 3892.3 Best-BlastP=> >nrprot 55% Identities = 149/349 (42%), Positives = 207/349 (59%), Gaps = 3/349 (0%) ref|ZP\_00008996.1| COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Rhodopseudomonas palustris] Length = 379
- 3895.2 Best-BlastP=> >nrprot 48% Identities = 92/324 (28%), Positives = 160/324 (49%), Gaps = 11/324 (3%) ref|NP\_819818.1| multidrug resistance protein [Coxiella burnetii RSA 493] gb|AAO90332.1| multidrug resistance protein [Coxiella burnetii RSA 493] Length = 331
- 3898.2 Best-BlastP=> >nrprot No Hits found
- 3899.2 Best-BlastP=> >nrprot No Hits found
- 39.1 Best-BlastP=> >nrprot 96% Identities = 340/363 (93%), Positives = 352/363 (96%) emb|CAB60060.1| lvhB10 [Legionella pneumophila] Length = 363
- 390.2 Best-BlastP=> >nrprot 86% Identities = 80/106 (75%), Positives = 97/106 (91%) sp|P08811|FER\_PSEST Ferredoxin pir|JFEPSTV ferredoxin [3Fe-4S][4Fe-4S] - Pseudomonas stutzeri prf|1410240A ferredoxin Length = 106
- 3901.2 Best-BlastP=> >nrprot 75% Identities = 152/272 (55%), Positives = 204/272 (75%) ref|NP\_250460.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9J2X0|YH69\_PSEAE Hypothetical UPF0085 protein PA1769 pir|D83425 conserved hypothetical protein PA1769 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05158.1|AE004602\_9 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 274
- 3902.3 Best-BlastP=> >nrprot 79% Identities = 312/481 (64%), Positives = 382/481 (79%) ref|ZP\_00081898.1| COG2079: Uncharacterized protein involved in propionate catabolism [Geobacter metallireducens] Length = 481
- 3904.3 Best-BlastP=> >nrprot 54% Identities = 222/592 (37%), Positives = 332/592 (56%), Gaps = 16/592 (2%) ref|NP\_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589
- 3908.3 Best-BlastP=> >nrprot No Hits found
- 3909.3 Best-BlastP=> >nrprot No Hits found
- 3911.2 Best-BlastP=> >nrprot 78% Identities = 384/621 (61%), Positives = 489/621 (78%), Gaps = 3/621 (0%) sp|P58480|HTPG\_SALTY Chaperone protein htpG (Heat shock protein htpG) (High temperature protein G) Length = 624
- 3913.2 Best-BlastP=> >nrprot 71% Identities = 194/356 (54%), Positives = 267/356 (75%) ref|NP\_819581.1| rod shape-determining protein RodA [Coxiella burnetii RSA 493] gb|AAO90095.1| rod shape-determining protein RodA [Coxiella burnetii RSA 493] Length = 359

- 3914.3 Best-BlastP=> >nrprot 65% Identities = 286/604 (47%), Positives = 407/604 (67%), Gaps = 2/604 (0%) ref|NP\_819582.1| penicillin-binding protein 2 [Coxiella burnetii RSA 493] gb|AAO90096.1| penicillin-binding protein 2 [Coxiella burnetii RSA 493] Length = 612
- 3916.3 Best-BlastP=> >nrprot 72% Identities = 267/417 (64%), Positives = 331/417 (79%) ref|NP\_253428.1| polyribonucleotide nucleotidyltransferase [Pseudomonas aeruginosa PA01] pir|C83052 polyribonucleotide nucleotidyltransferase PA4740 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08126.1|AE004888\_1 polyribonucleotide nucleotidyltransferase [Pseudomonas aeruginosa PAO1] Length = 701
- 3917.1 Best-BlastP=> >nrprot 70% Identities = 56/88 (63%), Positives = 65/88 (73%) ref|ZP\_00091229.1| COG0184: Ribosomal protein S15P/S13E [Azotobacter vinelandii] Length = 132
- 3919.1
- 3920.1 Best-BlastP=> >nrprot 61% Identities = 138/299 (46%), Positives = 188/299 (62%), Gaps = 11/299 (3%) ref|XP\_306459.1| ENSANGP0000001690 [Anopheles gambiae] gb|EAA02278.1| ENSANGP0000001690 [Anopheles gambiae str. PEST] Length = 309
- 3920.1 Best-BlastP=> >nrprot 64% Identities = 60/113 (53%), Positives = 80/113 (70%), Gaps = 3/113 (2%) ref|NP\_840836.1| Ribosome-binding factor A [Nitrosomonas europaea ATCC 19718] sp|Q82WC9|RBFA\_NITEU Ribosome-binding factor A emb|CAD84673.1| Ribosome-binding factor A [Nitrosomonas europaea ATCC 19718] Length = 117
- 3923.2 Best-BlastP=> >nrprot 63% Identities = 244/604 (40%), Positives = 394/604 (65%), Gaps = 9/604 (1%) ref|NP\_622330.1| predicted nucleoside-diphosphate sugar epimerases [Thermoanaerobacter tengcongensis] gb|AAM23934.1| predicted nucleoside-diphosphate sugar epimerases [Thermoanaerobacter tengcongensis] Length = 623
- 3924.2
- 3925.2 Best-BlastP=> >nrprot 57% Identities = 90/279 (32%), Positives = 162/279 (58%), Gaps = 8/279 (2%) ref|NP\_348443.1| Conserved membrane protein, possible 4-hydroxybenzoate octaprenyltransferase [Clostridium acetobutylicum] pir|D97124 conserved membrane protein, probable 4-hydroxybenzoate octaprenyltransferase CAC1818 [imported] - Clostridium acetobutylicum gb|AAK79783.1|AE007691\_1 Conserved membrane protein, possible 4-hydroxybenzoate octaprenyltransferase [Clostridium acetobutylicum] Length = 290
- 3925.2 Best-BlastP=> >nrprot No Hits found
- 3927.2 Best-BlastP=> >nrprot 67% Identities = 228/453 (50%), Positives = 305/453 (67%), Gaps = 34/453 (7%) ref|NP\_820835.1| peptide ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] gb|AAO91349.1| peptide ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] Length = 465
- 3928.1 Best-BlastP=> >nrprot 99% Identities = 593/596 (99%), Positives = 594/596 (99%) emb|CAA67994.1| oxaloacetate decarboxylase alpha-chain [Legionella pneumophila] Length = 596
- 3929.2 Best-BlastP=> >nrprot 99% Identities = 542/543 (99%), Positives = 542/543 (99%) sp|P21347|PROA\_LEGPN Zinc metalloproteinase precursor (PEP1) (PRO A) pir|A35265 zinc metalloproteinase (EC 3.4.24.-) precursor - Legionella pneumophila gb|AAA25301.1| zinc metalloprotease precursor (EC 3.4.24) Length = 543
- 393.1
- 393.1 Best-BlastP=> >nrprot 67% Identities = 67/107 (62%), Positives = 87/107 (81%) ref|NP\_747247.1| (di)nucleoside polyphosphate hydrolase, putative [Pseudomonas putida KT2440] sp|Q88CN4|NUDH\_PSEPK Probable (di)nucleoside polyphosphate hydrolase gb|AAN70711.1|AE016714\_9 (di)nucleoside polyphosphate hydrolase, putative [Pseudomonas putida KT2440] Length = 159
- 3933.3 Best-BlastP=> >nrprot No Hits found

- 3936.2 Best-BlastP=> >nrprot 31% Identities = 95/227 (41%), Positives = 131/227 (57%), Gaps = 29/227 (12%) sp|Q9ZB07|PURQ\_LACLC Phosphoribosylformylglycinamide synthase I (FGAM synthase I) pir|T51700 phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component I [similarity] - Lactococcus lactis gb|AAD12625.1| phosphoribosylformylglycinamide synthetase I [Lactococcus lactis] Length = 226
- 3937.2 Best-BlastP=> >nrprot 65% Identities = 216/436 (49%), Positives = 286/436 (65%), Gaps = 4/436 (0%) ref|ZP\_00077753.1| COG0151: Phosphoribosylamine-glycine ligase [Methanosarcina barkeri] Length = 433
- 3938.2 Best-BlastP=> >nrprot 65% Identities = 75/186 (40%), Positives = 127/186 (68%), Gaps = 4/186 (2%) ref|NP\_632467.1| Phosphoribosylglycinamide formyltransferase [Methanosarcina mazei Goe1] gb|AAM30139.1| Phosphoribosylglycinamide formyltransferase [Methanosarcina mazei Goe1] Length = 202
- 3942.2 Best-BlastP=> >nrprot 76% Identities = 186/311 (59%), Positives = 241/311 (77%), Gaps = 2/311 (0%) ref|ZP\_00065258.1| COG2025: Electron transfer flavoprotein, alpha subunit [Microbulbifer degradans 2-40] Length = 312
- 3950.2 Best-BlastP=> >nrprot 46% Identities = 148/462 (32%), Positives = 248/462 (53%), Gaps = 23/462 (4%) ref|NP\_488265.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AB2334 hypothetical protein all4225 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB75924.1| ORF\_ID:all4225~hypothetical protein [Nostoc sp. PCC 7120] Length = 565
- 3953.1 Best-BlastP=> >nrprot 74% Identities = 231/395 (58%), Positives = 292/395 (73%), Gaps = 7/395 (1%) ref|NP\_840860.1| Amino transferases class-I [Nitrosomonas europaea ATCC 19718] emb|CAD84697.1| Amino transferases class-I [Nitrosomonas europaea ATCC 19718] Length = 397
- 3956.2 Best-BlastP=> >nrprot 50% Identities = 71/224 (31%), Positives = 124/224 (55%), Gaps = 11/224 (4%) ref|NP\_841085.1| SURF1 family [Nitrosomonas europaea ATCC 19718] emb|CAD84923.1| SURF1 family [Nitrosomonas europaea ATCC 19718] Length = 239
- 3957.1 Best-BlastP=> >nrprot 67% Identities = 28/65 (43%), Positives = 46/65 (70%) ref|NP\_518489.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD13896.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 69
- 3958.1 Best-BlastP=> >nrprot 42% Identities = 76/80 (95%), Positives = 77/80 (96%) gb|AAO61477.1| unknown [Legionella pneumophila] Length = 80
- 3959.2 Best-BlastP=> >nrprot 18% Identities = 60/197 (30%), Positives = 98/197 (49%), Gaps = 18/197 (9%) ref|NP\_660278.2| similar to RIKEN cDNA 1700007B22 [Homo sapiens] gb|AAH24189.2| Similar to RIKEN cDNA 1700007B22 [Homo sapiens] Length = 345
- 396.4 Best-BlastP=> >nrprot 68% Identities = 152/296 (51%), Positives = 203/296 (68%), Gaps = 2/296 (0%) ref|NP\_798532.1| L-asparaginase I [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC60416.1| L-asparaginase I [Vibrio parahaemolyticus] Length = 337
- 3960.2 Best-BlastP=> >nrprot No Hits found
- 3962.2 Best-BlastP=> >nrprot 57% Identities = 37/110 (33%), Positives = 65/110 (59%), Gaps = 1/110 (0%) ref|NP\_819167.1| cell division protein FtsL [Coxiella burnetii RSA 493] gb|AAO89681.1| cell division protein FtsL [Coxiella burnetii RSA 493] Length = 115
- 3964.1 Best-BlastP=> >nrprot 72% Identities = 166/311 (53%), Positives = 224/311 (72%), Gaps = 7/311 (2%) ref|NP\_930870.1| S-adenosyl-methyltransferase MraW [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16035.1| S-adenosyl-methyltransferase MraW [Photorhabdus luminescens subsp. laumondii TTO1] Length = 314

- 3965.1 Best-BlastP=> >nrprot 73% Identities = 89/152 (58%), Positives = 113/152 (74%) ref|NP\_819165.1| conserved hypothetical protein TIGR00242 [Coxiella burnetii RSA 493] gb|AAO89679.1| conserved hypothetical protein TIGR00242 [Coxiella burnetii RSA 493] Length = 152
- 3966.1 Best-BlastP=> >nrprot 64% Identities = 116/251 (46%), Positives = 166/251 (66%), Gaps = 4/251 (1%) ref|ZP\_00060306.1| COG1521: Putative transcriptional regulator, homolog of Bvg accessory factor [Clostridium thermocellum ATCC 27405] Length = 255
- 3967.1 Best-BlastP=> >nrprot 48% Identities = 73/139 (52%), Positives = 91/139 (65%), Gaps = 1/139 (0%) ref|NP\_819361.1| conserved domain protein [Coxiella burnetii RSA 493] gb|AAO89875.1| conserved domain protein [Coxiella burnetii RSA 493] Length = 214
- 3968.1 Best-BlastP=> >nrprot 39% Identities = 35/77 (45%), Positives = 48/77 (62%), Gaps = 3/77 (3%) ref|NP\_760035.1| Cytochrome c5 [Vibrio vulnificus CMCP6] gb|AAO09562.1|AE016800\_167 Cytochrome c5 [Vibrio vulnificus CMCP6] dbj|BAC92805.1| cytochrome c5 [Vibrio vulnificus YJ016] Length = 150
- 3969.1 Best-BlastP=> >nrprot 49% Identities = 69/204 (33%), Positives = 115/204 (56%), Gaps = 5/204 (2%) ref|NP\_252040.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|C83227 hypothetical protein PA3350 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06738.1|AE004757\_7 hypothetical protein PA3350 [Pseudomonas aeruginosa PAO1] Length = 232
- 397.2 Best-BlastP=> >nrprot 59% Identities = 68/133 (51%), Positives = 100/133 (75%) ref|ZP\_00043701.1| COG1974: SOS-response transcriptional repressors (RecA-mediated autopeptidases) [Magnetococcus sp. MC-1] Length = 238
- 3970.1 Best-BlastP=> >nrprot 37% Identities = 23/57 (40%), Positives = 40/57 (70%) ref|ZP\_00084200.1| COG2747: Negative regulator of flagellin synthesis (anti-sigma28 factor) [Pseudomonas fluorescens PfO-1] Length = 131
- 3971.2 Best-BlastP=> >nrprot 43% Identities = 41/149 (27%), Positives = 72/149 (48%), Gaps = 6/149 (4%) ref|ZP\_00136724.1| hypothetical protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 156
- 3972.2 Best-BlastP=> >nrprot 71% Identities = 139/251 (55%), Positives = 178/251 (70%), Gaps = 5/251 (1%) ref|NP\_819867.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Coxiella burnetii RSA 493] gb|AAO90381.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Coxiella burnetii RSA 493] Length = 254
- 3974.2 Best-BlastP=> >nrprot 64% Identities = 76/181 (41%), Positives = 118/181 (65%), Gaps = 1/181 (0%) ref|NP\_252535.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|A83164 hypothetical protein PA3846 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07233.1|AE004802\_2 hypothetical protein PA3846 [Pseudomonas aeruginosa PAO1] Length = 180
- 3977.2 Best-BlastP=> >nrprot 23% Identities = 105/397 (26%), Positives = 174/397 (43%), Gaps = 43/397 (10%) ref|ZP\_00008208.1| COG0665: Glycine/D-amino acid oxidases (deaminating) [Rhodobacter sphaeroides] Length = 533
- 3979.2 Best-BlastP=> >nrprot 61% Identities = 270/546 (49%), Positives = 356/546 (65%), Gaps = 14/546 (2%) ref|NP\_298274.1| gamma-glutamyltranspeptidase [Xylella fastidiosa 9a5c] pir|C82738 gamma-glutamyltranspeptidase XF0984 [imported] - Xylella fastidiosa 9a5c) gb|AAF83794.1|AE003936\_8 gamma-glutamyltranspeptidase [Xylella fastidiosa 9a5c] Length = 603
- 398.2 Best-BlastP=> >nrprot 62% Identities = 203/420 (48%), Positives = 267/420 (63%), Gaps = 7/420 (1%) ref|ZP\_00043700.1| COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Magnetococcus sp. MC-1] Length = 421
- 3980.1 Best-BlastP=> >nrprot 68% Identities = 90/158 (56%), Positives = 116/158 (73%) ref|ZP\_00021201.1| COG0669: Phosphopantetheine adenylyltransferase [Ralstonia metalldurans] Length = 161

- 3982.2 Best-BlastP=> >nrprot 55% Identities = 62/185 (33%), Positives = 110/185 (59%), Gaps = 4/185 (2%) ref|NP\_820808.1| outer membrane lipoprotein LolB, putative [Coxiella burnetii] RSA 493| gb|AAO91322.1| outer membrane lipoprotein LolB, putative [Coxiella burnetii] RSA 493| Length = 210
- 3985.1 Best-BlastP=> >nrprot 34% Identities = 40/148 (27%), Positives = 70/148 (47%) gb|AAC01725.1| rifamycin efflux protein [Amycolatopsis mediterranei] Length = 522
- 3986.1 Best-BlastP=> >nrprot 59% Identities = 155/374 (41%), Positives = 222/374 (59%), Gaps = 11/374 (2%) ref|NP\_485927.1| hypothetical protein [Nostoc sp. PCC 7120] pir|A|2041 hypothetical protein all1887 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB73586.1| ORF\_ID:all1887~hypothetical protein [Nostoc sp. PCC 7120] Length = 375
- 3988.3 Best-BlastP=> >nrprot 21% Identities = 60/228 (26%), Positives = 106/228 (46%), Gaps = 16/228 (7%) dbj|BAB84935.1| FLJ00180 protein [Homo sapiens] Length = 499
- 3989.1 Best-BlastP=> >nrprot 70% Identities = 84/147 (57%), Positives = 106/147 (72%), Gaps = 3/147 (2%) ref|NP\_457097.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_461503.1| putative Cytosine/adenosine deaminase [Salmonella typhimurium LT2] ref|NP\_804165.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|AF0827 conserved hypothetical protein STY2814 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAL21462.1| putative cytosine/adenosine deaminase [Salmonella typhimurium LT2] emb|CAD02770.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO68014.1| conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 183
- 399.2 Best-BlastP=> >nrprot 20% Identities = 79/403 (19%), Positives = 171/403 (42%), Gaps = 54/403 (13%) gb|EAA16038.1| repeat organellar protein-related [Plasmodium yoelii yoelii] Length = 1441
- 3991.3 Best-BlastP=> >nrprot 10% Identities = 35/108 (32%), Positives = 60/108 (55%), Gaps = 4/108 (3%) ref|XP\_316738.1| ENSANGP00000016119 [Anopheles gambiae] gb|EAA11974.1| ENSANGP00000016119 [Anopheles gambiae str. PEST] Length = 602
- 3993.2 Best-BlastP=> >nrprot No Hits found
- 3994.5 Best-BlastP=> >nrprot 29% Identities = 41/133 (30%), Positives = 65/133 (48%), Gaps = 27/133 (20%) dbj|BAB21508.1| protein-glutaminase [Chryseobacterium proteolyticum] Length = 320
- 3995.5 Best-BlastP=> >nrprot 29% Identities = 85/264 (32%), Positives = 125/264 (47%), Gaps = 26/264 (9%) ref|NP\_810963.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO77157.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 425
- 3996.2 Best-BlastP=> >nrprot No Hits found
- 3998.3 Best-BlastP=> >nrprot 42% Identities = 36/142 (25%), Positives = 66/142 (46%), Gaps = 10/142 (7%) ref|NP\_751974.1| Putative glutamate dehydrogenase [Escherichia coli CFT073] gb|AAN78518.1| AE016755\_18 Putative glutamate dehydrogenase [Escherichia coli CFT073] Length = 678
- 3999.3 Best-BlastP=> >nrprot 99% Identities = 641/644 (99%), Positives = 642/644 (99%) sp|O32482|DNAK\_LEGPN Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) dbj|BAA22783.1| DnaK [Legionella pneumophila] Length = 644

- 4.1 Best-BlastP=> >nrrprot 59% Identities = 120/298 (40%), Positives = 181/298 (60%), Gaps = 1/298 (0%) ref|NP\_907748.1| conserved hypothetical protein [Wolinella succinogenes] emb|CAE10648.1| conserved hypothetical protein [Wolinella succinogenes] Length = 332
- 400.1 Best-BlastP=> >nrrprot 30% Identities = 45/177 (25%), Positives = 80/177 (45%), Gaps = 25/177 (14%) ref|NP\_587991.1| hypothetical structural protein [Schizosaccharomyces pombe] pir|T41077 hypothetical structural protein - fission yeast (Schizosaccharomyces pombe) emb|CAB53076.1| SPCC16A11.04 [Schizosaccharomyces pombe] Length = 1010
- 4000.2 Best-BlastP=> >nrrprot 45% Identities = 42/110 (38%), Positives = 64/110 (58%), Gaps = 5/110 (4%) ref|NP\_925923.1| MarR family transcriptional regulatory protein [Gloeobacter violaceus] dbj|BAC90918.1| MarR family transcriptional regulatory protein [Gloeobacter violaceus] Length = 143
- 4002.2 Best-BlastP=> >nrrprot 24% Identities = 99/340 (29%), Positives = 154/340 (45%), Gaps = 53/340 (15%) ref|NP\_623249.1| Cell division protein FtsI/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] gb|AAM24853.1| Cell division protein FtsI/penicillin-binding protein 2 [Thermoanaerobacter tengcongensis] Length = 678
- 4003.1 Best-BlastP=> >nrrprot 50% Identities = 151/498 (30%), Positives = 248/498 (49%), Gaps = 51/498 (10%) ref|ZP\_00112433.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Nostoc punctiforme] Length = 544
- 4004.2 Best-BlastP=> >nrrprot 61% Identities = 244/575 (42%), Positives = 366/575 (63%), Gaps = 8/575 (1%) ref|NP\_359923.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1| multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589
- 4005.2 Best-BlastP=> >nrrprot 76% Identities = 309/502 (61%), Positives = 381/502 (75%), Gaps = 7/502 (1%) gb|AAP40013.1| lysine tRNA synthetase [Citrobacter freundii] Length = 505
- 4009.1 Best-BlastP=> >nrrprot 85% Identities = 254/332 (76%), Positives = 288/332 (86%) ref|NP\_457439.1| peptide chain release factor 2 (RF-2) [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_806651.1| peptide chain release factor 2 [Salmonella enterica subsp. enterica serovar Typhi Ty2] sp|P28353|RF2\_SALTY Peptide chain release factor 2 (RF-2) pir|A36480 translation releasing factor RF-2 - Salmonella typhimurium pir|AG0871 peptide chain release factor 2 (RF-2) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) gb|AAA72914.1| peptide chain release factor 2 emb|CAD02871.1| peptide chain release factor 2 (RF-2) [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO70511.1| peptide chain release factor 2 [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 365
- 401.2 Best-BlastP=> >nrrprot 44% Identities = 128/335 (38%), Positives = 180/335 (53%), Gaps = 12/335 (3%) ref|ZP\_00005503.1| hypothetical protein [Rhodobacter sphaeroides] Length = 458
- 4010.1 Best-BlastP=> >nrrprot 42% Identities = 26/118 (22%), Positives = 58/118 (49%), Gaps = 13/118 (11%) ref|NP\_903543.1| hypothetical protein CV3873 [Chromobacterium violaceum ATCC 12472] gb|AAQ61535.1| hypothetical protein CV3873 [Chromobacterium violaceum ATCC 12472] Length = 117

4012.1

Best-BlastP=> >nrprot 54% Identities = 98/248 (39%), Positives = 150/248 (60%), Gaps = 14/248 (5%) ref|NP\_250152.1| probable chemotaxis protein [Pseudomonas aeruginosa PAO1] ref|ZP\_00139088.1| COG1360: Flagellar motor protein [Pseudomonas aeruginosa UCBPP-PA14] pir|T46617 probable chemotaxis protein PA1461 [imported] - Pseudomonas aeruginosa (strain PAO1) dbj|BAA33552.1| ORF2 [Pseudomonas aeruginosa] gb|AAG04850.1|AE004575\_9 probable chemotaxis protein [Pseudomonas aeruginosa PAO1] Length = 296

4013.1

Best-BlastP=> >nrprot 67% Identities = 129/244 (52%), Positives = 175/244 (71%) ref|NP\_746451.1| flagellar motor protein MotA [Pseudomonas putida KT2440] gb|AAN69915.1|AE016630\_6 flagellar motor protein MotA [Pseudomonas putida KT2440] Length = 246

4014.1

Best-BlastP=> >nrprot 97% Identities = 231/238 (97%), Positives = 234/238 (98%) emb|CAA67397.1| sigma factor 28 [Legionella pneumophila] Length = 238

4015.1

Best-BlastP=> >nrprot 76% Identities = 119/229 (51%), Positives = 178/229 (77%) gb|AAC62540.2| MotR [Pseudomonas aeruginosa] Length = 275

4016.1

Best-BlastP=> >nrprot 49% Identities = 124/284 (43%), Positives = 187/284 (65%), Gaps = 5/284 (1%) gb|AAF32412.1| flagellar biosynthesis protein FlhF [Vibrio parahaemolyticus] Length = 503

4017.4

Best-BlastP=> >nrprot 80% Identities = 433/701 (61%), Positives = 560/701 (79%), Gaps = 9/701 (1%) ref|NP\_250143.1| flagellar biosynthesis protein FlhA [Pseudomonas aeruginosa PAO1] ref|ZP\_00139079.1| COG1298: Flagellar biosynthesis pathway, component FlhA [Pseudomonas aeruginosa UCBPP-PA14] pir|F83465 flagellar biosynthesis protein FlhA PA1452 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04841.1|AE004574\_12 flagellar biosynthesis protein FlhA [Pseudomonas aeruginosa PAO1] Length = 707

Best-BlastP=> >nrprot No Hits found

402.2

4020.2

Best-BlastP=> >nrprot 48% Identities = 177/535 (33%), Positives = 277/535 (51%), Gaps = 29/535 (5%) ref|NP\_819244.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89758.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 578

Best-BlastP=> >nrprot 41% Identities = 53/162 (32%), Positives = 81/162 (50%), Gaps = 3/162 (1%) ref|NP\_643713.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri] str. 306] sp|Q8PH54|YY06\_XANAC Hypothetical UPF0149 protein XAC3406 gb|AAM38249.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri] str. 306] Length = 180

Best-BlastP=> >nrprot 69% Identities = 221/433 (51%), Positives = 306/433 (70%), Gaps = 1/433 (0%) ref|ZP\_00092323.1| COG0006: Xaa-Pro aminopeptidase [Azotobacter vinelandii] Length = 537

4023.2

4025.1

Best-BlastP=> >nrprot 56% Identities = 161/389 (41%), Positives = 227/389 (58%), Gaps = 12/389 (3%) ref|NP\_253910.1| ubiH protein [Pseudomonas aeruginosa PAO1] pir|G82992 ubiH protein PA5223 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG08608.1|AE004935\_5 ubiH protein [Pseudomonas aeruginosa PAO1] Length = 394

4026.2

Best-BlastP=> >nrprot 59% Identities = 171/394 (43%), Positives = 229/394 (58%), Gaps = 9/394 (2%) ref|NP\_716409.1| oxidoreductase, FAD-binding, UbiH/Coq6 family [Shewanella oneidensis MR-1] gb|AAN53854.1|AE015522\_9 oxidoreductase, FAD-binding, UbiH/Coq6 family [Shewanella oneidensis MR-1] Length = 407



- 4030.1 Best-BlastP=> >nrprot 35% Identities = 33/123 (26%), Positives = 54/123 (43%), Gaps = 30/123 (24%) ref|NP\_604443.1| dystonin isoform b; bullous pemphigoid antigen 1; dystonia musculorum [Mus musculus] sp|Q91ZU6|BPA1\_MOUSE Bullous pemphigoid antigen 1, isoforms 1/2/3/4 (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin) gb|AAK83384.1|AF396879\_1 bullous pemphigoid antigen 1-b [Mus musculus] Length = 7389
- 4032.3 Best-BlastP=> >nrprot 76% Identities = 179/322 (55%), Positives = 242/322 (75%), Gaps = 7/322 (2%) ref|ZP\_00090005.1| hypothetical protein [Azotobacter vinelandii] Length = 328
- 4035.1 Best-BlastP=> >nrprot 55% Identities = 47/121 (38%), Positives = 68/121 (56%), Gaps = 7/121 (5%) gb|AAL25256.1| TraK [Legionella pneumophila] Length = 114
- 4036.2 Best-BlastP=> >nrprot 50% Identities = 30/99 (30%), Positives = 48/99 (48%), Gaps = 6/99 (6%) ref|NP\_903527.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61519.2| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 576
- 4037.2 Best-BlastP=> >nrprot 75% Identities = 42/78 (53%), Positives = 60/78 (76%) ref|NP\_759375.1| Predicted transcriptional regulator [Vibrio vulnificus CMCP6] gb|AAO08902.1|AE016798\_62 Predicted transcriptional regulator [Vibrio vulnificus CMCP6] Length = 85
- 4039.2 Best-BlastP=> >nrprot 62% Identities = 206/434 (47%), Positives = 273/434 (62%), Gaps = 5/434 (1%) ref|NP\_932051.1| HipA protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE17272.1| HipA protein [Photobacterium luminescens subsp. laumondii TTO1] Length = 439
- 4040.1 Best-BlastP=> >nrprot 32% Identities = 19/53 (35%), Positives = 32/53 (60%), Gaps = 2/53 (3%) ref|NP\_297921.1| phage-related integrase [Xylella fastidiosa 9a5c] pir|E82782 phage-related integrase XF0631 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83441.1|AE003908\_9 phage-related integrase [Xylella fastidiosa 9a5c] Length = 413
- 4041.1 Best-BlastP=> >nrprot No Hits found
- 4042.1 Best-BlastP=> >nrprot 84% Identities = 169/231 (73%), Positives = 198/231 (85%) ref|NP\_435396.1| hypothetical protein [Sinorhizobium meliloti] pir|F95280 hypothetical protein SMa0280 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA gb|AAK64808.1| hypothetical protein [Sinorhizobium meliloti] Length = 262
- 4043.1 Best-BlastP=> >nrprot 65% Identities = 63/126 (50%), Positives = 88/126 (69%), Gaps = 5/126 (3%) ref|NP\_435397.1| putative regulator, MerR family [Sinorhizobium meliloti] pir|G95280 probable regulator, MerR family [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA gb|AAK64809.1| putative regulator, MerR family [Sinorhizobium meliloti] Length = 134
- 4045.2 Best-BlastP=> >nrprot No Hits found
- 4047.3 Best-BlastP=> >nrprot 57% Identities = 142/327 (43%), Positives = 195/327 (59%), Gaps = 7/327 (2%) ref|NP\_819580.1| lytic murein transglycosylase [Coxiella burnetii RSA 493] gb|AAO90094.1| lytic murein transglycosylase [Coxiella burnetii RSA 493] Length = 334
- 4048.3 Best-BlastP=> >nrprot 86% Identities = 443/598 (74%), Positives = 520/598 (86%) ref|ZP\_00090179.1| COG0481: Membrane GTPase LepA [Azotobacter vinelandii] Length = 599
- 405.3 Best-BlastP=> >nrprot 11% Identities = 44/140 (31%), Positives = 73/140 (52%), Gaps = 4/140 (2%) pir|OXRTGU L-gulonolactone oxidase (EC 1.1.3.8) - rat dbj|BAA02232.1| L-gulonolactone oxidase [Rattus norvegicus] Length = 440
- 4050.1 Best-BlastP=> >nrprot 73% Identities = 133/254 (52%), Positives = 184/254 (72%), Gaps = 9/254 (3%) ref|NP\_820098.1| signal peptidase I [Coxiella burnetii RSA 493] gb|AAO90612.1| signal peptidase I [Coxiella burnetii RSA 493] Length = 259

- 4051.2 Best-BlastP=> >nrprot 51% Identities = 37/118 (31%), Positives = 67/118 (56%), Gaps = 6/118 (5%) ref|NP\_842322.1| possible transmembrane protein [Nitrosomonas europaea ATCC 19718] emb|CAD86237.1| possible transmembrane protein [Nitrosomonas europaea ATCC 19718] Length = 126
- 4054.2 Best-BlastP=> >nrprot 68% Identities = 122/222 (54%), Positives = 155/222 (69%), Gaps = 4/222 (1%) ref|NP\_716968.1| ribonuclease III [Shewanella oneidensis MR-1] gb|AAN54413.1|AE015579\_2 ribonuclease III [Shewanella oneidensis MR-1] Length = 226
- 4055.1
- Best-BlastP=> >nrprot 67% Identities = 309/628 (49%), Positives = 418/628 (66%), Gaps = 14/628 (2%) ref|ZP\_00092302.1| COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Azotobacter vinelandii] Length = 830
- 4056.2 Best-BlastP=> >nrprot 75% Identities = 247/407 (60%), Positives = 308/407 (75%) ref|NP\_052356.1| unnamed protein product [Coxiella burnetii] pir|S38238 hypothetical protein - Coxiella burnetii emb|CAA53126.1| unnamed protein product [Coxiella burnetii] emb|CAA63678.1| orf 410 [Coxiella burnetii] Length = 410
- 4058.2 Best-BlastP=> >nrprot No Hits found
- 406.1 Best-BlastP=> >nrprot 51% Identities = 95/241 (39%), Positives = 143/241 (59%), Gaps = 6/241 (2%) ref|NP\_107761.1| unknown protein [Mesorhizobium loti] db|BAB53547.1| unknown protein [Mesorhizobium loti] Length = 273
- 4060.1 Best-BlastP=> >nrprot 66% Identities = 208/400 (52%), Positives = 273/400 (68%), Gaps = 5/400 (1%) ref|NP\_747386.1| phosphopantothencysteine decarboxylase/phosphopantothenate--cysteine ligase [Pseudomonas putida KT2440] gb|AAN70850.1|AE016729\_8 phosphopantothencysteine decarboxylase/phosphopantothenate--cysteine ligase [Pseudomonas putida KT2440] Length = 403
- 4061.1 Best-BlastP=> >nrprot 79% Identities = 108/147 (73%), Positives = 121/147 (82%) ref|ZP\_00134300.1| COG0756: dUTPase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 151
- 4063.1 Best-BlastP=> >nrprot 66% Identities = 229/455 (50%), Positives = 310/455 (68%) ref|NP\_747389.1| phosphomannomutase [Pseudomonas putida KT2440] sp|Q88C93|ALGC\_PSEPK Phosphomannomutase/phosphoglucomutase (PMM / PGM) gb|AAN70853.1|AE016729\_11 phosphomannomutase [Pseudomonas putida KT2440] Length = 463
- 4065.3 Best-BlastP=> >nrprot 50% Identities = 181/557 (32%), Positives = 290/557 (52%), Gaps = 17/557 (3%) ref|NP\_819579.1| TPR domain protein [Coxiella burnetii RSA 493] gb|AAO90093.1| TPR domain protein [Coxiella burnetii RSA 493] Length = 561
- 4066.2 Best-BlastP=> >nrprot 69% Identities = 102/190 (53%), Positives = 136/190 (71%), Gaps = 2/190 (1%) ref|NP\_928489.1| hypothetical protein [Photothabdus luminescens subsp. laumondii TTO1] emb|CAE13471.1| unnamed protein product [Photothabdus luminescens subsp. laumondii TTO1] Length = 197
- 4067.2 Best-BlastP=> >nrprot No Hits found
- 4068.2 Best-BlastP=> >nrprot 56% Identities = 174/381 (45%), Positives = 240/381 (62%), Gaps = 6/381 (1%) ref|NP\_296878.1| sodium:dicarboxylate symporter family protein [Chlamydia muridarum] gb|AAF73565.1| sodium:dicarboxylate symporter family protein [Chlamydia muridarum] Length = 415
- 407.4 Best-BlastP=> >nrprot 78% Identities = 295/449 (65%), Positives = 356/449 (79%) ref|NP\_253299.1| DNA repair protein RadA [Pseudomonas aeruginosa PA01] sp|P96963|RADA\_PSEAE DNA repair protein radA homolog (DNA repair protein sms homolog) pir|A83069 DNA repair protein RadA PA4609 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07997.1|AE004875\_3 DNA repair protein RadA [Pseudomonas aeruginosa PAO1] Length = 453

4070.3

- Best-BlastP=> >nrprot 82% Identities = 322/464 (69%), Positives = 387/464 (83%) ref|NP\_415450.1| asparagine tRNA synthetase [Escherichia coli K12] ref|NP\_752997.1| AsparaginyI-tRNA synthetase [Escherichia coli CFT073] ref|NP\_836636.1| asparagine tRNA synthetase [Shigella flexneri 2a str. 2457T] sp|P17242|SYN\_ECOLI AsparaginyI-tRNA synthetase (Asparagine--tRNA ligase) (AsnRS) pir|SYECNT asparagine-tRNA ligase (EC 6.1.1.22) - Escherichia coli (strain K-12) emb|CAA48274.1| AsparaginyI-tRNA synthetase [Escherichia coli] gb|AAA24666.1| asparaginyI-tRNA synthetase (asnS) dbj|BAA35682.1| AsparaginyI-tRNA synthetase (EC 6.1.1.22) (asparagine-tRNA ligase) (asnRS). [Escherichia coli K12] gb|AAC74016.1| asparagine tRNA synthetase [Escherichia coli K12] gb|AAN79540.1|AE016758\_144 AsparaginyI-tRNA synthetase [Escherichia coli CFT073] gb|AAP16442.1| asparagine tRNA synthetase [Shigella flexneri 2a str. 2457T] Length = 466
- 4071.1 Best-BlastP=> >nrprot No Hits found
- 4072.1 Best-BlastP=> >nrprot 98% Identities = 215/218 (98%), Positives = 216/218 (99%) gb|AAC32842.1| unknown [Legionella pneumophila] Length = 218
- 4073.1 Best-BlastP=> >nrprot 99% Identities = 355/357 (99%), Positives = 356/357 (99%) gb|AAC32841.1| unknown [Legionella pneumophila] Length = 357
- 4075.3 Best-BlastP=> >nrprot 58% Identities = 69/160 (43%), Positives = 93/160 (58%), Gaps = 4/160 (2%) ref|ZP\_00051893.1| COG3012: Uncharacterized protein conserved in bacteria [Magnetospirillum magnetotacticum] Length = 163
- 4076.1 Best-BlastP=> >nrprot No Hits found
- 4078.1 Best-BlastP=> >nrprot 70% Identities = 227/395 (57%), Positives = 303/395 (76%), Gaps = 1/395 (0%) ref|ZP\_00031357.1| COG0038: Chloride channel protein Eric [Burkholderia fungorum] Length = 443
- 408.3 Best-BlastP=> >nrprot 47% Identities = 152/478 (31%), Positives = 258/478 (53%), Gaps = 28/478 (5%) ref|NP\_820790.1| outer membrane efflux family protein [Coxiella burnetii RSA 493] gb|AAO91304.1| outer membrane efflux family protein [Coxiella burnetii RSA 493] Length = 507
- 4080.2 Best-BlastP=> >nrprot 89% Identities = 377/385 (97%), Positives = 381/385 (98%) gb|AAD47247.1| putative transport protein [Legionella pneumophila] Length = 387
- 4082.2 Best-BlastP=> >nrprot 34% Identities = 78/288 (27%), Positives = 138/288 (47%), Gaps = 2/288 (0%) ref|NP\_931673.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE16879.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 833
- 4083.3 Best-BlastP=> >nrprot No Hits found
- 4084.2 Best-BlastP=> >nrprot 55% Identities = 143/383 (37%), Positives = 217/383 (56%), Gaps = 1/383 (0%) ref|ZP\_00058706.1| COG0438: Glycosyltransferase [Thermobifida fusca] Length = 426
- 4087.2 Best-BlastP=> >nrprot 61% Identities = 175/436 (40%), Positives = 262/436 (60%), Gaps = 25/436 (5%) ref|NP\_845547.1| conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP27033.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 445
- 4088.2 Best-BlastP=> >nrprot 75% Identities = 182/288 (63%), Positives = 224/288 (77%) gb|AAM00632.1| unknown [Legionella pneumophila] Length = 294
- 409.2 Best-BlastP=> >nrprot 56% Identities = 123/352 (34%), Positives = 210/352 (59%), Gaps = 8/352 (2%) ref|NP\_820789.1| lipoprotein, putative [Coxiella burnetii RSA 493] gb|AAO91303.1| lipoprotein, putative [Coxiella burnetii RSA 493] Length = 391

- 4093.1 Best-BlastP=> >nrprot 72% Identities = 255/481 (53%), Positives = 346/481 (71%), Gaps = 9/481 (1%) ref|NP\_820458.1| glutamyl-tRNA(Gln) amidotransferase, B subunit [Coxiella burnetii] RSA 493] gb|AAO90972.1| glutamyl-tRNA(Gln) amidotransferase, B subunit [Coxiella burnetii] RSA 493] Length = 477
- 4094.2 Best-BlastP=> >nrprot 75% Identities = 284/480 (59%), Positives = 366/480 (76%), Gaps = 1/480 (0%) ref|NP\_820457.1| glutamyl-tRNA(Gln) amidotransferase, A subunit [Coxiella burnetii] RSA 493] gb|AAO90971.1| glutamyl-tRNA(Gln) amidotransferase, A subunit [Coxiella burnetii] RSA 493] Length = 483
- 4096.1 Best-BlastP=> >nrprot 70% Identities = 86/155 (55%), Positives = 113/155 (72%) ref|NP\_841624.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP\_841817.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP\_842206.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] ref|NP\_842438.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD85496.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD86113.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD85700.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb|CAD86358.1| Transposase IS4 family [Nitrosomonas europaea ATCC 19718] Length = 191
- 4097.1 Best-BlastP=> >nrprot 62% Identities = 26/34 (76%), Positives = 31/34 (91%) ref|ZP\_00111545.1| COG4644: Transposase and inactivated derivatives, TnpA family [Nostoc punctiforme] Length = 1014
- 4098.1 Best-BlastP=> >nrprot 62% Identities = 33/89 (37%), Positives = 57/89 (64%) gb|AAO92366.1| transposase [Listonella anguillarum] Length = 980
- 410.1 Best-BlastP=> >nrprot 70% Identities = 125/226 (55%), Positives = 166/226 (73%) ref|NP\_721272.1| putative ABC transporter, ATP-binding protein [Streptococcus mutans UA159] gb|AAN58578.1|AE014927\_7 putative ABC transporter, ATP-binding protein [Streptococcus mutans UA159] Length = 235
- 4101.1 Best-BlastP=> >nrprot 50% Identities = 22/49 (44%), Positives = 34/49 (69%) ref|NP\_277100.1| putative transposase [Deinococcus radiodurans] Length = 828
- 4104.2 Best-BlastP=> >nrprot 44% Identities = 121/430 (28%), Positives = 195/430 (45%), Gaps = 67/430 (15%) ref|NP\_873428.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] gb|AAP95817.1| conserved hypothetical protein [Haemophilus ducreyi 35000HP] Length = 481
- 4105.1 Best-BlastP=> >nrprot 48% Identities = 74/241 (30%), Positives = 126/241 (52%), Gaps = 19/241 (7%) ref|ZP\_00132729.1| hypothetical protein [Haemophilus somnus 2336] Length = 270
- 4106.1 Best-BlastP=> >nrprot 39% Identities = 47/197 (23%), Positives = 88/197 (44%), Gaps = 18/197 (9%) ref|ZP\_00123126.1| hypothetical protein [Haemophilus somnus 129PT] Length = 212
- 4107.1 Best-BlastP=> >nrprot No Hits found
- 4108.1 Best-BlastP=> >nrprot 34% Identities = 61/215 (28%), Positives = 97/215 (45%), Gaps = 29/215 (13%) ref|NP\_928397.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13363.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 245

- 4109.2 Best-BlastP=> >nrprot 34% Identities = 36/145 (24%), Positives = 67/145 (46%), Gaps = 16/145 (11%) ref|XP\_323218.1| hypothetical protein (AL356172) conserved hypothetical protein [Neurospora crassa] emb|CAD11783.1| conserved hypothetical protein [Neurospora crassa] gb|EAA28302.1| hypothetical protein ((AL356172) conserved hypothetical protein [Neurospora crassa]) Length = 743
- 4111.2 Best-BlastP=> >nrprot 97% Identities = 350/359 (97%), Positives = 350/359 (97%), Gaps = 8/359 (2%) emb|CAB65206.1| RmlB protein [Legionella pneumophila] Length = 351
- 4112.1 Best-BlastP=> >nrprot 99% Identities = 294/294 (100%), Positives = 294/294 (100%) emb|CAB65207.1| RmlD protein [Legionella pneumophila] Length = 294
- 4113.1 Best-BlastP=> >nrprot 94% Identities = 172/188 (91%), Positives = 177/188 (94%), Gaps = 1/188 (0%) emb|CAB65208.1| RmlC protein [Legionella pneumophila] Length = 188
- 4115.1 Best-BlastP=> >nrprot 97% Identities = 331/334 (99%), Positives = 332/334 (99%) emb|CAB65212.1| N-acetylneuraminic acid condensing enzyme [Legionella pneumophila] Length = 338
- 4116.3 Best-BlastP=> >nrprot 99% Identities = 232/232 (100%), Positives = 232/232 (100%) emb|CAB65213.1| CMP-N-acetylneuraminic acid synthetase [Legionella pneumophila] Length = 232
- 4118.3 Best-BlastP=> >nrprot 99% Identities = 213/213 (100%), Positives = 213/213 (100%) sp|Q9RDX3|HIS5\_LEGPN Imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH) emb|CAB65214.1| glutamine amidotransferase [Legionella pneumophila] Length = 213
- 4119.2 Best-BlastP=> >nrprot 82% Identities = 207/210 (98%), Positives = 210/210 (100%) sp|Q9RDX2|HIS6\_LEGPN Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF) emb|CAB65215.1| HisF protein [Legionella pneumophila] Length = 212
- 412.3 Best-BlastP=> >nrprot 66% Identities = 189/397 (47%), Positives = 263/397 (66%) ref|NP\_820787.1| ABC transporter, permease protein [Coxiella burnetii RSA 493] gb|AAO91301.1| ABC transporter, permease protein [Coxiella burnetii RSA 493] Length = 404
- 4123.2 Best-BlastP=> >nrprot 63% Identities = 39/74 (52%), Positives = 54/74 (72%), Gaps = 1/74 (1%) gb|AAM08234.1| putative phage repressor [Legionella pneumophila] Length = 227
- 4126.2 Best-BlastP=> >nrprot 54% Identities = 118/267 (44%), Positives = 164/267 (61%), Gaps = 2/267 (0%) gb|AAM08235.1| LvrA [Legionella pneumophila] Length = 289
- 4127.1 Best-BlastP=> >nrprot 51% Identities = 47/155 (30%), Positives = 77/155 (49%), Gaps = 20/155 (12%) gb|AAM08236.1| LvrB [Legionella pneumophila] Length = 150
- 4128.1 Best-BlastP=> >nrprot 61% Identities = 25/62 (40%), Positives = 45/62 (72%), Gaps = 2/62 (3%) emb|CAB60050.1| lvrC [Legionella pneumophila] Length = 67
- 4129.1 Best-BlastP=> >nrprot 40% Identities = 37/114 (32%), Positives = 62/114 (54%), Gaps = 4/114 (3%) gb|AAL05416.1| PilL [Yersinia pseudotuberculosis] Length = 356
- 413.5 Best-BlastP=> >nrprot 23% Identities = 104/399 (26%), Positives = 187/399 (46%), Gaps = 28/399 (7%) ref|NP\_486788.1| hypothetical protein [Nostoc sp. PCC 7120] pir|AE2149 hypothetical protein all2748 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB74447.1| ORF\_ID:all2748~hypothetical protein [Nostoc sp. PCC 7120] Length = 426

- 4130.2 Best-BlastP=> >nrprot 45% Identities = 33/104 (31%), Positives = 60/104 (57%), Gaps = 6/104 (5%) ref|NP\_819572.1| SMC family protein [Coxiella burnetii RSA 493] emb|CAD66594.1| SMC protein [Coxiella burnetii] gb|AAO90086.1| SMC family protein [Coxiella burnetii RSA 493] Length = 1169
- 4131.3 Best-BlastP=> >nrprot 31% Identities = 60/185 (32%), Positives = 87/185 (47%), Gaps = 8/185 (4%) gb|AAN62293.1|AF440524\_80 hypothetical protein [Pseudomonas aeruginosa] Length = 241
- 4132.3 Best-BlastP=> >nrprot 45% Identities = 42/99 (42%), Positives = 58/99 (58%), Gaps = 2/99 (2%) ref|ZP\_00123136.1| hypothetical protein [Haemophilus somnus 129PT] Length = 170
- 4133.1 Best-BlastP=> >nrprot 75% Identities = 39/61 (63%), Positives = 49/61 (80%) ref|NP\_403868.1| 50S ribosomal protein L29 [Yersinia pestis] ref|NP\_671291.1| 50S ribosomal subunit protein L29 [Yersinia pestis KIM] sp|Q8ZJA4|RL29\_YERPE 50S ribosomal protein L29 pir|AB0027 50S ribosomal protein L29 [imported] - Yersinia pestis (strain CO92) emb|CAC89077.1| 50S ribosomal protein L29 [Yersinia pestis CO92] gb|AAM87542.1|AE014002\_15 50S ribosomal subunit protein L29 [Yersinia pestis KIM] Length = 63
- 4134.1 Best-BlastP=> >nrprot 77% Identities = 54/79 (68%), Positives = 66/79 (83%) ref|ZP\_00090912.1| COG0186: Ribosomal protein S17 [Azotobacter vinelandii] Length = 90
- 4135.1 Best-BlastP=> >nrprot 90% Identities = 100/122 (81%), Positives = 110/122 (90%), Gaps = 1/122 (0%) ref|ZP\_00067983.1| COG0093: Ribosomal protein L14 [Microbulbifer degradans 2-40] Length = 122
- 4136.1 Best-BlastP=> >nrprot 70% Identities = 58/106 (54%), Positives = 77/106 (72%), Gaps = 1/106 (0%) ref|NP\_273211.1| 50S ribosomal protein L24 [Neisseria meningitidis MC58] ref|NP\_282968.1| 50S ribosomal protein L24 [Neisseria meningitidis Z2491] pir|C81232 50S ribosomal protein L24 NMB0153 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) gb|AAF40611.1| 50S ribosomal protein L24 [Neisseria meningitidis MC58] emb|CAB83433.1| 50S ribosomal protein L24 [Neisseria meningitidis Z2491] Length = 107
- 4138.1 Best-BlastP=> >nrprot 83% Identities = 128/178 (71%), Positives = 153/178 (85%) ref|NP\_273212.1| 50S ribosomal protein L5 [Neisseria meningitidis MC58] pir|D81232 50S ribosomal protein L5 NMB0154 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF40612.1| 50S ribosomal protein L5 [Neisseria meningitidis MC58] Length = 179
- 4139.1 Best-BlastP=> >nrprot 65% Identities = 49/101 (48%), Positives = 66/101 (65%), Gaps = 1/101 (0%) ref|ZP\_00004335.1| COG0199: Ribosomal protein S14 [Rhodobacter sphaeroides] Length = 101
- 4140.1 Best-BlastP=> >nrprot 78% Identities = 79/133 (59%), Positives = 103/133 (77%), Gaps = 5/133 (3%) ref|NP\_273214.1| 30S ribosomal protein S8 [Neisseria meningitidis MC58] ref|NP\_282965.1| 30S ribosomal protein S8 [Neisseria meningitidis Z2491] sp|Q9JR58|RS8\_NEIMA 30S ribosomal protein S8 pir|F81232 30S ribosomal protein S8 NMB0156 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) gb|AAF40614.1| 30S ribosomal protein S8 [Neisseria meningitidis MC58] emb|CAB83430.1| 30S ribosomal protein S8 [Neisseria meningitidis Z2491] Length = 130

4141.1

Best-BlastP=> >nprot 71% Identities = 102/179 (56%), Positives = 129/179 (72%), Gaps = 2/179 (1%) ref|NP\_289866.1| 50S ribosomal subunit protein L6 [Escherichia coli O157:H7 EDL933] ref|NP\_312197.1| 50S ribosomal subunit protein L6 [Escherichia coli O157:H7] ref|NP\_417764.1| 50S ribosomal subunit protein L6 [Escherichia coli K12] ref|NP\_709093.1| 50S ribosomal subunit protein L6 [Shigella flexneri 2a str. 301] ref|NP\_755932.1| 50S ribosomal protein L6 [Escherichia coli CFT073] ref|NP\_839565.1| 50S ribosomal subunit protein L6 [Shigella flexneri 2a str. 2457T] sp|P02390|RL6\_ECOLI 50S ribosomal protein L6 pir|R5EC6 ribosomal protein L6 [validated] - cherichia coli (strain K-12) pir|B91150 50S ribosomal subunit protein L6 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) 995 50S ribosomal subunit protein L6 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) gb|AA58102.1| 50S ribosomal subunit protein L6 [Escherichia coli] gb|AAC76330.1| 50S ribosomal subunit protein L6 [Escherichia coli K12] E05556\_19 50S ribosomal subunit protein L6 [Escherichia coli O157:H7 EDL933] db|BAB37593.1| 50S ribosomal subunit protein L6 [Escherichia coli O157:H7 E015343 16 50S ribosomal subunit protein L6 [Shigella flexneri 2a str. 301]]

4142.3

Best-BlastP=> >nrprot 71% Identities = 65/117 (55%), Positives = 86/117 (73%), Gaps = 4/117 (3%) ref|NP\_252937.1| 50S ribosomal protein L18 [Pseudomonas aeruginosa PAO1] ref|ZP\_00137735.1| COG0256: Ribosomal protein L18 [Pseudomonas aeruginosa UCBPP-PA14] pir||E83114 50S ribosomal protein L18 PA4247 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07635.1|AE004841\_13 50S ribosomal protein L18 [Pseudomonas aeruginosa PAO1] Length = 116

### 4143.3

Best-BlastP=> >nrrprot 75% Identities = 105/158 (66%), Positives = 127/158 (80%) ref|P\_00067978.1| COG0098: Ribosomal protein S5  
[Microbulfifer degradans 2-40] Length = 170

4144.3

Best-BlastP=> >nrrprot 66% Identities = 31/56 (55%), Positives = 41/56 (73%) ref|NP\_563303.1| 50S ribosomal protein L30 [Clostridium perfringens] db|BAB82093.1| 50S ribosomal protein L30 [Clostridium perfringens str. 13] Length = 57

4145.3

Best-BlastP=> >nrprot 76% Identities = 92/144 (63%), Positives = 111/144 (77%) ref|ZP\_00067977.1| COG0200: Ribosomal protein L15  
[Microbublifer degradans 2-40] Length = 144

4148.3

Best-BlastP=> >nprot 81% Identities = 293/437 (67%), Positives = 364/437 (83%) refNP\_819302.1 preprotein translocase, SecY subunit. [Coxiella burnetii RSA 493] gb|AAO89816.1 preprotein translocase, SecY subunit [Coxiella burnetii RSA 493] Length = 442

4149.1

Best-BlastP=> >nprot 81% Identities = 83/114 (72%), Positives = 97/114 (85%) ref|ZP\_00125957.1| COG0099: Ribosomal protein S13 [Pseudomonas syringae pv. syringae B728a] ref|NP\_790495.1| ribosomal protein S13 [Pseudomonas syringae pv. tomato str. DC3000] sp|Q889U9|RS13\_PSESM 30S ribosomal protein S13 gb|AAO54190.1| ribosomal protein S13 [Pseudomonas syringae pv. tomato str. DC3000]  
Length = 118

## 415.2

Best-BlastP=> >nprot 57% Identities = 176/280 (62%), Positives = 213/280 (76%), Gaps = 2/280 (0%) ref|NP\_838055.1| putative transposase [Shigella flexneri 2a str. 2457T] gb|AAK64580.1| putative transposase [Vibrio cholerae] dbj|BAB79611.1| orf6 [Salmonella enterica subsp. enterica serovar Choleraesuis] gb|AAL59686.1| putative transposase [Vibrio cholerae] gb|AAP17865.1| putative transposase [Shigella flexneri 2a str. 2457T] dbj|BAC79056.1| putative transposase [Vibrio cholerae] Length = 497

4151.1

Best-BlastP=> >nprot 80% Identities = 91/130 (70%), Positives = 107/130 (82%) ref|NP\_660814.1| 30S ribosomal protein S11 [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp|Q8K972|RS11\_BUCAP 30S ribosomal protein S11 gb|AAM68025.1| 30S ribosomal protein S11 [Buchnera aphidicola str. Sg (Schizaphis graminum)] Length = 130



4153.1

- Best-BlastP=> >nrprot 81% Identities = 139/206 (67%), Positives = 169/206 (82%) ref|NP\_289857.1| 30S ribosomal subunit protein S4 [Escherichia coli O157:H7 EDL933] ref|NP\_312188.1| 30S ribosomal subunit protein S4 [Escherichia coli O157:H7] ref|NP\_417755.1| 30S ribosomal subunit protein S4 [Escherichia coli K12] ref|NP\_755921.1| 30S ribosomal protein S4 [Escherichia coli CFT073] 54|RS4\_ECOLI 30S ribosomal protein S4 pir|JR3EC4 ribosomal protein S4 [validated] - Escherichia coli (strain K-12) pir|A91149 30S ribosomal subunit protein S4 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) emb|CAA26394.1| unnamed protein product [Escherichia coli] gb|AAA58094.1| 30S ribosomal subunit protein S4 [Escherichia coli] gb|AAC76321.1| 30S ribosomal subunit protein S4 [Escherichia coli K12].1|AE005556\_10 30S ribosomal subunit protein S4 [Escherichia coli O157:H7 EDL933] dbj|BAB37584.1| 30S ribosomal subunit protein S4 [Escherichia coli CFT073] Length = 206  
gb|AAN82495.1|AE016767\_255 30S ribosomal protein S4 [Escherichia coli CFT073] Length = 206
- 4154.2 Best-BlastP=> >nrprot 79% Identities = 216/328 (65%), Positives = 264/328 (80%), Gaps = 3/328 (0%) gb|AAM33636.1|AF506984\_1 RpoA [Pseudomonas putida] Length = 333
- 4156.3 Best-BlastP=> >nrprot 99% Identities = 283/283 (100%), Positives = 283/283 (100%) emb|CAB65193.1| Wzm protein [Legionella pneumophila] Length = 283
- 4157.2 Best-BlastP=> >nrprot 99% Identities = 473/474 (99%), Positives = 473/474 (99%) emb|CAB65192.1| Wzt protein [Legionella pneumophila] Length = 474
- 4158.1 Best-BlastP=> >nrprot 98% Identities = 379/382 (99%), Positives = 379/382 (99%) emb|CAB65191.1| hypothetical protein [Legionella pneumophila] Length = 382
- 4159.1 Best-BlastP=> >nrprot 91% Identities = 273/279 (97%), Positives = 275/279 (98%) emb|CAB65190.1| putative glycosyl transferase [Legionella pneumophila] Length = 297
- 4160.3 Best-BlastP=> >nrprot 97% Identities = 281/282 (99%), Positives = 281/282 (99%) emb|CAD43478.1| putative glycosyltransferase [Legionella pneumophila] Length = 297
- 4161.3 Best-BlastP=> >nrprot 99% Identities = 336/339 (99%), Positives = 338/339 (99%) emb|CAB65189.1| putative glycosyl transferase [Legionella pneumophila] Length = 339
- 4162.2 Best-BlastP=> >nrprot 37% Identities = 188/579 (32%), Positives = 316/579 (54%), Gaps = 35/579 (6%) ref|NP\_834965.1| Sensory box/GGDEF family protein [Bacillus cereus ATCC 14579] gb|AAP12166.1| Sensory box/GGDEF family protein [Bacillus cereus ATCC 14579] Length = 909
- 4164.1 Best-BlastP=> >nrprot 57% Identities = 138/138 (100%), Positives = 138/138 (100%) gb|AAD41585.1|AF057704\_1 EnhA [Legionella pneumophila] Length = 164
- 4165.1 Best-BlastP=> >nrprot 68% Identities = 127/133 (95%), Positives = 130/133 (97%) gb|AAD41586.1|AF057704\_2 EnhB [Legionella pneumophila] Length = 142
- 4167.4 Best-BlastP=> >nrprot 99% Identities = 1193/1201 (99%), Positives = 1198/1201 (99%), Gaps = 1/1201 (0%) gb|AAD41587.1|AF057704\_3 enhanced entry protein EnhC [Legionella pneumophila] Length = 1201
- 4168.2 Best-BlastP=> >nrprot No Hits found
- 417.3 Best-BlastP=> >nrprot 30% Identities = 45/190 (23%), Positives = 83/190 (43%), Gaps = 2/190 (1%) ref|ZP\_00091084.1| COG0582: Integrase [Azotobacter vinelandii] Length = 287

- 4170.1 Best-BlastP=> >nrprot 6% Identities = 36/117 (30%), Positives = 57/117 (48%), Gaps = 10/117 (8%) ref[NP\_701057.1] hypothetical protein [Plasmodium falciparum 3D7] gblAAN35781.1|AE014838\_59 hypothetical protein [Plasmodium falciparum 3D7] Length = 371
- 4171.4 Best-BlastP=> >nrprot 52% Identities = 69/147 (46%), Positives = 93/147 (63%), Gaps = 1/147 (0%) ref[ZP\_00080184.1] COG1881: Phospholipid-binding protein [Geobacter metallireducens] Length = 176
- 4172.2 Best-BlastP=> >nrprot 11% Identities = 22/63 (34%), Positives = 39/63 (61%), Gaps = 1/63 (1%) gb|EAA24489.1| hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 265
- 4173.2 Best-BlastP=> >nrprot 62% Identities = 68/129 (52%), Positives = 84/129 (65%), Gaps = 4/129 (3%) ref[NP\_230027.1] conserved hypothetical protein [Vibrio cholerae] pir|A82330 conserved hypothetical protein VC0373 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93546.1| conserved hypothetical protein [Vibrio cholerae] Length = 139
- 4174.1 Best-BlastP=> >nrprot 66% Identities = 57/143 (39%), Positives = 93/143 (65%), Gaps = 7/143 (4%) gb|AAC44222.1| hemin binding protein Hbp [Legionella pneumophila] Length = 141
- 4175.1 Best-BlastP=> >nrprot 54% Identities = 115/302 (38%), Positives = 169/302 (55%), Gaps = 11/302 (3%) ref[ZP\_00086085.1] hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 300
- 4177.2 Best-BlastP=> >nrprot 13% Identities = 48/172 (27%), Positives = 70/172 (40%), Gaps = 25/172 (14%) dbj|BAC27865.1| unnamed protein product [Mus musculus] Length = 531
- 4179.2 Best-BlastP=> >nrprot 27% Identities = 86/423 (20%), Positives = 183/423 (43%), Gaps = 69/423 (16%) gb|EAA18183.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 1154
- 418.4 Best-BlastP=> >nrprot 69% Identities = 119/215 (55%), Positives = 156/215 (72%), Gaps = 3/215 (1%) ref[NP\_286845.1] putative carrier/transport protein [Escherichia coli O157:H7 EDL933] ref[NP\_309081.1] putative carrier/transport protein [Escherichia coli O157:H7] pir|D85624 probable carrier/transport protein yccA [imported] - Escherichia coli (strain O157:H7, substrain EDL933) pir|F90760 probable carrier/transport protein ECs1054 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) gb|AAG55456.1|AE005287\_3 putative carrier/transport protein [Escherichia coli O157:H7 EDL933] dbj|BAB34477.1| putative carrier/transport protein [Escherichia coli O157:H7] Length = 219
- 4181.1 Best-BlastP=> >nrprot No Hits found
- 4184.1 Best-BlastP=> >nrprot 53% Identities = 34/97 (35%), Positives = 56/97 (57%) ref[NP\_820123.1] conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90637.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 106
- 4186.1 Best-BlastP=> >nrprot 70% Identities = 155/310 (50%), Positives = 210/310 (67%), Gaps = 16/310 (5%) ref[NP\_841212.1] DnaJ N-terminal domain:DnaJ C terminal domain [Nitrosomonas europaea ATCC 19718] emb|CAD85066.1| DnaJ N-terminal domain:DnaJ C terminal domain [Nitrosomonas europaea ATCC 19718] Length = 314
- 4188.1 Best-BlastP=> >nrprot 65% Identities = 171/397 (43%), Positives = 244/397 (61%), Gaps = 36/397 (9%) ref[ZP\_00016589.1] hypothetical protein [Rhodospirillum rubrum] Length = 402
- 419.2 Best-BlastP=> >nrprot 67% Identities = 136/265 (51%), Positives = 182/265 (68%), Gaps = 4/265 (1%) ref[NP\_253165.1] conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir|E83086 conserved hypothetical protein PA4475 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07863.1|AE004861\_4 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 282

- 4191.1 Best-BlastP=> >nrprot 71% Identities = 258/457 (56%), Positives = 333/457 (72%), Gaps = 3/457 (0%) ref|ZP\_000093339.1| hypothetical protein [Rhodopseudomonas palustris] Length = 471
- 4192.2 Best-BlastP=> >nrprot 66% Identities = 305/605 (50%), Positives = 398/605 (65%), Gaps = 21/605 (3%) ref|ZP\_00029131.1| hypothetical protein [Burkholderia fungorum] Length = 642
- 4194.3 Best-BlastP=> >nrprot 99% Identities = 428/429 (99%), Positives = 428/429 (99%) gb|AAM00638.1| unknown [Legionella pneumophila] Length = 429
- 4195.3 Best-BlastP=> >nrprot 46% Identities = 100/388 (25%), Positives = 180/388 (46%), Gaps = 7/388 (1%) ref|NP\_820942.1| drug resistance transporter, Bcr/CfIA family [Coxiella burnetii RSA 493] gb|AAO91456.1| drug resistance transporter, Bcr/CfIA family [Coxiella burnetii RSA 493] Length = 409
- 4197.2 Best-BlastP=> >nrprot 91% Identities = 725/730 (99%), Positives = 727/730 (99%) gb|AAK35045.2|AF330136\_1 type II protein secretion LspD [Legionella pneumophila] Length = 730
- 42.1 Best-BlastP=> >nrprot 98% Identities = 243/250 (97%), Positives = 247/250 (98%) gb|AAM08246.1| probable conjugal transfer protein [Legionella pneumophila] Length = 250
- 4200.2 Best-BlastP=> >nrprot No Hits found
- 4203.2 Best-BlastP=> >nrprot 47% Identities = 121/412 (29%), Positives = 202/412 (49%), Gaps = 29/412 (7%) ref|ZP\_00034486.1| COG0642: Signal transduction histidine kinase [Burkholderia fungorum] Length = 479
- 4205.2 Best-BlastP=> >nrprot No Hits found
- 4206.2 Best-BlastP=> >nrprot 33% Identities = 156/825 (18%), Positives = 318/825 (38%), Gaps = 118/825 (14%) gb|EAA20682.1| rhopty protein [Plasmodium yoelii yoelii] Length = 2719
- 4209.2 Best-BlastP=> >nrprot 42% Identities = 72/314 (22%), Positives = 139/314 (44%), Gaps = 28/314 (8%) gb|AAB03184.1| TnpA [Pseudomonas putida] Length = 584
- 421.2
- 4211.2 Best-BlastP=> >nrprot 78% Identities = 307/479 (64%), Positives = 377/479 (78%), Gaps = 4/479 (0%) ref|NP\_520780.1| PROBABLE TLDD PROTEIN [Ralstonia solanacearum] emb|CAD16366.1| PROBABLE TLDD PROTEIN [Ralstonia solanacearum] Length = 486
- 4212.1 Best-BlastP=> >nrprot 61% Identities = 182/449 (40%), Positives = 276/449 (61%), Gaps = 11/449 (2%) ref|ZP\_00056132.1| COG1355: Predicted dioxigenase [Magnetospirillum magnetotacticum] Length = 468
- 4212.1 Best-BlastP=> >nrprot 72% Identities = 229/348 (65%), Positives = 263/348 (75%) ref|NP\_217654.1| pflA [Mycobacterium tuberculosis H37Rv] ref|NP\_337751.1| pyruvate formate lyase-activating enzyme, putative [Mycobacterium tuberculosis CDC1551] pir|C70646 probable pflA protein - Mycobacterium tuberculosis (strain H37RV) emb|CAB06292.1| pflA [Mycobacterium tuberculosis H37Rv] gb|AAK47565.1| pyruvate formate lyase-activating enzyme, putative [Mycobacterium tuberculosis CDC1551] Length = 362
- 4214.3 Best-BlastP=> >nrprot 54% Identities = 176/517 (34%), Positives = 286/517 (55%), Gaps = 21/517 (4%) ref|NP\_790671.1| sensor protein PilS [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54366.1| sensor protein PilS [Pseudomonas syringae pv. tomato str. DC3000] Length = 531
- 422.3
- 422.3 Best-BlastP=> >nrprot 63% Identities = 127/295 (43%), Positives = 187/295 (63%), Gaps = 14/295 (4%) ref|NP\_460713.1| putative phosphoesterase [Salmonella typhimurium LT2] gb|AAL20672.1| putative phosphoesterase [Salmonella typhimurium LT2] Length = 301

- 4220.2 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 4221.3 Best-BlastP=> >nrprot 58% Identities = 38/86 (44%), Positives = 54/86 (62%) dbj|BAC94314.1| acylphosphatase [Vibrio vulnificus YJ016] Length = 90
- 4222.3 Best-BlastP=> >nrprot 45% Identities = 33/83 (39%), Positives = 48/83 (57%) gb|EAA16908.1| Drosophila melanogaster CG8797 gene product-related [Plasmodium yoelii yoelii] Length = 2198
- 4225.1 Best-BlastP=> >nrprot No Hits found
- 4226.2 Best-BlastP=> >nrprot 82% Identities = 578/861 (67%), Positives = 714/861 (82%), Gaps = 5/861 (0%) gb|AAB95117.1| DNA gyrase [Serratia marcescens] Length = 880
- 4227.1
- Best-BlastP=> >nrprot 65% Identities = 238/489 (48%), Positives = 322/489 (65%), Gaps = 4/489 (0%) ref|NP\_899921.1| glycerol kinase [Chromobacterium violaceum ATCC 12472] gb|AAQ57930.1| glycerol kinase [Chromobacterium violaceum ATCC 12472] Length = 500
- 4228.2 Best-BlastP=> >nrprot 64% Identities = 229/504 (45%), Positives = 327/504 (64%), Gaps = 15/504 (2%) ref|ZP\_00091277.1| COG0578: Glycerol-3-phosphate dehydrogenase [Azotobacter vinelandii] Length = 510
- 423.2 Best-BlastP=> >nrprot 47% Identities = 139/430 (32%), Positives = 204/430 (47%), Gaps = 28/430 (6%) ref|NP\_407457.1| hypothetical protein [Yersinia pestis] pir|AD0489 hypothetical protein YPO4021 [imported] - Yersinia pestis (strain CO92) emb|CAC93480.1| hypothetical protein [Yersinia pestis CO92] Length = 414
- 4231.2 Best-BlastP=> >nrprot 16% Identities = 49/205 (23%), Positives = 81/205 (39%), Gaps = 31/205 (15%) emb|CAE02991.1| OSJNBa0043L09.10 [Oryza sativa (japonica cultivar-group)] Length = 687
- 4232.3 Best-BlastP=> >nrprot 42% Identities = 73/161 (45%), Positives = 103/161 (63%), Gaps = 1/161 (0%) ref|ZP\_00088088.1| COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Pseudomonas fluorescens PfO-1] Length = 241
- 4233.3 Best-BlastP=> >nrprot No Hits found
- 4234.3 Best-BlastP=> >nrprot No Hits found
- 4236.3 Best-BlastP=> >nrprot 58% Identities = 257/678 (37%), Positives = 391/678 (57%), Gaps = 37/678 (5%) ref|ZP\_00087890.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 701
- 4238.1 Best-BlastP=> >nrprot No Hits found
- 4239.4 Best-BlastP=> >nrprot No Hits found
- 424.1 Best-BlastP=> >nrprot 73% Identities = 63/103 (61%), Positives = 76/103 (73%) ref|ZP\_00082900.1| COG0662: Mannose-6-phosphate isomerase [Pseudomonas fluorescens PfO-1] Length = 103
- 4242.2 Best-BlastP=> >nrprot 34% Identities = 67/250 (26%), Positives = 112/250 (44%), Gaps = 18/250 (7%) ref|XP\_340725.1| iron/ascorbate oxidoreductase family protein, putative [Trypanosoma brucei] gb|AAQ16084.1| iron/ascorbate oxidoreductase family protein, putative [Trypanosoma brucei] Length = 319
- 4243.2 Best-BlastP=> >nrprot 67% Identities = 76/154 (49%), Positives = 101/154 (65%), Gaps = 8/154 (5%) ref|NP\_360925.1| unknown [Rickettsia conorii] pir|H97860 hypothetical protein RC1288 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL03826.1| unknown [Rickettsia conorii] Length = 154

- 4244.1 Best-BlastP=> >nrprot No Hits found
- 4246.2 Best-BlastP=> >nrprot 54% Identities = 95/280 (33%), Positives = 154/280 (55%), Gaps = 7/280 (2%) gb|AAM73852.1|AF454863\_1 putative lipase LipA [Legionella pneumophila] Length = 282
- 4247.2 Best-BlastP=> >nrprot 40% Identities = 63/264 (23%), Positives = 117/264 (44%), Gaps = 9/264 (3%) ref|ZP\_00118032.1| COG1560: Lauroyl/myristoyl acyltransferase [Cytophaga hutchinsonii] Length = 307
- 4248.1 Best-BlastP=> >nrprot 52% Identities = 31/74 (41%), Positives = 47/74 (63%), Gaps = 6/74 (8%) ref|ZP\_00066809.1| COG1748: Saccharopine dehydrogenase and related proteins [Microbulbifer degradans 2-40] Length = 371
- 4249.1 Best-BlastP=> >nrprot 36% Identities = 89/354 (25%), Positives = 144/354 (40%), Gaps = 39/354 (11%) gb|EAA22829.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 2694
- 425.1 Best-BlastP=> >nrprot No Hits found
- 4250.1 Best-BlastP=> >nrprot No Hits found
- 4251.2 Best-BlastP=> >nrprot No Hits found
- 4253.1 Best-BlastP=> >nrprot 55% Identities = 173/457 (37%), Positives = 272/457 (59%), Gaps = 19/457 (4%) ref|NP\_654426.1| aa\_permeases, Amino acid permease [Bacillus anthracis A2012] ref|NP\_843029.1| amino acid permease family protein [Bacillus anthracis str. Ames] gb|AAP24515.1| amino acid permease family protein [Bacillus anthracis str. Ames] Length = 473
- 4254.2 Best-BlastP=> >nrprot No Hits found
- 4255.1 Best-BlastP=> >nrprot No Hits found
- 4259.2 Best-BlastP=> >nrprot 57% Identities = 104/292 (35%), Positives = 167/292 (57%), Gaps = 31/292 (10%) ref|ZP\_00065076.1| COG1766: Flagellar biosynthesis/type III secretory pathway lipoprotein [Microbulbifer degradans 2-40] Length = 556
- 426.3 Best-BlastP=> >nrprot No Hits found
- 4262.2 Best-BlastP=> >nrprot 47% Identities = 42/141 (29%), Positives = 72/141 (51%) ref|NP\_249796.1| flagellar protein FljJ [Pseudomonas aeruginosa PA01] ref|ZP\_00138693.1| COG2882: Flagellar biosynthesis chaperone [Pseudomonas aeruginosa UCBPP-PA14] pir|B83509 flagellar protein FljJ PA1105 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04494.1|AE004540\_14 flagellar protein FljJ [Pseudomonas aeruginosa PAO1] Length = 147
- 4266.3 Best-BlastP=> >nrprot 35% Identities = 82/312 (26%), Positives = 145/312 (46%), Gaps = 51/312 (16%) gb|AAN63820.1| lysophospholipase A [Legionella pneumophila] Length = 309
- 4267.5 Best-BlastP=> >nrprot 68% Identities = 360/694 (51%), Positives = 475/694 (68%), Gaps = 15/694 (2%) emb|CAA86935.1| polyphosphate kinase [Acinetobacter sp. ADP1] Length = 691
- 4269.3 Best-BlastP=> >nrprot No Hits found
- 427.3 Best-BlastP=> >nrprot 67% Identities = 127/239 (53%), Positives = 174/239 (72%), Gaps = 5/239 (2%) ref|NP\_743000.1| RNA methyltransferase, TrmH family, group 1 [Pseudomonas putida KT2440] gb|AAN66464.1|AE016275\_9 RNA methyltransferase, TrmH family, group 1 [Pseudomonas putida KT2440] Length = 251
- 4272.3 Best-BlastP=> >nrprot No Hits found
- 4273.1 Best-BlastP=> >nrprot 35% Identities = 83/286 (29%), Positives = 133/286 (46%), Gaps = 2/286 (0%) ref|ZP\_00065171.1| COG0583: Transcriptional regulator [Microbulbifer degradans 2-40] Length = 299

- 4275.2 Best-Blast[P=> >nrprot 49% Identities = 77/244 (31%), Positives = 120/244 (49%), Gaps = 19/244 (7%) ref|NP\_661075.1| oxidoreductase, short-chain dehydrogenase/reductase family [Chlorobium tepidum TLS] Length = 246
- 4276.2 Best-Blast[P=> >nrprot 11% Identities = 46/172 (26%), Positives = 73/172 (42%), Gaps = 36/172 (20%) dbj|BAC96628.1| conserved hypothetical protein [Vibrio vulnificus YJ016] Length = 442
- 428.1 Best-Blast[P=> >nrprot 75% Identities = 142/257 (55%), Positives = 197/257 (76%) ref|NP\_820132.1| inositol-1-monophosphatase [Coxiella burnetii RSA 493] Length = 266
- 4281.2 Best-Blast[P=> >nrprot 50% Identities = 32/88 (36%), Positives = 45/88 (51%), Gaps = 4/88 (4%) ref|NP\_441652.1| unknown protein [Synechocystis sp. PCC 6803] pir|S75873 hypothetical protein slr1163 - Synechocystis sp. (strain PCC 6803) dbj|BAA18332.1| ORF\_ID:slr1163-unknown protein [Synechocystis sp. PCC 6803] Length = 556
- 4282.2 Best-Blast[P=> >nrprot 67% Identities = 126/249 (50%), Positives = 169/249 (67%), Gaps = 2/249 (0%) gb|AAM51645.1| putative transposase [Francisella tularensis subsp. tularensis] Length = 247
- 4284.2 Best-Blast[P=> >nrprot 41% Identities = 100/266 (37%), Positives = 142/266 (53%), Gaps = 35/266 (13%) ref|NP\_769986.1| bl|3346 [Bradyrhizobium japonicum] dbj|BAC48611.1| bl|3346 [Bradyrhizobium japonicum USDA 110] Length = 314
- 4285.1 Best-Blast[P=> >nrprot No Hits found
- 4288.2 Best-Blast[P=> >nrprot 98% Identities = 314/322 (97%), Positives = 318/322 (98%) gb|AAD43224.1|AF111940\_6 LspK precursor [Legionella pneumophila] Length = 322
- 4289.2 Best-Blast[P=> >nrprot 99% Identities = 203/205 (99%), Positives = 204/205 (99%) gb|AAD43223.1|AF111940\_5 LspJ precursor [Legionella pneumophila] Length = 205
- 429.2 Best-Blast[P=> >nrprot 60% Identities = 149/315 (47%), Positives = 207/315 (65%), Gaps = 4/315 (1%) ref|NP\_793611.1| signal peptide peptidase SppA, 36K type [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57306.1| signal peptide peptidase SppA, 36K type [Pseudomonas syringae pv. tomato str. DC3000] Length = 332
- 4291.1 Best-Blast[P=> >nrprot 98% Identities = 123/125 (98%), Positives = 124/125 (99%) gb|AAD43222.1|AF111940\_4 Lspl precursor [Legionella pneumophila] Length = 125
- 4293.2 Best-Blast[P=> >nrprot 67% Identities = 116/253 (45%), Positives = 173/253 (68%), Gaps = 1/253 (0%) ref|NP\_927916.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE12861.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 258
- 4294.3 Best-Blast[P=> >nrprot 57% Identities = 107/276 (38%), Positives = 161/276 (58%) ref|NP\_720100.1| cell division ABC transporter, permease protein FtsX [Shewanella oneidensis MR-1] gb|AAN57544.1|AE015890\_5 cell division ABC transporter, permease protein FtsX [Shewanella oneidensis MR-1] Length = 321
- 4295.3 Best-Blast[P=> >nrprot 69% Identities = 210/424 (49%), Positives = 301/424 (70%) ref|NP\_820879.1| peptidase, M16 family [Coxiella burnetii RSA 493] gb|AAO91393.1| peptidase, M16 family [Coxiella burnetii RSA 493] Length = 459
- 4296.1 Best-Blast[P=> >nrprot 63% Identities = 164/388 (42%), Positives = 248/388 (63%) ref|NP\_820878.1| peptidase, M16 family [Coxiella burnetii RSA 493] gb|AAO91392.1| peptidase, M16 family [Coxiella burnetii RSA 493] Length = 443
- 4297.2 Best-Blast[P=> >nrprot 64% Identities = 85/182 (46%), Positives = 117/182 (64%), Gaps = 6/182 (3%) ref|ZP\_00134417.1| COG0742: N6-adenine-specific methylase [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 197

- 43.1 Best-BlastP=> >nrrprot 97% Identities = 228/238 (95%), Positives = 233/238 (97%) gb|AAM08245.1| probable conjugal transfer protein  
[Legionella pneumophila] Length = 238
- 4301.1 Best-BlastP=> >nrrprot 63% Identities = 130/287 (45%), Positives = 188/287 (65%), Gaps = 2/287 (0%) ref|XP\_306575.1|  
ENSANGP00000014633 [Anopheles gambiae] gb|EAA02168.1| ENSANGP00000014633 [Anopheles gambiae str. PEST] Length = 304
- 4302.1 Best-BlastP=> >nrrprot 81% Identities = 190/271 (70%), Positives = 227/271 (83%) ref|NP\_459218.1| 2,3,4,5-tetrahydropyridine-2-carboxylate N-  
succinyltransferase [Salmonella typhimurium LT2] gb|AAL19177.1| 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase  
[Salmonella typhimurium LT2] Length = 274
- 4303.1 Best-BlastP=> >nrrprot 68% Identities = 203/374 (54%), Positives = 258/374 (68%), Gaps = 1/374 (0%) ref|ZP\_00064957.1| COG0624:  
Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases [Microbulifer degradans 2-40]  
Length = 382
- 4305.2 Best-BlastP=> >nrrprot No Hits found
- 4307.2 Best-BlastP=> >nrrprot No Hits found
- 4309.2 Best-BlastP=> >nrrprot 37% Identities = 79/320 (24%), Positives = 143/320 (44%), Gaps = 16/320 (5%) gb|AAC83363.1| outer membrane  
secretion protein Y [Pseudomonas alcaligenes] Length = 381
- 431.1 Best-BlastP=> >nrrprot No Hits found
- 4310.1 Best-BlastP=> >nrrprot 45% Identities = 34/139 (24%), Positives = 71/139 (51%), Gaps = 3/139 (2%) ref|NP\_755574.1| Putative general  
secretion pathway protein M-type yghD [Escherichia coli CFT073] gb|AAN82147.1| AE016766\_235 Putative general secretion pathway  
protein M-type yghD [Escherichia coli CFT073] Length = 178
- 4311.1 Best-BlastP=> >nrrprot 41% Identities = 47/173 (27%), Positives = 74/173 (42%), Gaps = 14/173 (8%) ref|NP\_232963.1| DamX-related protein  
[Vibrio cholerae O1 biovar eltor str. N16961] pir|B82443 DamX-related protein VCA0573 [imported] - Vibrio cholerae (strain N16961  
serogroup O1) gb|AAF96475.1| DamX-related protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 195
- 4312.2 Best-BlastP=> >nrrprot 57% Identities = 186/432 (43%), Positives = 253/432 (58%), Gaps = 8/432 (1%) ref|NP\_231613.1|  
deoxyguanosinetriphosphate triphosphohydrolase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KQL9|DG1A\_VIBCH  
Deoxyguanosinetriphosphate triphosphohydrolase-like protein 1 pir|B82132 deoxyguanosinetriphosphate triphosphohydrolase VC1979 [imported]  
- Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95127.1| deoxyguanosinetriphosphate triphosphohydrolase [Vibrio cholerae O1  
biovar eltor str. N16961] Length = 441
- 4316.4 Best-BlastP=> >nrrprot 23% Identities = 87/391 (22%), Positives = 154/391 (39%), Gaps = 61/391 (15%) gb|AAC21558.1| paramyosin related  
protein [Echinococcus granulosus] Length = 601
- 4319.2 Best-BlastP=> >nrrprot 38% Identities = 56/226 (24%), Positives = 95/226 (42%), Gaps = 24/226 (10%) ref|NP\_820254.1| ompA-like  
transmembrane domain protein [Coxiella burnetii RSA 493] gb|AAO90768.1| ompA-like transmembrane domain protein [Coxiella burnetii RSA  
493] Length = 248
- 432.1 Best-BlastP=> >nrrprot No Hits found



- 4320.1 Best-BlastP=> >nrprot 61% Identities = 163/420 (38%), Positives = 265/420 (63%), Gaps = 4/420 (0%) ref|NP\_249285.1| peptidyl-prolyl cis-trans isomerase SurA [Pseudomonas aeruginosa PA01] pir|B83572 peptidyl-prolyl cis-trans isomerase SurA PA0594 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG03983.1|AE004495\_7 peptidyl-prolyl cis-trans isomerase SurA [Pseudomonas aeruginosa PAO1] Length = 430
- 4321.2 Best-BlastP=> >nrprot 48% Identities = 274/816 (33%), Positives = 410/816 (50%), Gaps = 61/816 (7%) ref|NP\_820953.1| organic solvent tolerance protein [Coxiella burnetii RSA 493] gb|AAO91467.1| organic solvent tolerance protein [Coxiella burnetii RSA 493] Length = 870
- 4322.1 Best-BlastP=> >nrprot 57% Identities = 133/323 (41%), Positives = 187/323 (57%), Gaps = 9/323 (2%) ref|NP\_840285.1| Domain of unknown function DUF227 [Nitrosomonas europaea ATCC 19718] emb|CAD84102.1| Domain of unknown function DUF227 [Nitrosomonas europaea ATCC 19718] Length = 332
- 4323.1 Best-BlastP=> >nrprot 65% Identities = 105/218 (48%), Positives = 145/218 (66%), Gaps = 4/218 (1%) ref|ZP\_00126866.1| COG1208: Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon) [Pseudomonas syringae pv. syringae B728a] Length = 223
- 4325.3 Best-BlastP=> >nrprot 66% Identities = 154/307 (50%), Positives = 205/307 (66%), Gaps = 1/307 (0%) ref|NP\_462824.1| porphobilinogen deaminase (hydroxymethylbilane synthase) [Salmonella typhimurium LT2] gb|AAF33453.1| 89% identity with E. coli porphobilinogen deaminase (HEMC) (SP:P06983); contains similarity to Pfam family PF01379 (Porphobilinogen deaminase), score=627.8, E=6.2e-185, N=1 [Salmonella typhimurium LT2] gb|AAL22783.1| porphobilinogen deaminase [Salmonella typhimurium LT2] Length = 318
- 4326.1 Best-BlastP=> >nrprot 50% Identities = 75/233 (32%), Positives = 127/233 (54%), Gaps = 3/233 (1%) dbj|BAC92844.1| uroporphyrinogen-III synthase [Vibrio vulnificus YJ016] Length = 260
- 4327.1 Best-BlastP=> >nrprot 40% Identities = 86/318 (27%), Positives = 151/318 (47%), Gaps = 26/318 (8%) ref|ZP\_00065835.1| COG2959: Uncharacterized enzyme of heme biosynthesis [Microbulifer degradans 2-40] Length = 494
- 4328.1 Best-BlastP=> >nrprot 56% Identities = 139/389 (35%), Positives = 224/389 (57%), Gaps = 3/389 (0%) ref|NP\_821051.1| hemY protein [Coxiella burnetii RSA 493] gb|AAO91565.1| hemY protein [Coxiella burnetii RSA 493] Length = 392
- 433.1 Best-BlastP=> >nrprot 99% Identities = 1007/1009 (99%), Positives = 1008/1009 (99%) pir|T18339 icmB protein - Legionella pneumophila emb|CAA75170.1| IcmB protein [Legionella pneumophila] gb|AAC38183.1| DotO [Legionella pneumophila] emb|CAA75336.1| IcmB protein [Legionella pneumophila] Length = 1009
- 4332.1 Best-BlastP=> >nrprot 59% Identities = 82/151 (54%), Positives = 107/151 (70%) ref|ZP\_00024252.1| COG0412: Dienelactone hydrolase and related enzymes [Ralstonia metallidurans] Length = 435
- 4333.1 Best-BlastP=> >nrprot 61% Identities = 128/282 (45%), Positives = 174/282 (61%), Gaps = 4/282 (1%) ref|ZP\_00077190.1| COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Methanosarcina barkeri] Length = 286
- 4334.1 Best-BlastP=> >nrprot 62% Identities = 135/293 (46%), Positives = 187/293 (63%), Gaps = 6/293 (2%) ref|NP\_421406.1| conserved hypothetical protein [Caulobacter crescentus CB15] pir|B87572 conserved hypothetical protein CC2605 [imported] - Caulobacter crescentus gb|AAK24574.1| conserved hypothetical protein [Caulobacter crescentus CB15] Length = 304

- 4336.2 Best-BlastP=> >nrprot 59% Identities = 163/401 (40%), Positives = 242/401 (60%), Gaps = 1/401 (0%) ref|NP\_626512.1| putative integral membrane protein. [Streptomyces coelicolor A3(2)] pir|T50573 probable integral membrane protein [imported] - Streptomyces coelicolor emb|CAB61710.1| putative integral membrane protein. [Streptomyces coelicolor A3(2)] Length = 431
- 4337.3 Best-BlastP=> >nrprot 57% Identities = 36/63 (57%), Positives = 48/63 (76%), Gaps = 2/63 (3%) ref|NP\_799393.1| putative signal peptide protein [Vibrio parahaemolyticus RMD 2210633] dbj|BAC61277.1| putative signal peptide protein [Vibrio parahaemolyticus] Length = 86
- 4338.3 Best-BlastP=> >nrprot 68% Identities = 147/290 (50%), Positives = 206/290 (71%), Gaps = 1/290 (0%) ref|NP\_781198.1| myo-inositol catabolism protein iolE [Clostridium tetani E88] gb|AAO35135.1| myo-inositol catabolism protein iolE [Clostridium tetani E88] Length = 298
- 4339.1 Best-BlastP=> >nrprot 72% Identities = 347/644 (53%), Positives = 451/644 (70%), Gaps = 25/644 (3%) ref|ZP\_00131855.1| COG3962: Acetolactate synthase [Haemophilus somnus 2336] Length = 645
- 434.3 Best-BlastP=> >nrprot 99% Identities = 207/208 (99%), Positives = 207/208 (99%) pir|T18338 icmJ protein - Legionella pneumophila emb|CAA75169.1| IcmJ protein [Legionella pneumophila] gb|AAC38184.1| DoIN [Legionella pneumophila] emb|CAA75335.1| IcmJ protein [Legionella pneumophila] Length = 208
- 4340.2 Best-BlastP=> >nrprot 36% Identities = 179/356 (50%), Positives = 232/356 (65%), Gaps = 4/356 (1%) ref|ZP\_00122182.1| COG3892: Uncharacterized protein conserved in bacteria [Haemophilus somnus 129PT] Length = 636
- 4341.3 Best-BlastP=> >nrprot No Hits found
- 4342.1 Best-BlastP=> >nrprot 53% Identities = 29/77 (37%), Positives = 44/77 (57%) ref|NP\_289764.1| orf, hypothetical protein [Escherichia coli O157:H7 EDL933] ref|NP\_312096.1| hypothetical protein [Escherichia coli O157:H7] ref|NP\_417657.1| hypothetical protein [Escherichia coli K12] ref|NP\_708989.1| orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref|NP\_755814.1| Protein yrbA [Escherichia coli CFT073] ref|NP\_838699.1| hypothetical protein [Shigella flexneri 2a str. 2457T] pir|H65109 hypothetical 9.5 kD protein in murZ-rpoN intergenic region - Escherichia coli (strain K-12) pir|E91137 hypothetical protein ECs4069 [imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952) pir|H85982 hypothetical protein yrbA [imported] - Escherichia coli (strain O157:H7, substrate EDL933) gb|AAA57991.1| ORF\_f89 [Escherichia coli] gb|AAC76222.1| orf, hypothetical protein [Escherichia coli K12] gb|AAF21251.1|AF053073\_4 YrbA [Shigella flexneri] gb|AAG58324.1|AE005547\_10 orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj|BAB37492.1| hypothetical protein [Escherichia coli O157:H7] gb|AAN44696.1|AE015334\_10 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] gb|AAN82388.1|AE016767\_148 F
- 4344.1 Best-BlastP=> >nrprot 80% Identities = 272/419 (64%), Positives = 339/419 (80%) ref|NP\_794195.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57890.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Pseudomonas syringae pv. tomato str. DC3000] Length = 421
- 4345.1 Best-BlastP=> >nrprot 71% Identities = 136/252 (53%), Positives = 182/252 (72%), Gaps = 3/252 (1%) ref|NP\_718206.1| conserved hypothetical protein TIGR00486 [Shewanella oneidensis MR-1] gb|AAN55650.1|AE015704\_1 conserved hypothetical protein TIGR00486 [Shewanella oneidensis MR-1] Length = 250
- 4346.2 Best-BlastP=> >nrprot 71% Identities = 153/286 (53%), Positives = 207/286 (72%), Gaps = 1/286 (0%) ref|NP\_249701.1| dihydrodipicolinate synthase [Pseudomonas aeruginosa PAO1] sp|Q914W3|DAPA\_PSEAE Dihydrodipicolinate synthase (DHDPS) pir|C83520 dihydrodipicolinate synthase PA1010 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04399.1|AE004533\_10 dihydrodipicolinate synthase [Pseudomonas aeruginosa PAO1] Length = 292

- 4347.2 Best-BlastP=> >nrprot 44% Identities = 31/68 (45%), Positives = 38/68 (55%), Gaps = 7/68 (10%) ref|ZP\_00035058.1| COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Burkholderia fungorum] Length = 237
- 4349.2 Best-BlastP=> >nrprot 81% Identities = 180/260 (69%), Positives = 213/260 (81%) ref|NP\_900365.1| 3-hydroxybutyrate dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ58371.1| 3-hydroxybutyrate dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 260
- 4350.2 Best-BlastP=> >nrprot 59% Identities = 152/375 (40%), Positives = 230/375 (61%), Gaps = 4/375 (1%) ref|ZP\_00008996.1| COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Rhodopseudomonas palustris] Length = 379
- 4351.2 Best-BlastP=> >nrprot 73% Identities = 161/286 (56%), Positives = 221/286 (77%) ref|NP\_522970.1| PROBABLE CHEMOTAXIS (MOTILITY PROTEIN A) TRANSMEMBRANE [Ralstonia solanacearum] emb|CAD18562.1| PROBABLE CHEMOTAXIS (MOTILITY PROTEIN A) TRANSMEMBRANE [Ralstonia solanacearum] Length = 286
- 4352.3 Best-BlastP=> >nrprot 61% Identities = 140/284 (49%), Positives = 191/284 (67%), Gaps = 1/284 (0%) ref|NP\_840146.1| Bacterial outer membrane protein [Nitrosomonas europaea ATCC 19718] emb|CAD83956.1| Bacterial outer membrane protein [Nitrosomonas europaea ATCC 19718] Length = 307
- 4353.2 Best-BlastP=> >nrprot No Hits found
- 4354.2 Best-BlastP=> >nrprot No Hits found
- 4355.2 Best-BlastP=> >nrprot 64% Identities = 161/310 (51%), Positives = 204/310 (65%), Gaps = 5/310 (1%) ref|NP\_438574.1| hypothetical protein [Haemophilus influenzae Rd] sp|P44433|RLUC\_HAEIN Ribosomal large subunit pseudouridine synthase C (Pseudouridylyl synthase) (Uracil hydrolyase) pir|G64151| hypothetical protein H10412 - Haemophilus influenzae (strain Rd KW20) gb|AAC22071.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 322
- 4356.2 Best-BlastP=> >nrprot 52% Identities = 77/215 (35%), Positives = 116/215 (53%), Gaps = 8/215 (3%) ref|ZP\_00013688.1| hypothetical protein [Rhodospirillum rubrum] Length = 236
- 4357.3 Best-BlastP=> >nrprot 98% Identities = 414/424 (97%), Positives = 420/424 (99%) gb|AAM00604.1| putative histidine kinase [Legionella pneumophila] Length = 424
- 4358.2 Best-BlastP=> >nrprot 49% Identities = 64/187 (34%), Positives = 91/187 (48%), Gaps = 7/187 (3%) ref|NP\_761114.1| Guanylate cyclase-related protein [Vibrio vulnificus CMCP6] gb|AAO10641.1|AE016804\_151 Guanylate cyclase-related protein [Vibrio vulnificus CMCP6] dbj|BAC94846.1| guanylate cyclase-related protein [Vibrio vulnificus YJ016] Length = 185
- 436.4 Best-BlastP=> >nrprot No Hits found
- 4363.2 Best-BlastP=> >nrprot 43% Identities = 68/183 (37%), Positives = 106/183 (57%), Gaps = 2/183 (1%) ref|ZP\_00073054.1| COG3555: Aspartyl/asparaginyl beta-hydroxylase and related dioxygenases [Trichodesmium erythraeum IMS101] Length = 283
- 4364.2 Best-BlastP=> >nrprot 41% Identities = 36/77 (46%), Positives = 44/77 (57%) pir|D72548| hypothetical protein APE1672 - Aeropyrum pernix (strain K1) dbj|BAA80673.1| 113aa long hypothetical protein [Aeropyrum pernix] Length = 113
- 4365.4 Best-BlastP=> >nrprot 63% Identities = 78/175 (44%), Positives = 115/175 (65%), Gaps = 6/175 (3%) ref|ZP\_00021197.1| COG0262: Dihydrofolate reductase [Ralstonia metallidurans] Length = 177
- 4366.1 Best-BlastP=> >nrprot 47% Identities = 37/123 (30%), Positives = 66/123 (53%), Gaps = 4/123 (3%) ref|NP\_800262.1| glutathione S-transfersae-related protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62095.1| glutathione S-transfersae-related protein [Vibrio parahaemolyticus] Length = 128

- 4367.1 Best-BlastP=> >nrrprot No Hits found
- 4369.1 Best-BlastP=> >nrrprot 35% Identities = 53/153 (34%), Positives = 79/153 (51%), Gaps = 2/153 (1%) ref|ZP\_00026335.1| COG3714: Predicted membrane protein [Ralstonia metallidurans] Length = 233
- 4370.1 Best-BlastP=> >nrrprot No Hits found
- 4371.1 Best-BlastP=> >nrrprot 57% Identities = 122/252 (48%), Positives = 171/252 (67%), Gaps = 4/252 (1%) ref|NP\_819457.1| polysaccharide deacetylase-related protein [Coxiella burnetii RSA 493] gb|AAO89971.1| polysaccharide deacetylase-related protein [Coxiella burnetii RSA 493] Length = 276
- 4372.3 Best-BlastP=> >nrrprot 61% Identities = 167/391 (42%), Positives = 247/391 (63%), Gaps = 5/391 (1%) ref|NP\_820110.1| membrane-bound lytic murein transglycosylase family protein [Coxiella burnetii RSA 493] gb|AAO90624.1| membrane-bound lytic murein transglycosylase family protein [Coxiella burnetii RSA 493] Length = 400
- 4373.3 Best-BlastP=> >nrrprot 64% Identities = 45/105 (42%), Positives = 68/105 (64%), Gaps = 7/105 (6%) ref|NP\_800642.1| hypothetical protein VPA1132 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62475.1| hypothetical protein [Vibrio parahaemolyticus] Length = 108
- 4374.4 Best-BlastP=> >nrrprot 68% Identities = 262/502 (52%), Positives = 358/502 (71%) ref|NP\_819429.1| integral membrane protein MviN [Coxiella burnetii RSA 493] gb|AAO89943.1| integral membrane protein MviN [Coxiella burnetii RSA 493] Length = 515
- 4376.3 Best-BlastP=> >nrrprot 63% Identities = 105/215 (48%), Positives = 143/215 (66%) pdb|1AZO| Dna Mismatch Repair Protein Muth From E. Coli Length = 232
- 4377.4 Best-BlastP=> >nrrprot No Hits found
- 4378.2 Best-BlastP=> >nrrprot 75% Identities = 135/205 (65%), Positives = 167/205 (81%), Gaps = 1/205 (0%) ref|NP\_799538.1| antibiotic acetyltransferase [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61371.1| antibiotic acetyltransferase [Vibrio parahaemolyticus] Length = 212
- 4379.1 Best-BlastP=> >nrrprot 40% Identities = 85/221 (38%), Positives = 120/221 (54%), Gaps = 8/221 (3%) ref|ZP\_00108724.1| COG3393: Predicted acetyltransferase [Nostoc punctiforme] Length = 222
- 4381.2 Best-BlastP=> >nrrprot 79% Identities = 276/420 (65%), Positives = 340/420 (80%) ref|NP\_819962.1| amino acid permease family protein [Coxiella burnetii RSA 493] gb|AAO90476.1| amino acid permease family protein [Coxiella burnetii RSA 493] Length = 437
- 4383.2 Best-BlastP=> >nrrprot 37% Identities = 83/190 (43%), Positives = 109/190 (57%), Gaps = 3/190 (1%) ref|NP\_435788.1| hypothetical protein [Sinorhizobium meliloti] pir|F95329 hypothetical protein Sma1005 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA gb|AAK65200.1| hypothetical protein [Sinorhizobium meliloti] Length = 266
- 4384.2 Best-BlastP=> >nrrprot 55% Identities = 171/477 (35%), Positives = 267/477 (55%), Gaps = 9/477 (1%) ref|NP\_819538.1| proton/peptide symporter family protein [Coxiella burnetii RSA 493] gb|AAO90052.1| proton/peptide symporter family protein [Coxiella burnetii RSA 493] Length = 492
- 4385.1 Best-BlastP=> >nrrprot 85% Identities = 411/546 (75%), Positives = 474/546 (86%), Gaps = 3/546 (0%) ref|NP\_230848.1| urocanate hydratase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KSQ3|HUTJ\_VIBCH Urocanate hydratase (Urocanase) (Imidazolonepropionate hydrolase) pir|F82228 urocanate hydratase VC1203 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94362.1| urocanate hydratase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 565

- 4386.2 Best-BlastP=> >nrprot 73% Identities = 296/486 (60%), Positives = 375/486 (77%), Gaps = 1/486 (0%) ref|NP\_230847.1| histidine ammonia-lyase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9K5Q4|HUTH\_VIBCH Histidine ammonia-lyase (Histidase) pir|E82228 histidine ammonia-lyase (EC 4.3.1.3) [similarity] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94361.1| histidine ammonia-lyase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 511
- 4387.3 Best-BlastP=> >nrprot 62% Identities = 96/190 (50%), Positives = 128/190 (67%), Gaps = 1/190 (0%) ref|NP\_246159.1| Dam [Pasteurella multocida] gb|AAK03306.1| Dam [Pasteurella multocida] gb|AAL05864.1| AF411317\_2 DNA adenine methylase [Pasteurella multocida] Length = 301
- 4388.1 Best-BlastP=> >nrprot 54% Identities = 151/402 (37%), Positives = 232/402 (57%), Gaps = 5/402 (1%) ref|NP\_819596.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO90110.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 421
- 4389.2 Best-BlastP=> >nrprot 62% Identities = 206/405 (50%), Positives = 270/405 (66%), Gaps = 8/405 (1%) ref|NP\_820255.1| D-alanyl-D-alanine carboxypeptidase [Coxiella burnetii RSA 493] gb|AAO90769.1| D-alanyl-D-alanine carboxypeptidase [Coxiella burnetii RSA 493] Length = 418
- 4391.1 Best-BlastP=> >nrprot 98% Identities = 270/278 (97%), Positives = 275/278 (98%) emb|CAD90964.1| putative D-Ala-amino transferase [Legionella pneumophila] Length = 278
- 4392.1 Best-BlastP=> >nrprot 60% Identities = 35/87 (40%), Positives = 53/87 (60%) ref|NP\_841528.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] sp|Q82UJ7|YE87\_NITEU Hypothetical UPF0250 protein NE1487 emb|CAD85398.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 87
- 4393.1 Best-BlastP=> >nrprot 98% Identities = 192/199 (96%), Positives = 196/199 (98%) emb|CAD90955.1| LssX protein [Legionella pneumophila] Length = 199
- 4394.4 Best-BlastP=> >nrprot 98% Identities = 666/678 (98%), Positives = 672/678 (99%) emb|CAD90962.1| LssY protein [Legionella pneumophila] Length = 678
- 4395.2 Best-BlastP=> >nrprot 63% Identities = 337/723 (46%), Positives = 453/723 (62%), Gaps = 27/723 (3%) ref|NP\_251738.1| conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir|A83266 conserved hypothetical protein PA3048 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06436.1| AE004729\_10 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 725
- 4396.1 Best-BlastP=> >nrprot 59% Identities = 66/157 (42%), Positives = 95/157 (60%) ref|ZP\_00090069.1| COG3028: Uncharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 172
- 4398.2 Best-BlastP=> >nrprot 48% Identities = 70/252 (27%), Positives = 135/252 (53%), Gaps = 4/252 (1%) ref|NP\_784615.1| integral membrane protein [Lactobacillus plantarum WCFS1] emb|CAD63460.1| integral membrane protein [Lactobacillus plantarum WCFS1] Length = 293
- 44.1 Best-BlastP=> >nrprot 97% Identities = 335/346 (96%), Positives = 339/346 (97%) gb|AAM08244.1| probable conjugal transfer protein [Legionella pneumophila] Length = 346
- 440.4 Best-BlastP=> >nrprot 14% Identities = 134/534 (25%), Positives = 215/534 (40%), Gaps = 106/534 (19%) pir|JC6009 surface-located membrane protein Imp3 precursor - Mycoplasma hominis emb|CAA64858.1| Lmp3 protein [Mycoplasma hominis] Length = 1302

- 4402.2 Best-BlastP=> >nrprot 65% Identities = 83/174 (47%), Positives = 119/174 (68%), Gaps = 2/174 (1%) ref|NP\_930722.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii] TTO1] emb|CAE15878.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii] TTO1] Length = 176
- 4403.2 Best-BlastP=> >nrprot 60% Identities = 124/258 (48%), Positives = 160/258 (62%) ref|NP\_252268.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01] sp|Q9HY42|YZ78\_PSEAE Hypothetical protein PA3578 pir|E83199 conserved hypothetical protein PA3578 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06966.1|AE004778\_10 conserved hypothetical protein [Pseudomonas aeruginosa PAO1] Length = 261
- 4404.1 Best-BlastP=> >nrprot 49% Identities = 51/124 (41%), Positives = 69/124 (55%) ref|NP\_105863.1| transcriptional regulator [Mesorhizobium loti] dbj|BAB51649.1| transcriptional regulator [Mesorhizobium loti] Length = 143
- 4405.1 Best-BlastP=> >nrprot 73% Identities = 77/148 (52%), Positives = 112/148 (75%) ref|NP\_662760.1| conserved hypothetical protein [Chlorobium tepidum TLS] gb|AAM73102.1| conserved hypothetical protein [Chlorobium tepidum TLS] Length = 155
- 4406.1 Best-BlastP=> >nrprot 63% Identities = 78/187 (41%), Positives = 121/187 (64%), Gaps = 1/187 (0%) ref|ZP\_00092584.1| COG1278: Cold shock proteins [Azotobacter vinelandii] Length = 333
- 4407.1 Best-BlastP=> >nrprot 65% Identities = 39/69 (56%), Positives = 51/69 (73%) ref|NP\_743260.1| cold-shock domain family protein [Pseudomonas putida KT2440] gb|AAN66724.1|AE016300\_9 cold-shock domain family protein [Pseudomonas putida KT2440] Length = 69
- 4408.1 Best-BlastP=> >nrprot No Hits found
- 4409.1 Best-BlastP=> >nrprot 71% Identities = 120/212 (56%), Positives = 150/212 (70%), Gaps = 3/212 (1%) ref|NP\_403711.1| orotate phosphoribosyltransferase [Yersinia pestis] ref|NP\_667439.1| orotate phosphoribosyltransferase [Yersinia pestis KIM] sp|Q8ZJP7|PYRE\_YERPE Orotate phosphoribosyltransferase (OPRT) (OPRTase) pir|AF0006 orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Yersinia pestis (strain CO92) emb|CAC88912.1| orotate phosphoribosyltransferase [Yersinia pestis CO92] gb|AAM83690.1|AE013610\_2 orotate phosphoribosyltransferase [Yersinia pestis KIM] Length = 215
- 4415.3 Best-BlastP=> >nrprot 55% Identities = 157/417 (37%), Positives = 239/417 (57%), Gaps = 8/417 (1%) ref|ZP\_00034486.1| COG0642: Signal transduction histidine kinase [Burkholderia fungorum] Length = 479
- 4419.2 Best-BlastP=> >nrprot 72% Identities = 161/317 (50%), Positives = 233/317 (73%) ref|NP\_794895.1| proline iminopeptidase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58590.1| proline iminopeptidase [Pseudomonas syringae pv. tomato str. DC3000] Length = 323
- 4421.2 Best-BlastP=> >nrprot 41% Identities = 77/254 (30%), Positives = 111/254 (43%), Gaps = 51/254 (20%) ref|NP\_052363.1| unnamed protein product [Coxiella burnetii] ref|NP\_819024.1| hypothetical protein [Coxiella burnetii RSA 493] pir|S38245 hypothetical protein - Coxiella burnetii emb|CAA53133.1| unnamed protein product [Coxiella burnetii] gb|AAO91584.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 341
- 4422.1 Best-BlastP=> >nrprot No Hits found
- 4424.1 Best-BlastP=> >nrprot No Hits found
- 4425.1 Best-BlastP=> >nrprot 46% Identities = 57/160 (35%), Positives = 80/160 (50%), Gaps = 3/160 (1%) ref|NP\_105070.1| hypothetical protein, acetyltransferase, putative [Mesorhizobium loti] dbj|BAB50856.1| hypothetical protein [Mesorhizobium loti] Length = 168

- 4427.1 Best-BlastP=> >nrprot No Hits found
- 4428.1 Best-BlastP=> >nrprot No Hits found
- 4429.2 Best-BlastP=> >nrprot No Hits found
- 443.3 Best-BlastP=> >nrprot 99% Identities = 190/191 (100%) pir|T18327 lcmQ protein - Legionella pneumophila emb|CAA73239.1| lcmQ protein [Legionella pneumophila] Length = 191
- 4431.2 Best-BlastP=> >nrprot 14% Identities = 61/293 (20%), Positives = 128/293 (43%), Gaps = 33/293 (11%) dbj|BAC86266.1| unnamed protein product [Homo sapiens] Length = 486
- 4432.2 Best-BlastP=> >nrprot No Hits found
- 4433.1 Best-BlastP=> >nrprot 42% Identities = 64/200 (32%), Positives = 86/200 (43%), Gaps = 12/200 (6%) ref|NP\_799850.1| putative tellurite resistance protein-related protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61683.1| putative tellurite resistance protein-related protein [Vibrio parahaemolyticus] Length = 195
- 4434.1 Best-BlastP=> >nrprot 34% Identities = 52/215 (24%), Positives = 91/215 (42%), Gaps = 23/215 (10%) ref|NP\_788733.1| multiple ankyrin repeats single KH domain CG33106-PA [Drosophila melanogaster] ref|NP\_788734.1| multiple ankyrin repeats single KH domain CG33106-PB [Drosophila melanogaster] gb|AAO41600.1| CG33106-PA [Drosophila melanogaster] gb|AAO41601.1| CG33106-PB [Drosophila melanogaster] Length = 4001
- 4435.4 Best-BlastP=> >nrprot 13% Identities = 50/196 (25%), Positives = 92/196 (46%), Gaps = 32/196 (16%) ref|NP\_001804.1| centromere protein E; Centromere autoantigen E (312kD); centromere protein E (312kD); kinesin family member 10 [Homo sapiens] sp|Q02224|CENE\_HUMAN Centromeric protein E (CENP-E protein) pir|S28261 centromere protein E - human emb|CAA78727.1| CENP-E [Homo sapiens] Length = 2663
- 444.2 Best-BlastP=> >nrprot 96% Identities = 116/120 (96%), Positives = 117/120 (97%) pir|T18326 lcmR protein - Legionella pneumophila emb|CAA73238.1| lcmR protein [Legionella pneumophila] emb|CAA75323.1| lcmR protein [Legionella pneumophila] Length = 120
- 4440.1 Best-BlastP=> >nrprot 73% Identities = 71/144 (49%), Positives = 104/144 (72%), Gaps = 4/144 (2%) ref|ZP\_00065054.1| COG1558: Flagellar basal body rod protein [Microbulbifer degradans 2-40] Length = 148
- 4441.1 Best-BlastP=> >nrprot 61% Identities = 61/132 (46%), Positives = 80/132 (60%), Gaps = 1/132 (0%) gb|AAN08637.1| FlgB [Aeromonas hydrophila] Length = 132
- 4442.1 Best-BlastP=> >nrprot 75% Identities = 202/297 (68%), Positives = 235/297 (79%) ref|NP\_928683.1| oxygen-dependent coproporphyrinogen III oxidase [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE13676.1| oxygen-dependent coproporphyrinogen III oxidase [Photorhabdus luminescens subsp. laumondii TTO1] Length = 302
- 4444.2 Best-BlastP=> >nrprot 57% Identities = 168/420 (40%), Positives = 249/420 (59%), Gaps = 12/420 (2%) ref|ZP\_00030428.1| COG0477: Permeases of the major facilitator superfamily [Burkholderia fungorum] Length = 645
- 4452.2 Best-BlastP=> >nrprot 34% Identities = 127/238 (53%), Positives = 161/238 (67%) ref|ZP\_00112372.1| COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Nostoc punctiforme] Length = 616
- 4453.2 Best-BlastP=> >nrprot 41% Identities = 97/469 (20%), Positives = 194/469 (41%), Gaps = 60/469 (12%) gb|EAA15516.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 585
- 4454.4 Best-BlastP=> >nrprot 87% Identities = 258/329 (78%), Positives = 290/329 (88%) gb|AAB58447.1| spectinomycin phosphotransferase [Legionella pneumophila] Length = 331



- 4457.2 Best-BlastP=> >nrprot 51% Identities = 102/334 (30%), Positives = 174/334 (52%), Gaps = 14/334 (4%) ref|NP\_249522.1| transcriptional regulator OruR [Pseudomonas aeruginosa PA01] ref|ZP\_00138425.1| COG2207: AraC-type DNA-binding domain-containing proteins [Pseudomonas aeruginosa UCBPP-PA14] sp|P72171|ORUR\_PSEAE Ornithine utilization regulator pir|G83540 transcription regulator OruR PA0831 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAB94774.1| OruR [Pseudomonas aeruginosa] gb|AAG04220.1|AE004518\_1 transcriptional regulator OruR [Pseudomonas aeruginosa PAO1] Length = 339
- 4462.3 Best-BlastP=> >nrprot 71% Identities = 115/192 (59%), Positives = 145/192 (75%) ref|ZP\_00067991.1| COG0088: Ribosomal protein L4 [Microbulbifer degradans 2-40] Length = 204
- 4463.2 Best-BlastP=> >nrprot 80% Identities = 138/209 (66%), Positives = 175/209 (83%), Gaps = 1/209 (0%) ref|NP\_403860.1| 50S ribosomal protein L3 [Yersinia pestis] ref|NP\_671283.1| 50S ribosomal subunit protein L3 [Yersinia pestis KIM] pir|AB0026 50S ribosomal protein L3 [imported] - Yersinia pestis (strain CO92) emb|CAC89069.1| 50S ribosomal protein L3 [Yersinia pestis CO92] gb|AAM87534.1|AE014002\_7 50S ribosomal subunit protein L3 [Yersinia pestis KIM] Length = 209
- 4464.1 Best-BlastP=> >nrprot 87% Identities = 86/103 (83%), Positives = 93/103 (90%) ref|NP\_778069.1| 30S ribosomal protein S10 [Buchnera aphidicola (Baizongia pistaciae)] sp|Q89A67|RS10\_BUCBP 30S ribosomal protein S10 gb|AAO27174.1| 30S ribosomal protein S10 [Buchnera aphidicola str. Bp (Baizongia pistaciae)] Length = 104
- 4465.3 Best-BlastP=> >nrprot 37% Identities = 43/118 (36%), Positives = 61/118 (51%), Gaps = 10/118 (8%) pir|H71023 hypothetical protein PH1485 - Pyrococcus horikoshii dbj|BAA30592.1| 156aa long hypothetical protein [Pyrococcus horikoshii] Length = 156
- 4466.3 Best-BlastP=> >nrprot 93% Identities = 338/397 (85%), Positives = 370/397 (93%), Gaps = 1/397 (0%) ref|ZP\_00090901.1| COG0050: GTPases - translation elongation factors [Azotobacter vinelandii] Length = 397
- 4468.2 Best-BlastP=> >nrprot 89% Identities = 527/691 (76%), Positives = 621/691 (89%) ref|NP\_819279.1| translation elongation factor G [Coxiella burnetii RSA 493] sp|Q83ES7|EFG\_COXBU Elongation factor G (EF-G) gb|AAO89793.1| translation elongation factor G [Coxiella burnetii RSA 493] Length = 699
- 4469.2 Best-BlastP=> >nrprot 48% Identities = 86/277 (31%), Positives = 138/277 (49%), Gaps = 23/277 (8%) ref|NP\_519890.1| PROBABLE OXIDOREDUCTASE DEHYDROGENASE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] emb|CAD15471.1| PROBABLE OXIDOREDUCTASE DEHYDROGENASE SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum] Length = 300
- 447.2 Best-BlastP=> >nrprot 99% Identities = 114/114 (100%), Positives = 114/114 (100%) pir|T18325 icmS protein - Legionella pneumophila emb|CAA73237.1| IcmS protein [Legionella pneumophila] emb|CAA75322.1| IcmS protein [Legionella pneumophila] Length = 114
- 4470.1 Best-BlastP=> >nrprot 64% Identities = 156/329 (47%), Positives = 223/329 (67%), Gaps = 6/329 (1%) ref|NP\_742587.1| anthranilate phosphoribosyltransferase [Pseudomonas putida KT2440] sp|Q88QR7|TRPD\_PSEPK Anthranilate phosphoribosyltransferase gb|AAN66051.1|AE016234\_4 anthranilate phosphoribosyltransferase [Pseudomonas putida KT2440] Length = 349
- 4471.3 Best-BlastP=> >nrprot 43% Identities = 47/160 (29%), Positives = 83/160 (51%), Gaps = 2/160 (1%) ref|NP\_819774.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90288.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 195

4472.2

Best-BlastP=> >nrprot 59% Identities = 116/247 (46%), Positives = 155/247 (62%), Gaps = 1/247 (0%) ref|NP\_902024.1| probable hydrolase [Chromobacterium violaceum ATCC 12472] gb|AAQ60026.1| probable hydrolase [Chromobacterium violaceum ATCC 12472] Length = 267

Best-BlastP=> >nrprot 59% Identities = 89/180 (49%), Positives = 122/180 (67%), Gaps = 1/180 (0%) ref|ZP\_00092748.1| hypothetical protein [Azotobacter vinelandii] Length = 397

4474.1

Best-BlastP=> >nrprot 52% Identities = 45/114 (39%), Positives = 65/114 (57%), Gaps = 4/114 (3%) ref|ZP\_00092749.1| hypothetical protein [Azotobacter vinelandii] Length = 135

4475.1

Best-BlastP=> >nrprot 42% Identities = 51/183 (27%), Positives = 96/183 (52%), Gaps = 14/183 (7%) ref|ZP\_00047462.1| COG4123: Predicted O-methyltransferase [Lactobacillus gasseri] Length = 338

4477.2

Best-BlastP=> >nrprot 46% Identities = 204/834 (24%), Positives = 357/834 (42%), Gaps = 142/834 (17%) ref|NP\_907987.1| PHOSPHOENOLPYRUVATE CARBOXYLASE PEPCASE PEPC [Wolinella succinogenes] emb|CAE10887.1| PHOSPHOENOLPYRUVATE CARBOXYLASE PEPCASE PEPC [Wolinella succinogenes] Length = 885

4479.2

Best-BlastP=> >nrprot 60% Identities = 46/119 (38%), Positives = 71/119 (59%), Gaps = 3/119 (2%) ref|NP\_769098.1| blr2458 [Bradyrhizobium japonicum] dbj|BAC47723.1| blr2458 [Bradyrhizobium japonicum USDA 110] Length = 163

448.1

Best-BlastP=> >nrprot 98% Identities = 86/86 (100%), Positives = 86/86 (100%) pir|T18324 icmT protein - Legionella pneumophila emb|CAA73236.1| icmT protein [Legionella pneumophila] emb|CAA75321.1| icmT protein [Legionella pneumophila] Length = 86

4480.4

Best-BlastP=> >nrprot 69% Identities = 234/416 (56%), Positives = 291/416 (69%) ref|NP\_812629.1| gamma-glutamyl phosphate reductase [Bacteroides thetaiotaomicron VPI-5482] gb|AAO78823.1| gamma-glutamyl phosphate reductase [Bacteroides thetaiotaomicron VPI-5482] Length = 417

4481.1

Best-BlastP=> >nrprot 70% Identities = 91/172 (52%), Positives = 124/172 (72%), Gaps = 3/172 (1%) ref|NP\_177142.1| expressed protein [Arabidopsis thaliana] ref|NP\_849870.1| expressed protein [Arabidopsis thaliana] pir|F96720 unknown protein, 58197-59415 [imported] - Arabidopsis thaliana gb|AAG52556.1| AC010675\_4 unknown protein; 58197-59415 [Arabidopsis thaliana] gb|AAM20691.1| unknown protein [Arabidopsis thaliana] gb|AAN15655.1| unknown protein [Arabidopsis thaliana] Length = 286

4482.1

Best-BlastP=> >nrprot 56% Identities = 119/320 (37%), Positives = 168/320 (52%), Gaps = 33/320 (10%) ref|ZP\_00119712.1| COG4823: Abortive infection bacteriophage resistance protein [Cytophaga hutchinsonii] Length = 331

4483.2

Best-BlastP=> >nrprot No Hits found

4484.1

Best-BlastP=> >nrprot No Hits found

4485.2

Best-BlastP=> >nrprot 98% Identities = 252/254 (99%), Positives = 252/254 (99%) gb|AAM73853.1| AF454864\_1 putative lipase LipB [Legionella pneumophila] Length = 254

4487.1

Best-BlastP=> >nrprot 70% Identities = 133/223 (59%), Positives = 163/223 (73%) ref|NP\_231545.1| orotidine 5'-phosphate decarboxylase [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KQT7|PYRF\_VIBCH Orotidine 5'-phosphate decarboxylase (OMP decarboxylase) (OMPDCase) pir|A82143 orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) VC1911 [similarity] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95059.1| orotidine 5'-phosphate decarboxylase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 231

- 4488.1 Best-BlastP=> >nrprot 72% Identities = 213/362 (58%), Positives = 270/362 (74%) ref|NP\_903794.1| probable aminotransferase [Chromobacterium violaceum ATCC 12472] gb|AAQ61785.1| probable aminotransferase [Chromobacterium violaceum ATCC 12472] Length = 365
- 4489.3 Best-BlastP=> >nrprot 67% Identities = 195/383 (50%), Positives = 263/383 (68%), Gaps = 2/383 (0%) ref|NP\_819562.1| TPR domain protein [Coxiella burnetii RSA 493] gb|AAO90076.1| TPR domain protein [Coxiella burnetii RSA 493] Length = 388
- 4490.2 Best-BlastP=> >nrprot 38% Identities = 65/177 (36%), Positives = 109/177 (61%), Gaps = 12/177 (6%) ref|NP\_808996.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb|AAO75190.1| conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] Length = 288
- 4491.3 Best-BlastP=> >nrprot No Hits found
- 4492.3 Best-BlastP=> >nrprot No Hits found
- 4493.1 Best-BlastP=> >nrprot No Hits found
- 4496.2 Best-BlastP=> >nrprot 51% Identities = 106/240 (44%), Positives = 141/240 (58%), Gaps = 3/240 (1%) emb|CAB60048.1| lvrA [Legionella pneumophila] Length = 288
- 4497.4 Best-BlastP=> >nrprot No Hits found
- 4498.1 Best-BlastP=> >nrprot No Hits found
- 45.1 Best-BlastP=> >nrprot 94% Identities = 115/131 (87%), Positives = 125/131 (95%) gb|AAM08243.1| LvrD [Legionella pneumophila] Length = 131
- 450.1 Best-BlastP=> >nrprot 39% Identities = 22/50 (44%), Positives = 28/50 (56%) gb|AAF87782.1| AF279293\_1 p76 membrane protein precursor [Mycoplasma hyopneumoniae] Length = 1427
- 4500.1 Best-BlastP=> >nrprot 82% Identities = 69/116 (59%), Positives = 97/116 (83%) ref|ZP\_00067079.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 117
- 4503.1 Best-BlastP=> >nrprot 77% Identities = 209/334 (62%), Positives = 266/334 (79%) ref|NP\_744617.1| phenylalanyl-tRNA synthetase, alpha subunit [Pseudomonas putida KT2440] gb|AAN68081.1| AE016440\_1 phenylalanyl-tRNA synthetase, alpha subunit [Pseudomonas putida KT2440] Length = 338
- 4505.3 Best-BlastP=> >nrprot 88% Identities = 98/118 (83%), Positives = 106/118 (89%) ref|NP\_929901.1| 50S ribosomal protein L20 [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE15040.1| 50S ribosomal protein L20 [Photorhabdus luminescens subsp. laumondii TTO1] Length = 118
- 4508.4 Best-BlastP=> >nrprot 77% Identities = 90/161 (55%), Positives = 126/161 (78%) ref|NP\_719351.1| conserved hypothetical protein [Shewanella oneidensis MR-1] sp|Q8EAS7|Y2B5\_SHEON Hypothetical UPF0234 protein SO3815 gb|AAN56795.1| AE015815\_1 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 161
- 451.3 Best-BlastP=> >nrprot No Hits found
- 4510.1 Best-BlastP=> >nrprot 83% Identities = 545/812 (67%), Positives = 672/812 (82%), Gaps = 10/812 (1%) ref|NP\_819766.1| ATP-dependent protease La [Coxiella burnetii RSA 493] gb|AAO90280.1| ATP-dependent protease La [Coxiella burnetii RSA 493] Length = 817
- 4511.1 Best-BlastP=> >nrprot 70% Identities = 53/90 (58%), Positives = 66/90 (73%) ref|ZP\_00119213.1| COG0776: Bacterial nucleoid DNA-binding protein [Cytophaga hutchinsonii] Length = 90

- 4512.4 Best-BlastP=> >nprot 49% Identities = 181/604 (29%), Positives = 311/604 (51%), Gaps = 28/604 (4%) ref|ZP\_00139461.1| COG0760: Parvulin-like peptidyl-prolyl isomerase [Pseudomonas aeruginosa UCBPP-PA14] Length = 621
- 4516.3 Best-BlastP=> >nprot 56% Identities = 157/337 (46%), Positives = 214/337 (63%), Gaps = 3/337 (0%) ref|ZP\_00030194.1| COG0845: Membrane-fusion protein [Burkholderia fungorum] Length = 513
- 4517.2 Best-BlastP=> >nprot 51% Identities = 97/274 (35%), Positives = 145/274 (52%), Gaps = 21/274 (7%) gb|AAK81664.1| MdcB [Burkholderia cepacia] Length = 290
- 4519.3 Best-BlastP=> >nprot 78% Identities = 341/546 (62%), Positives = 431/546 (78%), Gaps = 2/546 (0%) ref|NP\_640913.1| alpha subunit of malonate decarboxylase [Xanthomonas axonopodis pv. citri str. 306] gb|AAM35449.1| alpha subunit of malonate decarboxylase [Xanthomonas axonopodis pv. citri str. 306] Length = 548
- 4520.1 Best-BlastP=> >nprot 73% Identities = 225/396 (56%), Positives = 299/396 (75%), Gaps = 2/396 (0%) sp|Q8GDU2|ASSY\_HELMO Argininosuccinate synthase (Citrulline--aspartate ligase) gb|AAN87486.1| Argininosuccinate synthase [Heliobacillus mobilis] Length = 408
- 4521.1 Best-BlastP=> >nprot 60% Identities = 96/207 (46%), Positives = 135/207 (65%), Gaps = 15/207 (7%) ref|NP\_465264.1| similar to amino acid (glutamine) ABC transporter (ATP-binding protein) [Listeria monocytogenes EGD-e] pir|AC1292 amino acid (glutamine) ABC transporter (ATP-binding protein) homolog lmo1739 [imported] - Listeria monocytogenes (strain EGD-e) emb|CAC99817.1| lmo1739 [Listeria monocytogenes] Length = 215
- 4522.4 Best-BlastP=> >nprot 66% Identities = 94/203 (46%), Positives = 144/203 (70%), Gaps = 2/203 (0%) ref|NP\_359808.1| amino acid ABC transporter permease protein [Rickettsia conorii] ref|ZP\_00142355.1| amino acid ABC transporter permease protein [Rickettsia sibirica] pir|C97721 amino acid ABC transporter permease protein yqiY [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02709.1| amino acid ABC transporter permease protein [Rickettsia conorii] gb|EAA25764.1| amino acid ABC transporter permease protein [Rickettsia sibirica] Length = 218
- 4523.1 Best-BlastP=> >nprot 49% Identities = 56/159 (35%), Positives = 89/159 (55%), Gaps = 4/159 (2%) ref|NP\_714273.1| MutT/nudix family protein [Leptospira interrogans serovar lai str. 56601] gb|AAN51291.1| AE011563\_7 MutT/nudix family protein [Leptospira interrogans serovar lai str. 56601] Length = 223
- 4524.1 Best-BlastP=> >nprot 52% Identities = 79/246 (32%), Positives = 125/246 (50%), Gaps = 11/246 (4%) ref|NP\_670144.1| arginine 3rd transport system periplasmic binding protein [Yersinia pestis KIM] gb|AAM86395.1| AE013887\_2 arginine 3rd transport system periplasmic binding protein [Yersinia pestis KIM] Length = 252
- 4525.2 Best-BlastP=> >nprot 73% Identities = 317/556 (57%), Positives = 418/556 (75%), Gaps = 2/556 (0%) ref|NP\_718167.1| long-chain-fatty-acid--CoA ligase [Shewanella oneidensis MR-1] gb|AAN55611.1| AE015699\_9 long-chain-fatty-acid--CoA ligase [Shewanella oneidensis MR-1] Length = 557
- 4526.3 Best-BlastP=> >nprot 83% Identities = 64/111 (57%), Positives = 93/111 (83%), Gaps = 2/111 (1%) ref|ZP\_00065090.1| COG1886: Flagellar motor switch/type III secretory pathway protein [Microbulifer degradans 2-40] Length = 141
- 4528.2 Best-BlastP=> >nprot 21% Identities = 42/173 (57%), Positives = 56/173 (76%) gb|AAN34372.1| ORF2 transposase [Acinetobacter baumannii] Length = 76
- 453.3 Best-BlastP=> >nprot 87% Identities = 181/244 (74%), Positives = 220/244 (90%), Gaps = 6/244 (2%) ref|ZP\_00023826.1| COG0330: Membrane protease subunits, stomatin/prohibitin homologs [Ralstonia metallidurans] Length = 251

- 4530.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 4531.2 Best-BlastP=> >nrprot 53% Identities = 34/77 (44%), Positives = 47/77 (61%), Gaps = 5/77 (6%) gb|AAG53985.1|AF327444\_1 putative transposase A [Pantoea agglomerans] Length = 149
- 4532.2 Best-BlastP=> >nrprot 30% Identities = 127/185 (68%), Positives = 148/185 (80%), Gaps = 11/185 (5%) emb|CAC33489.1| hypothetical protein [Legionella pneumophila] Length = 189
- 4533.2 Best-BlastP=> >nrprot 50% Identities = 643/2158 (29%), Positives = 955/2158 (44%), Gaps = 397/2158 (18%) ref|NP\_758987.1| unknown [Zymomonas mobilis] gb|AAL36122.1| unknown [Zymomonas mobilis] Length = 2201
- 4535.2 Best-BlastP=> >nrprot 69% Identities = 226/438 (51%), Positives = 312/438 (71%), Gaps = 18/438 (4%) ref|ZP\_00089764.1| COG0793: Periplasmic protease [Azotobacter vinelandii] Length = 456
- 4536.1 Best-BlastP=> >nrprot 49% Identities = 114/349 (32%), Positives = 189/349 (54%), Gaps = 12/349 (3%) ref|ZP\_00065627.1| COG4942: Membrane-bound metalloproteinase [Microbulbifer degradans] 2-40] Length = 402
- 4538.2 Best-BlastP=> >nrprot 68% Identities = 273/506 (53%), Positives = 353/506 (69%), Gaps = 4/506 (0%) ref|ZP\_00141602.1| COG0696: Phosphoglyceromutase [Pseudomonas aeruginosa UCBPP-PA14] Length = 515
- 454.1
- Best-BlastP=> >nrprot 59% Identities = 215/454 (47%), Positives = 301/454 (66%), Gaps = 31/454 (6%) ref|NP\_820466.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO90980.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 458
- 4540.2 Best-BlastP=> >nrprot No Hits found
- 4542.4 Best-BlastP=> >nrprot 35% Identities = 136/313 (43%), Positives = 191/313 (61%), Gaps = 22/313 (7%) ref|ZP\_00033133.1| COG2010: Cytochrome c, mono- and diheme variants [Burkholderia fungorum] Length = 432
- 4546.3 Best-BlastP=> >nrprot 21% Identities = 47/163 (28%), Positives = 74/163 (45%), Gaps = 18/163 (11%) ref|ZP\_00011332.1| COG0183: Acetyl-CoA acetyltransferase [Rhodospseudomonas palustris] Length = 504
- 4547.4 Best-BlastP=> >nrprot 76% Identities = 206/337 (61%), Positives = 260/337 (77%), Gaps = 3/337 (0%) ref|ZP\_00125317.1| COG0604: NADPH:quinone reductase and related Zn-dependent oxidoreductases [Pseudomonas syringae pv. syringae B728a] Length = 337
- 4549.2 Best-BlastP=> >nrprot 21% Identities = 73/109 (66%), Positives = 94/109 (86%) ref|NP\_820449.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90963.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 113
- 4551.2 Best-BlastP=> >nrprot 55% Identities = 31/78 (39%), Positives = 49/78 (62%) ref|NP\_875585.1| Uncharacterized conserved membrane protein [Prochlorococcus marinus subsp. marinus str. CCMP1375] gb|AAQ00238.1| Uncharacterized conserved membrane protein [Prochlorococcus marinus subsp. marinus str. CCMP1375] Length = 91
- 4552.4 Best-BlastP=> >nrprot No Hits found
- 4553.2 Best-BlastP=> >nrprot 66% Identities = 107/240 (44%), Positives = 156/240 (65%), Gaps = 14/240 (5%) ref|NP\_867184.1| short chain alcohol dehydrogenase-like [Pirellula sp.] emb|CAD74729.1| short chain alcohol dehydrogenase-like [Pirellula sp.] Length = 247
- 4554.2 Best-BlastP=> >nrprot 35% Identities = 27/49 (55%), Positives = 31/49 (63%), Gaps = 1/49 (2%) ref|ZP\_00031568.1| COG1051: ADP-ribose pyrophosphatase [Burkholderia fungorum] Length = 181

- 4558.1 Best-BlastP=> >nrprot 29% Identities = 43/182 (23%), Positives = 82/182 (45%), Gaps = 9/182 (4%) gb|AAK27486.1|AF343323\_1 DNA gyrase B [Cycloclasticus sp. NOP-122A] gb|AAK27491.1|AF343328\_1 DNA gyrase B [Cycloclasticus sp. N-221A] gb|AAK27492.1|AF343329\_1 DNA gyrase B [Cycloclasticus sp. N-231B] gb|AAK27493.1|AF343330\_1 DNA gyrase B [Cycloclasticus sp. P-211A2] Length = 362
- 4559.1 Best-BlastP=> >nrprot 59% Identities = 206/502 (41%), Positives = 308/502 (61%), Gaps = 6/502 (1%) ref|NP\_819464.1| amino acid permease family protein [Coxiella burnetii RSA 493] gb|AAO89978.1| amino acid permease family protein [Coxiella burnetii RSA 493] Length = 531
- 4560.2 Best-BlastP=> >nrprot 26% Identities = 49/217 (22%), Positives = 98/217 (45%), Gaps = 30/217 (13%) ref|NP\_702678.1| hypothetical protein [Plasmodium falciparum 3D7] emb|CAD49112.1| hypothetical protein [Plasmodium falciparum 3D7] Length = 1248
- 4561.2 Best-BlastP=> >nrprot 48% Identities = 140/428 (32%), Positives = 222/428 (51%), Gaps = 3/428 (0%) ref|NP\_636850.1| outer membrane component of multidrug efflux pump [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM40774.1| outer membrane component of multidrug efflux pump [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 467
- 4564.2 Best-BlastP=> >nrprot 99% Identities = 198/200 (99%), Positives = 199/200 (99%) gb|AAM00391.1|AF386079\_1 CcmA [Legionella pneumophila] Length = 200
- 4566.1 Best-BlastP=> >nrprot 62% Identities = 93/192 (48%), Positives = 124/192 (64%), Gaps = 5/192 (2%) ref|ZP\_00071947.1| COG0693: Putative intracellular protease/amidase [Trichodesmium erythraeum IMS101] Length = 191
- 4567.2 Best-BlastP=> >nrprot 10% Identities = 44/175 (25%), Positives = 69/175 (39%), Gaps = 36/175 (20%) gb|AAK20704.1|AF316641\_10 WcIT [Streptococcus pneumoniae] Length = 242
- 457.2 Best-BlastP=> >nrprot 50% Identities = 180/528 (34%), Positives = 271/528 (51%), Gaps = 58/528 (10%) ref|NP\_820680.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91194.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 518
- 4571.2 Best-BlastP=> >nrprot 34% Identities = 29/58 (50%), Positives = 38/58 (65%) ref|NP\_819567.1| lipoprotein, putative [Coxiella burnetii RSA 493] gb|AAO90081.1| lipoprotein, putative [Coxiella burnetii RSA 493] Length = 323
- 4572.2 Best-BlastP=> >nrprot 63% Identities = 175/348 (50%), Positives = 227/348 (65%), Gaps = 2/348 (0%) ref|ZP\_00068140.1| COG1194: A/G-specific DNA glycosylase [Microbulifer degradans 2-40] Length = 355
- 4573.4 Best-BlastP=> >nrprot 43% Identities = 123/542 (22%), Positives = 226/542 (41%), Gaps = 78/542 (14%) ref|NP\_819951.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90465.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 502
- 4574.2 Best-BlastP=> >nrprot 44% Identities = 95/367 (25%), Positives = 164/367 (44%), Gaps = 55/367 (14%) ref|ZP\_00089878.1| COG1562: Phytoene/squalene synthetase [Azotobacter vinelandii] Length = 377
- 4577.2 Best-BlastP=> >nrprot 48% Identities = 101/231 (43%), Positives = 135/231 (58%), Gaps = 19/231 (8%) ref|NP\_819994.1| rare lipoprotein A family protein [Coxiella burnetii RSA 493] gb|AAO90508.1| rare lipoprotein A family protein [Coxiella burnetii RSA 493] Length = 261

- 4578.1 Best-BlastP=> >nrprot 80% Identities = 224/390 (57%), Positives = 314/390 (80%), Gaps = 1/390 (0%) ref|NP\_819495.1| sodium/hydrogen antiporter family protein [Coxiella burnetii RSA 493] Length = 389
- 458.3 Best-BlastP=> >nrprot 47% Identities = 93/334 (27%), Positives = 164/334 (49%), Gaps = 18/334 (5%) ref|NP\_819588.1| DNA polymerase III, delta subunit [Coxiella burnetii RSA 493] Length = 339
- 4580.1 Best-BlastP=> >nrprot 34% Identities = 41/110 (37%), Positives = 58/110 (52%), Gaps = 3/110 (2%) ref|NP\_742951.1| inner membrane protein AmpE [Pseudomonas putida KT2440] Length = 276
- 4581.2 Best-BlastP=> >nrprot 29% Identities = 22/97 (22%), Positives = 39/97 (40%), Gaps = 1/97 (1%) ref|NP\_820299.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 155
- 4584.3 Best-BlastP=> >nrprot No Hits found
- 4587.2 Best-BlastP=> >nrprot No Hits found
- 4588.2 Best-BlastP=> >nrprot No Hits found
- 4589.1 Best-BlastP=> >nrprot No Hits found
- 459.3 Best-BlastP=> >nrprot 56% Identities = 76/212 (35%), Positives = 119/212 (56%), Gaps = 2/212 (0%) ref|NP\_406133.1| putative nicotinate-nucleotide adenyllyltransferase [Yersinia pestis] sp|Q8ZDG1|NADD\_YERPE Probable nicotinate-nucleotide adenyllyltransferase (Deamido-NAD(+)-pyrophosphorylase) (Deamido-NAD(+) diphosphorylase) (Nicotinate mononucleotide adenyllyltransferase) (NaMN adenyllyltransferase) pir|AC0318 probable nicotinate-nucleotide adenyllyltransferase [EC 2.7.7.18] [imported] - Yersinia pestis (strain CO92) emb|CAC92850.1| putative nicotinate-nucleotide adenyllyltransferase [Yersinia pestis CO92] Length = 220
- 4590.1 Best-BlastP=> >nrprot 56% Identities = 57/130 (43%), Positives = 77/130 (59%), Gaps = 6/130 (4%) ref|ZP\_00086142.1| COG2764: Uncharacterized protein conserved in bacteria [Pseudomonas fluorescens PfO-1] Length = 137
- 4591.2 Best-BlastP=> >nrprot 71% Identities = 86/155 (55%), Positives = 113/155 (72%), Gaps = 4/155 (2%) ref|ZP\_00109160.1| COG3865: Uncharacterized protein conserved in bacteria [Nostoc punctiforme] Length = 165
- 4597.1 Best-BlastP=> >nrprot No Hits found
- 4598.2 Best-BlastP=> >nrprot 71% Identities = 132/248 (53%), Positives = 176/248 (70%), Gaps = 5/248 (2%) ref|NP\_902034.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ60036.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] Length = 246
- 4599.2 Best-BlastP=> >nrprot 78% Identities = 135/206 (65%), Positives = 169/206 (82%) ref|ZP\_00024696.1| COG1484: DNA replication protein [Ralstonia metallidurans] Length = 268
- 46.1 Best-BlastP=> >nrprot 97% Identities = 220/236 (93%), Positives = 230/236 (97%) gb|AAM08241.1| putative TraC protein [Legionella pneumophila] Length = 236
- 460.2 Best-BlastP=> >nrprot 53% Identities = 59/158 (37%), Positives = 95/158 (60%) ref|NP\_819911.1| colicin V production protein [Coxiella burnetii RSA 493] gb|AAO90425.1| colicin V production protein [Coxiella burnetii RSA 493] Length = 184



- 4600.2 Best-BlastP=> >nrprot 52% Identities = 83/238 (34%), Positives = 128/238 (53%), Gaps = 27/238 (11%) ref|NP\_932037.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE17256.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 255
- 4601.1 Best-BlastP=> >nrprot No Hits found
- 4602.3 Best-BlastP=> >nrprot 99% Identities = 300/302 (99%), Positives = 302/302 (100%) emb|CAC14311.1| putative transcriptional regulator [Legionella pneumophila] Length = 302
- 4604.3 Best-BlastP=> >nrprot 48% Identities = 48/182 (26%), Positives = 91/182 (50%), Gaps = 12/182 (6%) ref|NP\_251679.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|F83271 hypothetical protein PA2989 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06377.1|AE004724\_6 hypothetical protein PA2989 [Pseudomonas aeruginosa PAO1] Length = 254
- 4607.2 Best-BlastP=> >nrprot 79% Identities = 265/421 (62%), Positives = 335/421 (79%) ref|ZP\_00092427.1| hypothetical protein [Azotobacter vinelandii] Length = 838
- 4608.1 Best-BlastP=> >nrprot 33% Identities = 34/111 (30%), Positives = 60/111 (54%), Gaps = 3/111 (2%) ref|NP\_700535.1| hypothetical protein [Plasmodium falciparum 3D7] gb|AAN35259.1|AE014830\_3 hypothetical protein [Plasmodium falciparum 3D7] Length = 426
- 4609.2 Best-BlastP=> >nrprot No Hits found
- 4613.3 Best-BlastP=> >nrprot 48% Identities = 121/487 (24%), Positives = 240/487 (49%), Gaps = 29/487 (5%) ref|NP\_753921.1| Hypothetical transporter ydgR [Escherichia coli CFT073] gb|AAN80486.1|AE016761\_61 Hypothetical transporter ydgR [Escherichia coli CFT073] Length = 500
- 4615.3 Best-BlastP=> >nrprot No Hits found
- 4616.2 Best-BlastP=> >nrprot 48% Identities = 93/315 (29%), Positives = 150/315 (47%), Gaps = 35/315 (11%) ref|NP\_820641.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91155.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 429
- 4618.1 Best-BlastP=> >nrprot 58% Identities = 110/250 (44%), Positives = 151/250 (60%), Gaps = 7/250 (2%) dbj|BAB72031.1| lipopolysaccharide biosynthesis glycosyltransferase [Photobacterium damsela subsp. piscicida] Length = 255
- 462.2 Best-BlastP=> >nrprot 44% Identities = 71/278 (25%), Positives = 116/278 (41%), Gaps = 35/278 (12%) ref|NP\_718631.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56075.1|AE015743\_3 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 281
- 4620.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 4623.2 Best-BlastP=> >nrprot 52% Identities = 66/169 (39%), Positives = 93/169 (55%), Gaps = 5/169 (2%) ref|NP\_814807.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] gb|AAO80877.1| acetyltransferase, GNAT family [Enterococcus faecalis V583] Length = 168
- 4625.2 Best-BlastP=> >nrprot 68% Identities = 162/307 (52%), Positives = 215/307 (70%), Gaps = 1/307 (0%) ref|NP\_761810.1| S-malonyltransferase [Vibrio vulnificus CMCP6] gb|AAO11337.1|AE016807\_56 S-malonyltransferase [Vibrio vulnificus CMCP6] Length = 307

- 4626.1 Best-BlastP=> >nrprot 72% Identities = 172/314 (54%), Positives = 231/314 (73%), Gaps = 3/314 (0%) ref|NP\_930069.1| 3-oxoacyl-[acyl carrier-protein] synthase III (beta-ketoacyl-ACP synthase III) (KAS III) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE15209.1| 3-oxoacyl-[acyl carrier-protein] synthase III (beta-ketoacyl-ACP synthase III) (KAS III) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 317
- 4627.2 Best-BlastP=> >nrprot 72% Identities = 183/330 (55%), Positives = 241/330 (73%), Gaps = 2/330 (0%) ref|NP\_819526.1| fatty acid/phospholipid synthesis protein PlsX [Coxiella burnetii RSA 493] sp|Q83E40|PLSX\_COXBU Fatty acid/phospholipid synthesis protein plsX gb|AAO90040.1| fatty acid/phospholipid synthesis protein PlsX [Coxiella burnetii RSA 493] Length = 343
- 4628.2 Best-BlastP=> >nrprot 78% Identities = 45/55 (81%), Positives = 50/55 (90%) ref|ZP\_00135404.1| COG0333: Ribosomal protein L32 [Actinobacillus pleuropneumoniae serovar 1 str. 4074] ref|NP\_873288.1| 50S ribosomal protein L32 [Haemophilus ducreyi 35000HP] gb|AAP95677.1| 50S ribosomal protein L32 [Haemophilus ducreyi 35000HP] Length = 56
- 4629.2 Best-BlastP=> >nrprot 33% Identities = 23/98 (23%), Positives = 48/98 (48%), Gaps = 1/98 (1%) ref|ZP\_00136314.1| COG1399: Predicted metal-binding, possibly nucleic acid-binding protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 148
- 463.2 Best-BlastP=> >nrprot No Hits found
- 4632.1 Best-BlastP=> >nrprot No Hits found
- 4633.2 Best-BlastP=> >nrprot 82% Identities = 121/184 (65%), Positives = 154/184 (83%) ref|NP\_842482.1| Uncharacterized protein family UPF0016 [Nitrosomonas europaea ATCC 19718] emb|CAD86405.1| Uncharacterized protein family UPF0016 [Nitrosomonas europaea ATCC 19718] Length = 192
- 4634.2 Best-BlastP=> >nrprot 52% Identities = 222/716 (31%), Positives = 348/716 (48%), Gaps = 80/716 (11%) ref|NP\_924649.1| probable peptidase [Gloeobacter violaceus] dbj|BAC89644.1| gl|1703 [Gloeobacter violaceus] Length = 730
- 4636.4 Best-BlastP=> >nrprot 4% Identities = 49/164 (29%), Positives = 74/164 (45%), Gaps = 12/164 (7%) ref|ZP\_00009072.1| hypothetical protein [Rhodopseudomonas palustris] Length = 275
- 464.2 Best-BlastP=> >nrprot 60% Identities = 167/405 (41%), Positives = 258/405 (63%), Gaps = 4/405 (0%) ref|NP\_819909.1| FolC bifunctional protein [Coxiella burnetii RSA 493] gb|AAO90423.1| FolC bifunctional protein [Coxiella burnetii RSA 493] Length = 416
- 4640.2 Best-BlastP=> >nrprot 74% Identities = 466/845 (55%), Positives = 627/845 (74%), Gaps = 12/845 (1%) ref|NP\_820057.1| DNA mismatch repair protein MutS [Coxiella burnetii RSA 493] gb|AAO90571.1| DNA mismatch repair protein MutS [Coxiella burnetii RSA 493] Length = 859
- 4642.1 Best-BlastP=> >nrprot 63% Identities = 79/154 (51%), Positives = 107/154 (69%), Gaps = 1/154 (0%) ref|ZP\_00025457.1| COG1546: Uncharacterized protein (competence- and mitomycin-induced) [Ralstonia metallidurans] Length = 200
- 4643.2 Best-BlastP=> >nrprot 56% Identities = 176/176 (100%), Positives = 176/176 (100%) emb|CAC33483.1| hypothetical protein [Legionella pneumophila] Length = 176
- 4644.3 Best-BlastP=> >nrprot 41% Identities = 95/419 (22%), Positives = 174/419 (41%), Gaps = 31/419 (7%) ref|ZP\_00071833.1| hypothetical protein [Trichodesmium erythraeum IMS101] Length = 424
- 4645.2 Best-BlastP=> >nrprot 44% Identities = 96/328 (29%), Positives = 162/328 (49%), Gaps = 10/328 (3%) ref|ZP\_00056223.1| COG0477: Permeases of the major facilitator superfamily [Magnetospirillum magnetotacticum] Length = 407

- 4647.2 Best-BlastP=> >nrprot 25% Identities = 54/234 (23%), Positives = 94/234 (40%), Gaps = 8/234 (3%) ref|ZP\_00034418.1| COG0683: ABC-type branched-chain amino acid transport systems, periplasmic component [Burkholderia fungorum] Length = 451
- 4649.1 Best-BlastP=> >nrprot No Hits found
- 465.2 Best-BlastP=> >nrprot 75% Identities = 186/283 (65%), Positives = 222/283 (78%), Gaps = 3/283 (1%) ref|NP\_819908.1| acetyl-CoA carboxylase, carboxyl transferase, beta subunit [Coxiella burnetii RSA 493] gb|AAO90422.1| acetyl-CoA carboxylase, carboxyl transferase, beta subunit [Coxiella burnetii RSA 493] Length = 291
- 4650.3 Best-BlastP=> >nrprot 45% Identities = 301/1302 (23%), Positives = 574/1302 (44%), Gaps = 91/1302 (6%) ref|NP\_901766.1| probable transmembrane protein [Chromobacterium violaceum ATCC 12472] gb|AAQ59768.1| probable transmembrane protein [Chromobacterium violaceum ATCC 12472] Length = 1272
- 4652.2 Best-BlastP=> >nrprot 62% Identities = 51/115 (44%), Positives = 79/115 (68%) ref|NP\_353968.1| AGR\_C\_1731p [Agrobacterium tumefaciens] pir||H97474 hypothetical 14.1K protein in rpli-cpdb intergenic region [imported] - Agrobacterium tumefaciens (strain C58, Cereon) gb|AAK86753.1| AGR\_C\_1731p [Agrobacterium tumefaciens str. C58 (Cereon)] Length = 190
- 4653.2 Best-BlastP=> >nrprot 26% Identities = 50/154 (32%), Positives = 79/154 (51%), Gaps = 17/154 (11%) ref|NP\_440166.1| hypothetical protein [Synechocystis sp. PCC 6803] sp|P72831|YC98\_SYNY3 Hypothetical protein slr1298 pir||S74695 hypothetical protein slr1298 - Synechocystis sp. (strain PCC 6803) dbj|BAA16846.1| ORF\_ID:slr1298~hypothetical protein [Synechocystis sp. PCC 6803] Length = 755
- 4655.3 Best-BlastP=> >nrprot 47% Identities = 130/460 (28%), Positives = 216/460 (46%), Gaps = 31/460 (6%) ref|NP\_840264.1| Outer membrane efflux protein [Nitrosomonas europaea ATCC 19718] emb|CAD84081.1| Outer membrane efflux protein [Nitrosomonas europaea ATCC 19718] Length = 516
- 4656.2 Best-BlastP=> >nrprot 26% Identities = 69/366 (18%), Positives = 161/366 (43%), Gaps = 26/366 (7%) ref|XP\_230851.2| similar to hypothetical protein [Rattus norvegicus] Length = 396
- 4657.1 Best-BlastP=> >nrprot 62% Identities = 94/202 (46%), Positives = 131/202 (64%), Gaps = 7/202 (3%) ref|NP\_520142.1| PUTATIVE GST-RELATED PROTEIN [Ralstonia solanacearum] emb|CAD15723.1| PUTATIVE GST-RELATED PROTEIN [Ralstonia solanacearum] Length = 230
- 4658.2 Best-BlastP=> >nrprot 75% Identities = 94/134 (70%), Positives = 105/134 (78%), Gaps = 1/134 (0%) ref|NP\_105189.1| organic hydroperoxide resistance protein [Mesorhizobium loti] dbj|BAB50975.1| organic hydroperoxide resistance protein [Mesorhizobium loti] Length = 137
- 4659.2 Best-BlastP=> >nrprot No Hits found
- 4660.2 Best-BlastP=> >nrprot No Hits found
- 4662.1 Best-BlastP=> >nrprot No Hits found
- 4663.3 Best-BlastP=> >nrprot 98% Identities = 288/297 (96%), Positives = 294/297 (98%) pir||A42596 major outer membrane protein - Legionella pneumophila gb|AAA25300.1| major outer membrane protein Length = 297
- 4665.2 Best-BlastP=> >nrprot 45% Identities = 244/604 (40%), Positives = 363/604 (60%), Gaps = 38/604 (6%) ref|NP\_715981.1| sensory box protein [Shewanella oneidensis MR-1] gb|AAN53426.1|AE015481\_9 sensory box protein [Shewanella oneidensis MR-1] Length = 1515

- 4666.2 Best-BlastP=> >nrprot 53% Identities = 118/339 (34%), Positives = 174/339 (51%), Gaps = 44/339 (12%) ref|NP\_720115.1| ribonuclease, T2 family [Shewanella oneidensis MR-1] gb|AAN57559.1|AE015891\_10 ribonuclease, T2 family [Shewanella oneidensis MR-1] Length = 384
- 4668.1 Best-BlastP=> >nrprot 25% Identities = 75/198 (37%), Positives = 112/198 (56%), Gaps = 1/198 (0%) ref|ZP\_00054876.1| hypothetical protein [Magnetospirillum magnetotacticum] Length = 626
- 4669.2 Best-BlastP=> >nrprot 76% Identities = 48/71 (67%), Positives = 55/71 (77%), Gaps = 1/71 (1%) ref|NP\_232566.1| cold shock transcriptional regulator CspA [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KN00|CSPA\_VIBCH Cold shock-like protein cspA pir|G82492 cold shock transcription regulator CspA VCA0166 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF96079.1| cold shock transcriptional regulator CspA [Vibrio cholerae O1 biovar eltor str. N16961] Length = 70
- 4671.3 Best-BlastP=> >nrprot 58% Identities = 131/353 (37%), Positives = 208/353 (58%), Gaps = 5/353 (1%) ref|NP\_243998.1| endo-1,4-beta-glucanase [Bacillus halodurans] pir|D84041 endo-1,4-beta-glucanase BH3132 [imported] - Bacillus halodurans (strain C-125) dbj|BAB06851.1| endo-1,4-beta-glucanase [Bacillus halodurans] Length = 361
- 4672.1 Best-BlastP=> >nrprot 67% Identities = 119/224 (53%), Positives = 161/224 (71%), Gaps = 2/224 (0%) ref|ZP\_00131766.1| COG0220: Predicted S-adenosylmethionine-dependent methyltransferase [Haemophilus somnus 2336] Length = 251
- 4673.1 Best-BlastP=> >nrprot 83% Identities = 59/78 (75%), Positives = 66/78 (84%) ref|NP\_439112.1| ribosomal protein L28 [Haemophilus influenzae Rd] sp|P44364|RL28\_HAEIN 50S ribosomal protein L28 pir|E64104 ribosomal protein L28 - Haemophilus influenzae (strain Rd KW20) gb|AAC22612.1| ribosomal protein L28 (rplL28) [Haemophilus influenzae Rd] Length = 78
- 4676.2 Best-BlastP=> >nrprot 73% Identities = 262/488 (53%), Positives = 342/488 (70%), Gaps = 32/488 (6%) dbj|BAC93212.1| DNA-directed RNA polymerase specialized sigma subunit [Vibrio vulnificus YJ016] Length = 487
- 4678.3 Best-BlastP=> >nrprot No Hits found
- 468.3 Best-BlastP=> >nrprot 76% Identities = 81/121 (66%), Positives = 99/121 (81%) ref|ZP\_00089152.1| COG0251: Putative translation initiation inhibitor, yigF family [Azotobacter vinelandii] Length = 234
- 4680.2 Best-BlastP=> >nrprot 74% Identities = 129/219 (58%), Positives = 169/219 (77%) ref|NP\_642403.1| ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36939.1| ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] Length = 227
- 4683.3 Best-BlastP=> >nrprot 73% Identities = 215/417 (51%), Positives = 305/417 (73%), Gaps = 5/417 (1%) ref|NP\_820008.1| lipoprotein ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] gb|AAO90522.1| lipoprotein ABC transporter, permease protein, putative [Coxiella burnetii RSA 493] Length = 414
- 4688.2 Best-BlastP=> >nrprot 73% Identities = 199/352 (56%), Positives = 275/352 (78%) ref|NP\_643914.1| type II secretion system protein-like protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM38450.1| type II secretion system protein-like protein [Xanthomonas axonopodis pv. citri str. 306] Length = 377
- 469.3 Best-BlastP=> >nrprot 74% Identities = 411/703 (58%), Positives = 530/703 (75%), Gaps = 5/703 (0%) ref|NP\_819346.1| guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase [Coxiella burnetii RSA 493] gb|AAO89860.1| guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase [Coxiella burnetii RSA 493] Length = 707

- 4690.2 Best-BlastP=> >nrprot 4% Identities = 21/50 (42%), Positives = 31/50 (62%) ref|NP\_055206.1| cardiac ankyrin repeat protein; cytokine inducible nuclear protein [Homo sapiens] pir||A57291 cytokine inducible nuclear protein C193 - human emb|CAA58676.1| nuclear protein [Homo sapiens] Length = 319
- 4691.2 Best-BlastP=> >nrprot 82% Identities = 279/413 (67%), Positives = 356/413 (86%), Gaps = 3/413 (0%) ref|NP\_670162.1| probable serine transporter [Yersinia pestis KIM] gb|AAM86413.1|AE013888\_9 probable serine transporter [Yersinia pestis KIM] Length = 440
- 4692.5 Best-BlastP=> >nrprot 71% Identities = 232/427 (54%), Positives = 316/427 (74%), Gaps = 3/427 (0%) ref|NP\_820015.1| adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Coxiella burnetii RSA 493] gb|AAO90529.1| adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Coxiella burnetii RSA 493] Length = 442
- 4694.1 Best-BlastP=> >nrprot 59% Identities = 187/507 (36%), Positives = 297/507 (58%), Gaps = 30/507 (5%) ref|NP\_616892.1| serine-type D-Ala-D-Ala carboxypeptidase [Methanosarcina acetivorans str. C2A] gb|AAM05372.1| serine-type D-Ala-D-Ala carboxypeptidase [Methanosarcina acetivorans str. C2A] Length = 568
- 4695.1 Best-BlastP=> >nrprot No Hits found
- 4696.3 Best-BlastP=> >nrprot 31% Identities = 102/309 (33%), Positives = 170/309 (55%), Gaps = 8/309 (2%) ref|NP\_461159.1| putative membrane protein involved in resistance to lambda and N4 phages [Salmonella typhimurium LT2] gb|AAL21118.1| putative membrane protein involved in resistance to lambda and N4 phages [Salmonella typhimurium LT2] Length = 518
- 4699.3 Best-BlastP=> >nrprot 85% Identities = 315/417 (75%), Positives = 364/417 (87%), Gaps = 5/417 (1%) ref|NP\_793499.1| ATP-dependent Clp protease, ATP-binding subunit ClpX [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57194.1| ATP-dependent Clp protease, ATP-binding subunit ClpX [Pseudomonas syringae pv. tomato str. DC3000] Length = 427
- 47.1 Best-BlastP=> >nrprot 97% Identities = 784/826 (94%), Positives = 806/826 (97%) gb|AAM08240.1| putative type IV secretion protein B4 [Legionella pneumophila] Length = 826
- 470.3 Best-BlastP=> >nrprot 88% Identities = 48/68 (70%), Positives = 60/68 (88%) ref|ZP\_00085276.1| COG1758: DNA-directed RNA polymerase, subunit K/omega [Pseudomonas fluorescens PfO-1] Length = 87
- 4701.2 Best-BlastP=> >nrprot 58% Identities = 118/269 (43%), Positives = 163/269 (60%), Gaps = 14/269 (5%) ref|NP\_819610.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90124.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 273
- 4702.1 Best-BlastP=> >nrprot 65% Identities = 96/188 (51%), Positives = 131/188 (69%) ref|NP\_819608.1| glycosyl transferase, group 2 family protein [Coxiella burnetii RSA 493] gb|AAO90122.1| glycosyl transferase, group 2 family protein [Coxiella burnetii RSA 493] Length = 324
- 4703.2 Best-BlastP=> >nrprot 48% Identities = 53/118 (44%), Positives = 79/118 (66%) ref|NP\_900830.1| probable glycosyl transferase [Chromobacterium violaceum ATCC 12472] gb|AAQ58835.1| probable glycosyl transferase [Chromobacterium violaceum ATCC 12472] Length = 335
- 4704.2 Best-BlastP=> >nrprot 56% Identities = 81/220 (36%), Positives = 127/220 (57%), Gaps = 3/220 (1%) ref|ZP\_00021591.1| COG3376: High-affinity nickel permease [Ralstonia metalldurans] Length = 278

- 4705.3 Best-BlastP=> >nrprot 31% Identities = 55/205 (26%), Positives = 94/205 (45%), Gaps = 29/205 (14%) ref|NP\_052786.1| pXO1-90 [Bacillus anthracis] ref|NP\_652888.1| S-layer protein, (pXO1-90) [Bacillus anthracis str. A2012] pir|B59102 hypothetical protein pXO1-90 - Bacillus anthracis virulence plasmid pXO1 gb|AAD32394.1| pXO1-90 [Bacillus anthracis] gb|AAM26077.1| S-layer protein, (pXO1-90) [Bacillus anthracis str. A2012] Length = 652
- 4706.3 Best-BlastP=> >nrprot 86% Identities = 106/141 (75%), Positives = 123/141 (87%) dbj|BAC55152.1| nucleoside diphosphate kinase [Halomonas sp. #593] Length = 141
- 4709.1
- Best-BlastP=> >nrprot 73% Identities = 213/358 (59%), Positives = 281/358 (78%), Gaps = 1/358 (0%) ref|NP\_274327.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir|B81098 conserved hypothetical protein NMB1308 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF41683.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 364
- 4710.1 Best-BlastP=> >nrprot 40% Identities = 70/205 (34%), Positives = 107/205 (52%) ref|NP\_231252.1| fimbrial biogenesis and twitching motility protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir|F82178 probable fimbrial biogenesis and twitching motility protein VC1612 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94766.1| fimbrial biogenesis and twitching motility protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] Length = 237
- 4711.1
- Best-BlastP=> >nrprot 41% Identities = 42/159 (26%), Positives = 78/159 (49%), Gaps = 21/159 (13%) ref|NP\_820244.1| DNA-binding protein, putative [Coxiella burnetii RSA 493] gb|AAO90758.1| DNA-binding protein, putative [Coxiella burnetii RSA 493] Length = 203
- 4712.2 Best-BlastP=> >nrprot 71% Identities = 250/418 (59%), Positives = 306/418 (73%), Gaps = 2/418 (0%) ref|ZP\_00091666.1| Histidyl-tRNA synthetase [Azotobacter vinelandii] Length = 428
- 4713.1 Best-BlastP=> >nrprot No Hits found
- 4714.1 Best-BlastP=> >nrprot 47% Identities = 102/310 (32%), Positives = 159/310 (51%), Gaps = 5/310 (1%) ref|NP\_800300.1| putative YhfP protein [Vibrio parahaemolyticus RMD 2210633] dbj|BAC62133.1| putative YhfP protein [Vibrio parahaemolyticus] Length = 334
- 4715.3 Best-BlastP=> >nrprot 48% Identities = 43/158 (27%), Positives = 80/158 (50%), Gaps = 7/158 (4%) ref|ZP\_00084605.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 171
- 4716.2 Best-BlastP=> >nrprot 48% Identities = 88/323 (27%), Positives = 162/323 (50%), Gaps = 34/323 (10%) ref|ZP\_00144869.1| Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb|EAA23536.1| Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 351
- 4718.1 Best-BlastP=> >nrprot No Hits found
- 4719.2
- Best-BlastP=> >nrprot 42% Identities = 149/405 (36%), Positives = 217/405 (53%), Gaps = 35/405 (8%) pir|T03487 potential multicopper oxidase - Rhodobacter capsulatus gb|AAC16140.1| potential multicopper oxidase [Rhodobacter capsulatus] Length = 491
- 472.1 Best-BlastP=> >nrprot 73% Identities = 107/205 (52%), Positives = 155/205 (75%) ref|NP\_819344.1| guanylate kinase [Coxiella burnetii RSA 493] gb|AAO89858.1| guanylate kinase [Coxiella burnetii RSA 493] Length = 206
- 4721.2 Best-BlastP=> >nrprot 70% Identities = 91/161 (56%), Positives = 125/161 (77%), Gaps = 1/161 (0%) ref|NP\_440118.1| spore maturation protein A [Synechocystis sp. PCC 6803] pir|S74646 spore maturation protein A - Synechocystis sp. (strain PCC 6803) dbj|BAA16798.1| spore maturation protein A [Synechocystis sp. PCC 6803] Length = 182

- 4724.2 Best-BlastP=> >nrprot 70% Identities = 98/199 (49%), Positives = 142/199 (71%), Gaps = 5/199 (2%) ref|NP\_440119.1| spore maturation protein B [Synechocystis sp. PCC 6803] pir||S74647 spore maturation protein B - Synechocystis sp. (strain PCC 6803) dbj|BAA16799.1| spore maturation protein B [Synechocystis sp. PCC 6803] Length = 217
- 4725.2 Best-BlastP=> >nrprot 31% Identities = 73/267 (27%), Positives = 111/267 (41%), Gaps = 62/267 (23%) ref|NP\_230974.1| hypothetical protein VC1330 [Vibrio cholerae O1 biovar eltor str. N16961] pir||B82212 hypothetical protein VC1330 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF94488.1| hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 275
- 4726.1 Best-BlastP=> >nrprot No Hits found
- 4727.1 Best-BlastP=> >nrprot 42% Identities = 43/76 (56%), Positives = 57/76 (75%) ref|ZP\_00101887.1| COG5394: Uncharacterized protein conserved in bacteria [Desulfitobacterium hafniense] Length = 107
- 4729.3 Best-BlastP=> >nrprot 64% Identities = 111/246 (45%), Positives = 161/246 (65%), Gaps = 1/246 (0%) ref|NP\_902034.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] gb|AAQ60036.1| acetoacetyl-CoA reductase [Chromobacterium violaceum ATCC 12472] Length = 246
- 473.2 Best-BlastP=> >nrprot 63% Identities = 122/288 (42%), Positives = 183/288 (63%) ref|NP\_229866.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] pir||C82350 conserved hypothetical protein VC0209 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93385.1| conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] Length = 288
- 4732.3 Best-BlastP=> >nrprot 33% Identities = 30/96 (31%), Positives = 42/96 (43%), Gaps = 17/96 (17%) dbj|BAA89216.1| soluble cytochrome cA [Shewanella violacea] Length = 85
- 4733.2 Best-BlastP=> >nrprot 71% Identities = 154/296 (52%), Positives = 210/296 (70%), Gaps = 8/296 (2%) ref|NP\_820374.1| translation elongation factor Ts [Coxiella burnetii RSA 493] sp|Q9X5U9|EFTS\_COXBU Elongation factor Ts (EF-Ts) gb|AAD33343.1| AF127534\_2 elongation factor Ts [Coxiella burnetii] gb|AAO90888.1| translation elongation factor Ts [Coxiella burnetii RSA 493] Length = 296
- 4734.2 Best-BlastP=> >nrprot 65% Identities = 134/341 (39%), Positives = 213/341 (62%), Gaps = 16/341 (4%) ref|NP\_439856.1| hypothetical protein [Haemophilus influenzae Rd] sp|P45339|YJEQ\_HAEIN Hypothetical protein HI1714 pir||B64176 hypothetical protein HI1714 - Haemophilus influenzae (strain Rd KW20) gb|AAC23359.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 346
- 4736.2 Best-BlastP=> >nrprot 70% Identities = 219/403 (54%), Positives = 289/403 (71%), Gaps = 2/403 (0%) ref|NP\_232075.1| tRNA nucleotidyltransferase [Vibrio cholerae O1 biovar eltor str. N16961] pir||D82076 tRNA nucleotidyltransferase VC2446 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF95588.1| tRNA nucleotidyltransferase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 403
- 4737.1 Best-BlastP=> >nrprot 79% Identities = 122/178 (68%), Positives = 149/178 (83%) ref|ZP\_00066572.1| COG1949: Oligoribonuclease (3'->5' exonuclease) [Microbulifer degradans 2-40] Length = 185
- 4739.1 Best-BlastP=> >nrprot 81% Identities = 156/208 (75%), Positives = 180/208 (86%) ref|NP\_841903.1| DUF208 [Nitrosomonas europaea ATCC 19718] emb|CAD85792.1| DUF208 [Nitrosomonas europaea ATCC 19718] Length = 215



474.2

Best-BlastP=> >nrprot 44% Identities = 24/107 (22%), Positives = 49/107 (45%) ref|NP\_878011.1| Tn1546 transposase [Staphylococcus aureus] sp|Q06238|TNP6\_ENTFC Transposase for transposon Tn1546 pir|A40628 probable transposase - Enterococcus faecium transposon Tn1546 gb|AAA65951.1| transposase [Enterococcus faecium] gb|AAQ17155.1| Tn1546 transposase [Staphylococcus aureus] Length = 988

4740.2 Best-BlastP=> >nrprot 62% Identities = 137/287 (47%), Positives = 193/287 (67%), Gaps = 1/287 (0%) ref|NP\_478257.1| cation efflux system protein [Nostoc sp. PCC 7120] pir|AG2540 cation efflux system protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120beta dbj|BAB77253.1| cation efflux system protein [Nostoc sp. PCC 7120] Length = 304

4742.3 Best-BlastP=> >nrprot 48% Identities = 85/305 (27%), Positives = 148/305 (48%), Gaps = 14/305 (4%) ref|NP\_759924.1| Transcriptional regulator [Vibrio vulnificus CMCP6] gb|AAO09451.1| AE016800\_56 Transcriptional regulator [Vibrio vulnificus CMCP6] dbj|BAC35964.1| transcriptional regulator [Vibrio vulnificus YJ016] Length = 313

4744.3 Best-BlastP=> >nrprot 40% Identities = 66/257 (25%), Positives = 119/257 (46%), Gaps = 35/257 (13%) ref|ZP\_00143092.1| hypothetical protein [Rickettsia sibirica] gb|EAA26501.1| unknown [Rickettsia sibirica] Length = 290

4746.1 Best-BlastP=> >nrprot 52% Identities = 34/80 (42%), Positives = 48/80 (60%), Gaps = 3/80 (3%) ref|NP\_799393.1| putative signal peptide protein [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61277.1| putative signal peptide protein [Vibrio parahaemolyticus] Length = 86

4748.1 Best-BlastP=> >nrprot 71% Identities = 145/246 (58%), Positives = 182/246 (73%), Gaps = 2/246 (0%) ref|ZP\_00028198.1| COG4689: Acetoacetate decarboxylase [Burkholderia fungorum] Length = 442

4749.2 Best-BlastP=> >nrprot 39% Identities = 206/416 (49%), Positives = 284/416 (68%), Gaps = 3/416 (0%) ref|NP\_386185.1| PUTATIVE NADH DEHYDROGENASE TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] emb|CAC46658.1| PUTATIVE NADH DEHYDROGENASE TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti] Length = 422

475.1 Best-BlastP=> >nrprot No Hits found

4751.2 Best-BlastP=> >nrprot 44% Identities = 161/483 (33%), Positives = 245/483 (50%), Gaps = 72/483 (14%) gb|AAN78225.1| class 4 metalloprotease [Chromobacterium violaceum] Length = 489

4752.2 Best-BlastP=> >nrprot 60% Identities = 120/275 (43%), Positives = 180/275 (65%) ref|ZP\_00029901.1| COG0697: Permeases of the drug/metabolite transporter (DMT) superfamily [Burkholderia fungorum] Length = 341

4754.1 Best-BlastP=> >nrprot No Hits found

4755.2 Best-BlastP=> >nrprot 58% Identities = 74/170 (43%), Positives = 109/170 (64%) ref|NP\_310486.1| hypothetical protein [Escherichia coli O157:H7] pir|C90936 hypothetical protein ECs2459 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) dbj|BAB35882.1| hypothetical protein [Escherichia coli O157:H7] Length = 182

4757.2 Best-BlastP=> >nrprot 53% Identities = 60/192 (31%), Positives = 105/192 (54%), Gaps = 3/192 (1%) ref|ZP\_00111879.1| COG0259: Pyridoxamine-phosphate oxidase [Nostoc punctiforme] Length = 214

4758.2 Best-BlastP=> >nrprot 51% Identities = 44/92 (47%), Positives = 66/92 (71%) ref|NP\_926536.1| unknown protein [Gloeobacter violaceus] dbj|BAC91531.1| gsl3590 [Gloeobacter violaceus] Length = 98

4759.2 Best-BlastP=> >nrprot 70% Identities = 142/258 (55%), Positives = 181/258 (70%), Gaps = 5/258 (1%) ref|NP\_863091.1| putative oxidoreductase [Pseudomonas putida] gb|AAO64293.1| putative oxidoreductase [Pseudomonas putida] gb|AAP44207.1| putative dehydrogenase [Pseudomonas sp. ND6] Length = 257

- 4760.2 Best-BlastP=> >nrprot No Hits found
- 4763.2 Best-BlastP=> >nrprot 52% Identities = 133/408 (32%), Positives = 219/408 (53%), Gaps = 23/408 (5%) ref|NP\_903521.1| probable prophage integrase [Chromobacterium violaceum ATCC 12472] gb|AAQ61513.1| probable prophage integrase [Chromobacterium violaceum ATCC 12472] Length = 423
- 4764.2 Best-BlastP=> >nrprot No Hits found
- 4766.2
- Best-BlastP=> >nrprot 74% Identities = 80/144 (55%), Positives = 108/144 (75%), Gaps = 1/144 (0%) ref|NP\_820296.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90810.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 146
- 4767.2
- Best-BlastP=> >nrprot 62% Identities = 36/93 (38%), Positives = 57/93 (61%), Gaps = 3/93 (3%) ref|NP\_273838.1| conserved hypothetical protein [Neisseria meningitidis MC58] ref|NP\_283783.1| hypothetical protein MMA1005 [Neisseria meningitidis Z2491] sp|Q9JRC2|YA05\_NEIMA Hypothetical protein MMA1005/NMB0796 pir|C81157 conserved hypothetical protein NMB0796 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) gb|AAF41209.1| conserved hypothetical protein [Neisseria meningitidis MC58] emb|CAB84274.1| hypothetical protein MMA1005 [Neisseria meningitidis Z2491] Length = 92
- 4768.1 Best-BlastP=> >nrprot 52% Identities = 35/101 (34%), Positives = 62/101 (61%), Gaps = 12/101 (11%) ref|ZP\_00022930.1| COG2913: Small protein A (tmRNA-binding) [Ralstonia metallidurans] Length = 159
- 4769.1 Best-BlastP=> >nrprot 99% Identities = 135/136 (99%), Positives = 136/136 (100%) sp|Q48835|FUR\_LEGPN Ferric uptake regulation protein (Ferric uptake regulator) gb|AAA19656.1| Fur Length = 136
- 4770.1 Best-BlastP=> >nrprot 68% Identities = 25/46 (54%), Positives = 33/46 (71%), Gaps = 3/46 (6%) emb|CAB87569.1| FldC protein [Sphingomonas sp. LB126] Length = 533
- 4771.2 Best-BlastP=> >nrprot 26% Identities = 65/166 (39%), Positives = 94/166 (56%), Gaps = 7/166 (4%) ref|NP\_907052.1| COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wolinetia succinogenes] emb|CAE09952.1| COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wolinetia succinogenes] Length = 407
- 4773.3
- Best-BlastP=> >nrprot 77% Identities = 292/461 (63%), Positives = 362/461 (78%) ref|ZP\_00015785.1| hypothetical protein [Rhodospirillum rubrum] sp|Q59765|PNTB\_RHORU NAD(P) transhydrogenase subunit beta (Pyridine nucleotide transhydrogenase subunit beta) (Nicotinamide nucleotide transhydrogenase subunit beta) (Proton-translocating transhydrogenase NAD(P)(H)-binding component) (dIII) gb|AAC43257.1| nicotinamide nucleotide transhydrogenase, subunit beta gb|AAA62495.1| proton-translocating nicotinamide nucleotide transhydrogenase subunit PntB prf|J2102322C energy-transducing nicotinamide nucleotide transhydrogenase: Length = 464
- 4774.1 Best-BlastP=> >nrprot 74% Identities = 61/91 (67%), Positives = 74/91 (81%) ref|NP\_840934.1| probable transmembrane NAD(P) transhydrogenase (alpha subunit part 2) [Nitrosomonas europaea ATCC 19718] emb|CAD84771.1| probable transmembrane NAD(P) transhydrogenase (alpha subunit part 2) [Nitrosomonas europaea ATCC 19718] Length = 102
- 4775.2 Best-BlastP=> >nrprot 66% Identities = 179/361 (49%), Positives = 250/361 (69%), Gaps = 9/361 (2%) ref|NP\_840933.1| Alanine dehydrogenase and pyridine nucleotide transhydrogenase [Nitrosomonas europaea ATCC 19718] emb|CAD84770.1| Alanine dehydrogenase and pyridine nucleotide transhydrogenase [Nitrosomonas europaea ATCC 19718] Length = 375

- 4776.3 Best-BlastP=> >nrprot 51% Identities = 59/146 (40%), Positives = 89/146 (60%), Gaps = 8/146 (5%) ref|ZP\_00111831.1| COG2340: Uncharacterized protein with SCP/PR1 domains [Nostoc punctiforme] Length = 182
- 4777.2 Best-BlastP=> >nrprot No Hits found
- 4778.1 Best-BlastP=> >nrprot No Hits found
- 4779.1 Best-BlastP=> >nrprot 62% Identities = 68/152 (44%), Positives = 93/152 (61%), Gaps = 4/152 (2%) ref|ZP\_00125177.1| COG2153: Predicted acyltransferase [Pseudomonas syringae pv. syringae B728a] Length = 152
- 4780.2 Best-BlastP=> >nrprot No Hits found
- 4782.3 Best-BlastP=> >nrprot 99% Identities = 359/363 (98%), Positives = 362/363 (99%) emb|CAB65197.1| hypothetical protein [Legionella pneumophila] Length = 363
- 4785.1 Best-BlastP=> >nrprot No Hits found
- 4786.2 Best-BlastP=> >nrprot 52% Identities = 159/409 (38%), Positives = 250/409 (61%), Gaps = 8/409 (1%) ref|NP\_819388.1| d-xylose-proton symporter, putative [Coxiella burnetii RSA 493] gb|AAO89902.1| d-xylose-proton symporter, putative [Coxiella burnetii RSA 493] Length = 409
- 4788.3 Best-BlastP=> >nrprot 98% Identities = 200/204 (98%), Positives = 201/204 (98%) sp|P50024|DSBA\_LEGPN\_THIOL:DISULFIDE INTERCHANGE PROTEIN DSBA PRECURSOR gb|AAA67725.1| disulfide bond forming protein Length = 204
- 4790.3
- Best-BlastP=> >nrprot 77% Identities = 278/425 (65%), Positives = 336/425 (79%), Gaps = 1/425 (0%) ref|NP\_820750.1| ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] gb|AAO91264.1| ABC transporter, ATP-binding protein [Coxiella burnetii RSA 493] Length = 432
- 4791.3 Best-BlastP=> >nrprot 35% Identities = 37/91 (40%), Positives = 47/91 (51%) pir|A71007 hypothetical protein PH1351 - Pyrococcus horikoshii dbj|BAA30457.1| 101aa long hypothetical protein [Pyrococcus horikoshii] Length = 101
- 4793.2 Best-BlastP=> >nrprot 75% Identities = 306/545 (56%), Positives = 412/545 (75%) ref|NP\_820751.1| ABC transporter, permease protein [Coxiella burnetii RSA 493] gb|AAO91265.1| ABC transporter, permease protein [Coxiella burnetii RSA 493] Length = 581
- 4795.1 Best-BlastP=> >nrprot No Hits found
- 4796.1 Best-BlastP=> >nrprot 25% Identities = 24/70 (34%), Positives = 36/70 (51%), Gaps = 12/70 (17%) ref|NP\_650587.1| CG5225-PA [Drosophila melanogaster] gb|AAF55377.2| CG5225-PA [Drosophila melanogaster] Length = 594
- 4797.1 Best-BlastP=> >nrprot 91% Identities = 293/351 (83%), Positives = 324/351 (92%) ref|NP\_820537.1| ribonucleoside-diphosphate reductase, beta subunit [Coxiella burnetii RSA 493] gb|AAO91051.1| ribonucleoside-diphosphate reductase, beta subunit [Coxiella burnetii RSA 493] Length = 401
- 48.1 Best-BlastP=> >nrprot 98% Identities = 90/93 (96%), Positives = 93/93 (100%) emb|CAB60052.1| lvhB3 [Legionella pneumophila] gb|AAM08239.1| putative type IV secretion protein B3 [Legionella pneumophila] Length = 93
- 480.3
- Best-BlastP=> >nrprot 88% Identities = 373/475 (78%), Positives = 428/475 (90%), Gaps = 1/475 (0%) ref|NP\_820349.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90863.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 480
- 4800.2 Best-BlastP=> >nrprot 61% Identities = 102/252 (40%), Positives = 160/252 (63%), Gaps = 1/252 (0%) ref|ZP\_00110131.1| COG0300: Short-chain dehydrogenases of various substrate specificities [Nostoc punctiforme] Length = 270

- 4801.1 Best-BlastP=> >nrprot 33% Identities = 31/122 (25%), Positives = 56/122 (45%), Gaps = 24/122 (19%) ref|ZP\_00026008.1| COG4970: Tfp pilus assembly protein FimT [Ralstonia metallidurans] Length = 222
- 4802.2 Best-BlastP=> >nrprot 31% Identities = 34/110 (30%), Positives = 56/110 (50%), Gaps = 7/110 (6%) ref|ZP\_00030895.1| COG3161: 4-hydroxybenzoate synthetase (chorismate lyase) [Burkholderia fungorum] Length = 227
- 4803.2 Best-BlastP=> >nrprot 79% Identities = 148/247 (59%), Positives = 197/247 (79%) ref|NP\_793605.1| 3-oxoacyl-(acyl-carrier-protein) reductase [Pseudomonas syringae pv. tomato str. DC3000] Length = 247
- 4804.1 Best-BlastP=> >nrprot 84% Identities = 65/73 (89%), Positives = 70/73 (95%) pir|T12021| acyl carrier protein - Pseudomonas aeruginosa gb|AAB94392.1| acyl carrier protein [Pseudomonas aeruginosa] Length = 78
- 4805.1 Best-BlastP=> >nrprot 78% Identities = 258/411 (62%), Positives = 325/411 (79%) ref|NP\_251655.1| beta-ketoacyl-acyl carrier protein synthase II [Pseudomonas aeruginosa PA01] pir|T12022| 3-oxoacyl-[acyl-carrier-protein] synthase [EC 2.3.1.41] II - Pseudomonas aeruginosa gb|AAB94396.1| 3-oxoacyl-acyl carrier protein synthase II [Pseudomonas aeruginosa] gb|AAG06353.1| AE004722\_9 beta-ketoacyl-acyl carrier protein synthase II [Pseudomonas aeruginosa PA01] Length = 414
- 4806.4 Best-BlastP=> >nrprot 60% Identities = 127/330 (38%), Positives = 200/330 (60%), Gaps = 14/330 (4%) ref|NP\_819532.1| conserved hypothetical protein TIGR00247 [Coxiella burnetii RSA 493] Length = 370
- 4809.2 Best-BlastP=> >nrprot 46% Identities = 85/287 (29%), Positives = 130/287 (45%), Gaps = 15/287 (5%) ref|ZP\_00013543.1| hypothetical protein [Rhodospirillum rubrum] Length = 352
- 481.1 Best-BlastP=> >nrprot 57% Identities = 62/150 (41%), Positives = 88/150 (58%) ref|NP\_298766.1| conserved hypothetical protein [Xylella fastidiosa 9a5c] pir|H82676| conserved hypothetical protein XF1477 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF84286.1| AE003977\_9 conserved hypothetical protein [Xylella fastidiosa 9a5c] Length = 153
- 4810.1 Best-BlastP=> >nrprot No Hits found
- 4811.2 Best-BlastP=> >nrprot 67% Identities = 89/163 (54%), Positives = 110/163 (67%), Gaps = 1/163 (0%) ref|NP\_404518.1| putative membrane protein [Yersinia pestis] pir|AE0110| probable membrane protein YPO0899 [imported] - Yersinia pestis (strain CO92) emb|CAC89744.1| putative membrane protein [Yersinia pestis CO92] Length = 165
- 4813.2 Best-BlastP=> >nrprot 63% Identities = 161/389 (41%), Positives = 246/389 (63%), Gaps = 4/389 (1%) gb|AAD47247.1| putative transport protein [Legionella pneumophila] Length = 387
- 4814.2 Best-BlastP=> >nrprot 65% Identities = 101/199 (50%), Positives = 138/199 (69%), Gaps = 5/199 (2%) ref|NP\_820137.1| enhanced entry protein EnhA, putative [Coxiella burnetii RSA 493] gb|AAO90651.1| enhanced entry protein EnhA, putative [Coxiella burnetii RSA 493] Length = 248
- 4815.2 Best-BlastP=> >nrprot 59% Identities = 56/115 (48%), Positives = 82/115 (71%), Gaps = 1/115 (0%) ref|NP\_883806.1| flagellar protein FlIS [Bordetella parapertussis] emb|CAE36818.1| flagellar protein FlIS [Bordetella parapertussis] Length = 142
- 4817.4 Best-BlastP=> >nrprot No Hits found
- 4818.3 Best-BlastP=> >nrprot No Hits found

- 4819.2 Best-BlastP=> >nrprot 40% Identities = 70/290 (24%), Positives = 129/290 (44%), Gaps = 13/290 (4%) gb|AAF20289.1|AF121266\_11 malonyl-CoA:ACP transacylase MdcG [Acinetobacter calcoaceticus] Length = 307
- 482.2 Best-BlastP=> >nrprot 62% Identities = 257/538 (47%), Positives = 363/538 (67%), Gaps = 9/538 (1%) gb|AAM48100.1|AF353205\_1 poly-beta-hydroxybutyrate synthase [Azospirillum brasilense] Length = 618
- 4821.2 Best-BlastP=> >nrprot 44% Identities = 79/266 (29%), Positives = 125/266 (46%), Gaps = 34/266 (12%) ref|NP\_440042.1| alkaline phosphatase [Synechocystis sp. PCC 6803] pir|S74570 alkaline phosphatase (EC 3.1.3.1) phoA - Synechocystis sp. (strain PCC 6803) dbj|BAA16722.1| alkaline phosphatase [Synechocystis sp. PCC 6803] Length = 326
- 4822.3 Best-BlastP=> >nrprot 35% Identities = 73/276 (26%), Positives = 119/276 (43%), Gaps = 37/276 (13%) ref|ZP\_00123112.1| hypothetical protein [Haemophilus somnus 129PT] Length = 308
- 4826.2 Best-BlastP=> >nrprot 49% Identities = 64/203 (31%), Positives = 115/203 (56%), Gaps = 11/203 (5%) ref|NP\_819961.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90475.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 227
- 4830.2 Best-BlastP=> >nrprot 26% Identities = 39/135 (28%), Positives = 80/135 (59%) ref|ZP\_00060561.1| hypothetical protein [Clostridium thermocellum ATCC 27405] Length = 902
- 4833.2 Best-BlastP=> >nrprot 33% Identities = 44/162 (27%), Positives = 85/162 (52%), Gaps = 4/162 (2%) ref|NP\_149698.1| 235L [Invertebrate iridescent virus 6] gb|AAK82096.1|AF303741\_235 235L [Chilo iridescent virus] Length = 265
- 4834.4 Best-BlastP=> >nrprot No Hits found
- 4835.4
- Best-BlastP=> >nrprot 67% Identities = 101/174 (58%), Positives = 135/174 (77%) ref|ZP\_00126146.1| COG1187: 16S rRNA uridine-516 pseudouridylate synthase and related pseudouridylate synthases [Pseudomonas syringae pv. syringae B728a] Length = 210
- 4836.1 Best-BlastP=> >nrprot 48% Identities = 45/135 (33%), Positives = 79/135 (58%) ref|NP\_743096.1| rod shape-determining protein MreD [Pseudomonas putida KT2440] gb|AAN66560.1|AE016284\_8 rod shape-determining protein MreD [Pseudomonas putida KT2440] Length = 163
- 4837.1
- Best-BlastP=> >nrprot 63% Identities = 116/273 (42%), Positives = 178/273 (65%), Gaps = 3/273 (1%) ref|NP\_820453.1| rod shape-determining protein MreC [Coxiella burnetii RSA 493] gb|AAO90967.1| rod shape-determining protein MreC [Coxiella burnetii RSA 493] Length = 292
- 4841.2
- Best-BlastP=> >nrprot 92% Identities = 287/348 (82%), Positives = 320/348 (91%), Gaps = 3/348 (0%) ref|NP\_820454.1| rod shape-determining protein MreB [Coxiella burnetii RSA 493] gb|AAO90968.1| rod shape-determining protein MreB [Coxiella burnetii RSA 493] Length = 352
- 4844.2 Best-BlastP=> >nrprot No Hits found
- 4845.4 Best-BlastP=> >nrprot 22% Identities = 67/290 (23%), Positives = 129/290 (44%), Gaps = 34/290 (11%) ref|ZP\_00036809.1| COG0419: ATPase involved in DNA repair [Enterococcus faecium] Length = 1042
- 4847.2 Best-BlastP=> >nrprot No Hits found
- 4848.3 Best-BlastP=> >nrprot 52% Identities = 116/301 (38%), Positives = 178/301 (59%), Gaps = 1/301 (0%) ref|ZP\_00053871.1| COG0845: Membrane-fusion protein [Magnetospirillum magnetotacticum] Length = 335

- 485.3 Best-BlastP=> >nrprot 41% Identities = 106/439 (24%), Positives = 199/439 (45%), Gaps = 41/439 (9%) ref|NP\_932208.1| putative conjugative transfer protein TraB [Vibrio vulnificus YJ016] dbj|BAC97731.1| putative conjugative transfer protein TraB [Vibrio vulnificus YJ016] Length = 603
- 4850.2 Best-BlastP=> >nrprot No Hits found
- 4851.2 Best-BlastP=> >nrprot 67% Identities = 89/161 (55%), Positives = 109/161 (67%), Gaps = 2/161 (1%) ref|ZP\_00054128.1| COG3837: Uncharacterized conserved protein, contains double-stranded beta-helix domain [Magnetospirillum magnetotacticum] Length = 180
- 4855.2 Best-BlastP=> >nrprot 80% Identities = 67/91 (73%), Positives = 79/91 (86%) ref|NP\_717690.1| integration host factor, alpha subunit [Shewanella oneidensis MR-1] gb|AAN55134.1|AE015650\_4 integration host factor, alpha subunit [Shewanella oneidensis MR-1] Length = 98
- 4856.2 Best-BlastP=> >nrprot 67% Identities = 51/100 (51%), Positives = 72/100 (72%) ref|NP\_841896.1| putative ferredoxin 2fe-2s protein [Nitrosomonas europaea ATCC 19718] emb|CAD85785.1| putative ferredoxin 2fe-2s protein [Nitrosomonas europaea ATCC 19718] Length = 102
- 4859.2 Best-BlastP=> >nrprot No Hits found
- 486.2 Best-BlastP=> >nrprot No Hits found
- 4860.1 Best-BlastP=> >nrprot No Hits found
- 4863.4 Best-BlastP=> >nrprot 69% Identities = 220/430 (51%), Positives = 294/430 (68%), Gaps = 13/430 (3%) ref|NP\_406861.1| poly(A) polymerase [Yersinia pestis] pir|A10412 polynucleotide adenylyltransferase (EC 2.7.7.19) [imported] - Yersinia pestis (strain CO92) emb|CAC92629.1| poly(A) polymerase [Yersinia pestis CO92] Length = 440
- 4864.2 Best-BlastP=> >nrprot 66% Identities = 62/131 (47%), Positives = 88/131 (67%) ref|NP\_735626.1| Unknown [Streptococcus agalactiae NEM316] emb|CAD46839.1| Unknown [Streptococcus agalactiae NEM316] Length = 162
- 4865.2 Best-BlastP=> >nrprot 58% Identities = 48/146 (32%), Positives = 83/146 (56%), Gaps = 12/146 (8%) ref|NP\_841101.1| Universal stress protein (Usp) [Nitrosomonas europaea ATCC 19718] emb|CAD84939.1| Universal stress protein (Usp) [Nitrosomonas europaea ATCC 19718] Length = 148
- 4867.2 Best-BlastP=> >nrprot 62% Identities = 209/445 (46%), Positives = 293/445 (65%), Gaps = 3/445 (0%) ref|ZP\_00025176.1| COG1012: NAD-dependent aldehyde dehydrogenases [Ralstonia metallidurans] Length = 520
- 4868.2 Best-BlastP=> >nrprot 72% Identities = 155/269 (57%), Positives = 197/269 (73%), Gaps = 1/269 (0%) pir|T34105 hypothetical protein C17G10.8 - Caenorhabditis elegans Length = 938
- 4869.3 Best-BlastP=> >nrprot 75% Identities = 90/139 (64%), Positives = 108/139 (77%) ref|NP\_540374.1| RIBONUCLEASE HI [Brucella melitensis] ref|NP\_697505.1| ribonuclease H [Brucella suis 1330] sp|Q8YFR3|RNH\_BRUME Ribonuclease H (RNase H) pir|AC3434 calf thymus ribonuclease H (EC 3.1.26.4) [imported] - Brucella melitensis (strain 16M) gb|AAL52638.1| RIBONUCLEASE HI [Brucella melitensis 16M] gb|AAN29420.1|AE014357\_5 ribonuclease H [Brucella suis 1330] Length = 154
- 4872.3 Best-BlastP=> >nrprot 98% Identities = 511/520 (98%), Positives = 515/520 (99%) gb|AAM00608.1| unknown [Legionella pneumophila] Length = 520
- 4873.3 Best-BlastP=> >nrprot 99% Identities = 383/387 (98%), Positives = 385/387 (99%) gb|AAM00609.1| unknown [Legionella pneumophila] Length = 388

- 4874.2 Best-BlastP=> >nrprot 41% Identities = 108/445 (24%), Positives = 193/445 (43%), Gaps = 79/445 (17%) ref|NP\_621958.1| ATPase involved in DNA repair [Thermoanaerobacter tengcongensis] gb|AAM23562.1| ATPase involved in DNA repair [Thermoanaerobacter tengcongensis]  
Length = 1177
- 4875.1 Best-BlastP=> >nrprot 69% Identities = 73/119 (61%), Positives = 91/119 (76%), Gaps = 6/119 (5%) ref|ZP\_00033092.1| COG0316: Uncharacterized conserved protein [Burkholderia fungorum] Length = 121
- 4877.2 Best-BlastP=> >nrprot 74% Identities = 202/356 (56%), Positives = 269/356 (75%), Gaps = 1/356 (0%) ref|NP\_746144.1| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Pseudomonas putida KT2440] gb|AAN69608.1|AE016594\_5 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Pseudomonas putida KT2440] Length = 374
- 4878.2 Best-BlastP=> >nrprot 54% Identities = 161/418 (38%), Positives = 242/418 (57%), Gaps = 6/418 (1%) ref|ZP\_00086772.1| COG0739: Membrane proteins related to metalloendopeptidases [Pseudomonas fluorescens PfO-1] Length = 471
- 488.2 Best-BlastP=> >nrprot 75% Identities = 181/298 (60%), Positives = 230/298 (77%) ref|ZP\_00068320.1| COG1131: ABC-type multidrug transport system, ATPase component [Microbulbifer degradans 2-40] Length = 318
- 4880.2. Best-BlastP=> >nrprot 49% Identities = 92/270 (34%), Positives = 136/270 (50%), Gaps = 9/270 (3%) ref|NP\_085189.1| IS10 orf [Shigella flexneri] ref|NP\_858160.1| hypothetical protein [Shigella flexneri 2a] gb|AAK18345.1|AF348706\_34 IS10 orf [Shigella flexneri] gb|AAL72480.1| hypothetical protein [Shigella flexneri 2a] Length = 407
- 4881.4 Best-BlastP=> >nrprot 11% Identities = 72/284 (25%), Positives = 121/284 (42%), Gaps = 19/284 (6%) ref|ZP\_00112010.1| hypothetical protein [Nostoc punctiforme] Length = 427
- 4883.2
- 4884.1 Best-BlastP=> >nrprot 50% Identities = 45/105 (42%), Positives = 67/105 (63%), Gaps = 1/105 (0%) ref|NP\_819268.1| preprotein translocase, SecE subunit [Coxiella burnetii RSA 493] gb|AAO89782.1| preprotein translocase, SecE subunit [Coxiella burnetii RSA 493] Length = 127
- Best-BlastP=> >nrprot 80% Identities = 125/175 (71%), Positives = 148/175 (84%) ref|ZP\_00123792.1| COG0250: Transcription antiterminator [Pseudomonas syringae pv. syringae B728a] ref|NP\_790461.1| transcription antitermination protein NusG [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54156.1| transcription antitermination protein NusG [Pseudomonas syringae pv. tomato str. DC3000] Length = 177
- 4885.2 Best-BlastP=> >nrprot 87% Identities = 112/143 (78%), Positives = 127/143 (88%) ref|NP\_282996.1| 50S ribosomal protein L11 [Neisseria meningitidis Z2491] pir|H82007 50S ribosomal protein L11 NMA0146 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB83461.1| 50S ribosomal protein L11 [Neisseria meningitidis Z2491] Length = 144
- 4887.3 Best-BlastP=> >nrprot 57% Identities = 72/176 (40%), Positives = 102/176 (57%), Gaps = 6/176 (3%) ref|NP\_419908.1| acetyltransferase, GNAT family [Caulobacter crescentus CB15] pir|H87384 acetyltransferase, GNAT family [imported] - Caulobacter crescentus gb|AAK23076.1| acetyltransferase, GNAT family [Caulobacter crescentus CB15] Length = 181
- 4888.1 Best-BlastP=> >nrprot 59% Identities = 63/151 (41%), Positives = 103/151 (68%) emb|CAD31280.1| PUTATIVE TRANSCRIPTION REGULATOR PROTEIN [Mesorhizobium loti] Length = 151
- 4889.1 Best-BlastP=> >nrprot 49% Identities = 44/120 (36%), Positives = 66/120 (55%), Gaps = 3/120 (2%) ref|NP\_819252.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO89766.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 130
- 489.1 Best-BlastP=> >nrprot No Hits found



- 4891.2 Best-BlastP=> >nrprot 26% Identities = 39/138 (28%), Positives = 67/138 (48%), Gaps = 19/138 (13%) pir|A59234 slow myosin heavy chain 3 - quail gb|AAC59911.1| slow myosin heavy chain 3 gb|AAC59912.1| slow myosin heavy chain 3 Length = 1931
- 4894.1 Best-BlastP=> >nrprot 69% Identities = 52/121 (42%), Positives = 81/121 (66%), Gaps = 7/121 (5%) ref|NP\_746309.1| succinate dehydrogenase, hydrophobic membrane anchor protein [Pseudomonas putida KT2440] gb|AAN69773.1|AE016613\_8 succinate dehydrogenase, hydrophobic membrane anchor protein [Pseudomonas putida KT2440] Length = 122
- 4895.1 Best-BlastP=> >nrprot 69% Identities = 60/124 (48%), Positives = 87/124 (70%) ref|NP\_250272.1| succinate dehydrogenase (C subunit) [Pseudomonas aeruginosa PA01] pir|C83448 succinate dehydrogenase (C subunit) PA1581 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG04970.1|AE004586\_8 succinate dehydrogenase (C subunit) [Pseudomonas aeruginosa PA01] Length = 128
- 4897.2 Best-BlastP=> >nrprot 47% Identities = 103/370 (27%), Positives = 179/370 (48%), Gaps = 22/370 (5%) ref|NP\_761717.1| Predicted signal transduction protein [Vibrio vulnificus CMCP6] gb|AAO11244.1|AE016806\_234 Predicted signal transduction protein [Vibrio vulnificus CMCP6] Length = 404
- 4900.3 Best-BlastP=> >nrprot 41% Identities = 205/972 (21%), Positives = 412/972 (42%), Gaps = 110/972 (11%) ref|NP\_245295.1| unknown [Pasteurella multocida] gb|AAK02442.1| unknown [Pasteurella multocida] Length = 1113
- 4901.3 Best-BlastP=> >nrprot 76% Identities = 357/592 (60%), Positives = 454/592 (76%), Gaps = 1/592 (0%) ref|NP\_842254.1| aspartyl-tRNA synthetase [Nitrosomonas europaea ATCC 19718] emb|CAD86164.1| aspartyl-tRNA synthetase [Nitrosomonas europaea ATCC 19718] Length = 593
- 4902.1 Best-BlastP=> >nrprot 25% Identities = 23/43 (53%), Positives = 28/43 (65%) ref|NP\_275122.1| hypothetical protein [Neisseria meningitidis MC58] pir|G81001 hypothetical protein NMB2137 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF42445.1| hypothetical protein [Neisseria meningitidis MC58] Length = 70
- 4907.2 Best-BlastP=> >nrprot 72% Identities = 134/257 (52%), Positives = 186/257 (72%), Gaps = 9/257 (3%) ref|ZP\_00067917.1| COG1054: Predicted sulfurtransferase [Microbulifer degradans 2-40] Length = 309
- 4908.3 Best-BlastP=> >nrprot 58% Identities = 715/1981 (36%), Positives = 1108/1981 (55%), Gaps = 111/1981 (5%) ref|NP\_406102.1| putative membrane protein [Yersinia pestis] ref|NP\_668470.1| conserved hypothetical protein [Yersinia pestis KIM] sp|Q8ZDJ2|YP73\_YERPE Hypothetical UPF0192 protein YP02573/Y1143 precursor pir|AC0314 probable membrane protein YPO2573 [imported] - Yersinia pestis (strain CO92) emb|CAC91375.1| putative membrane protein [Yersinia pestis CO92] gb|AAM84721.1|AE013717\_3 conserved hypothetical protein [Yersinia pestis KIM] Length = 2004
- 491.1 Best-BlastP=> >nrprot 34% Identities = 62/271 (22%), Positives = 116/271 (42%), Gaps = 20/271 (7%) sp|O60610|DIA1\_HUMAN Diaphanous protein homolog 1 (Diaphanous-related formin 1) (DRF1) gb|AAC05373.1| diaphanous 1 [Homo sapiens] Length = 1248
- 4913.2 Best-BlastP=> >nrprot No Hits found
- 4914.2 Best-BlastP=> >nrprot No Hits found
- 4916.2 Best-BlastP=> >nrprot 30% Identities = 53/186 (28%), Positives = 93/186 (50%), Gaps = 11/186 (5%) ref|NP\_179611.1| leucine rich repeat protein family [Arabidopsis thaliana] pir|D84586 hypothetical protein At2g20210 [imported] - Arabidopsis thaliana gb|AAD21766.1| hypothetical protein [Arabidopsis thaliana] Length = 271
- 4917.2 Best-BlastP=> >nrprot No Hits found

- 4918.2 Best-Blast[P=> >nrprot 17% Identities = 31/114 (27%), Positives = 52/114 (45%), Gaps = 4/114 (3%) ref|NP\_281741.1| putative integral membrane protein [Campylobacter jejuni] pir|E81402 probable integral membrane protein Cj0557c [imported] - Campylobacter jejuni (strain NCTC 11168) emb|CAB75193.1| putative integral membrane protein [Campylobacter jejuni subsp. jejuni NCTC 11168] Length = 361
- 4919.1 Best-Blast[P=> >nrprot 44% Identities = 109/421 (25%), Positives = 192/421 (45%), Gaps = 24/421 (5%) ref|NP\_900103.1| outer membrane efflux protein [Chromobacterium violaceum ATCC 12472] gb|AAQ58111.1| outer membrane efflux protein [Chromobacterium violaceum ATCC 12472] Length = 466
- 492.4 Best-Blast[P=> >nrprot 59% Identities = 48/101 (47%), Positives = 70/101 (69%), Gaps = 1/101 (0%) ref|NP\_761137.1| SM-20-related protein [Vibrio vulnificus CMCP6] gb|AAO10664.1|AE016804\_174 SM-20-related protein [Vibrio vulnificus CMCP6] dbj|BAC94823.1| SM-20-related protein [Vibrio vulnificus YJ016] Length = 200
- 4920.4 Best-Blast[P=> >nrprot 56% Identities = 88/284 (30%), Positives = 143/284 (50%), Gaps = 38/284 (13%) ref|NP\_791175.1| sensory box/GGDEF domain/EAL domain protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54870.1| sensory box/GGDEF domain/EAL domain protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 763
- 4923.2 Best-Blast[P=> >nrprot 79% Identities = 433/634 (68%), Positives = 507/634 (79%) ref|ZP\_00066531.1| COG0441: Threonyl-tRNA synthetase [Microbulifer degradans 2-40] Length = 636
- 4927.1 Best-Blast[P=> >nrprot No Hits found
- 4929.2 Best-Blast[P=> >nrprot 72% Identities = 164/298 (55%), Positives = 223/298 (74%), Gaps = 2/298 (0%) ref|NP\_622015.1| uncharacterized enzyme involved in pigment biosynthesis [Thermoanaerobacter tengcongensis] gb|AAM23619.1| uncharacterized enzyme involved in pigment biosynthesis [Thermoanaerobacter tengcongensis] Length = 307
- 493.4 Best-Blast[P=> >nrprot 55% Identities = 83/216 (38%), Positives = 131/216 (60%) ref|NP\_634315.1| Zinc metalloprotease [Methanosarcina mazei Goe1] gb|AAM31987.1| Zinc metalloprotease [Methanosarcina mazei Goe1] Length = 238
- 4930.2 Best-Blast[P=> >nrprot 78% Identities = 51/90 (56%), Positives = 71/90 (78%) ref|NP\_819953.1| conserved hypothetical protein [Coxiella burnetii RSA 493] sp|Q83D06|Y941\_COXBU Hypothetical UPF0269 protein CBU0941 gb|AAO90467.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 90
- 4934.3 Best-Blast[P=> >nrprot 26% Identities = 59/198 (29%), Positives = 101/198 (51%), Gaps = 27/198 (13%) ref|NP\_628263.1| possible secreted peptidase [Streptomyces coelicolor A3(2)] emb|CAB56362.1| possible secreted peptidase [Streptomyces coelicolor A3(2)] Length = 279
- 4935.2 Best-Blast[P=> >nrprot 63% Identities = 168/345 (48%), Positives = 225/345 (65%) ref|NP\_216774.1| hypothetical protein Rv2258c [Mycobacterium tuberculosis H37Rv] ref|NP\_336787.1| methyltransferase-related protein [Mycobacterium tuberculosis CDC1551] ref|NP\_855931.1| Possible transcriptional regulatory protein [Mycobacterium bovis subsp. bovis AF2122/97] pir|F70862 probable helix-turn helix motif at aa 47-68 - Mycobacterium tuberculosis (strain H37RV) emb|CAA17295.1| hypothetical protein Rv2258c [Mycobacterium tuberculosis H37Rv] gb|AAK46601.1| methyltransferase-related protein [Mycobacterium tuberculosis CDC1551] emb|CAD97135.1| Possible transcriptional regulatory protein [Mycobacterium bovis subsp. bovis AF2122/97] Length = 353

- 494.2 Best-BlastP=> >nrprot 75% Identities = 160/283 (56%), Positives = 212/283 (74%), Gaps = 5/283 (1%) ref|NP\_518195.1| PROBABLE METALLOPROTEASE ZINC TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] sp|Q8Y3A6|HTPX\_RALSO Probable protease htpX homolog emb|CAD13602.1| PROBABLE METALLOPROTEASE ZINC TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 286
- 4941.2 Best-BlastP=> >nrprot No Hits found
- 4942.1 Best-BlastP=> >nrprot No Hits found
- 4943.2 Best-BlastP=> >nrprot No Hits found
- 4945.2 Best-BlastP=> >nrprot 79% Identities = 214/340 (62%), Positives = 268/340 (78%), Gaps = 11/340 (3%) ref|NP\_052843.1| hypothetical protein [Coxiella burnetii] ref|NP\_819053.1| repB protein, putative [Coxiella burnetii] RSA 493| pir|S52723| qsopB protein - Coxiella burnetii plasmid QpH1 gb|AAA69865.1| qsopB gene product emb|CAA59788.1| orf 334 [Coxiella burnetii] emb|CAA75818.1| hypothetical protein [Coxiella burnetii] gb|AAD33475.1|AF131076\_1 hypothetical protein [Coxiella burnetii] gb|AAO91613.1| repB protein, putative [Coxiella burnetii] RSA 493| prf|2117254B trans-acting factor Length = 334
- 4947.2 Best-BlastP=> >nrprot 93% Identities = 340/402 (84%), Positives = 377/402 (93%) ref|NP\_052336.1| unnamed protein product [Coxiella burnetii] ref|NP\_052844.1| hypothetical protein [Coxiella burnetii] ref|NP\_819052.1| parA protein, putative [Coxiella burnetii] RSA 493| pir|S68866| qsopA protein - Coxiella burnetii plasmid QpH1 emb|CAA53106.1| unnamed protein product [Coxiella burnetii] gb|AAA69864.1| qsopA gene product emb|CAA59789.1| orf 406 [Coxiella burnetii] emb|CAA75819.1| putative SopA protein (protein a) [Coxiella burnetii] gb|AAD33476.1|AF131076\_2 hypothetical protein [Coxiella burnetii] gb|AAO91612.1| parA protein, putative [Coxiella burnetii] RSA 493| prf|2117254A trans-acting factor Length = 406
- 4948.4 Best-BlastP=> >nrprot No Hits found
- 4951.2 Best-BlastP=> >nrprot 24% Identities = 25/79 (31%), Positives = 40/79 (50%), Gaps = 4/79 (5%) ref|ZP\_00103190.1| COG1396: Predicted transcriptional regulators [Desulfotobacterium hafniense] Length = 123
- 4952.1 Best-BlastP=> >nrprot No Hits found
- 4954.2 Best-BlastP=> >nrprot 53% Identities = 62/155 (40%), Positives = 92/155 (59%) ref|NP\_746668.1| polypeptide deformylase [Pseudomonas putida KT2440] sp|Q88EA7|DEF2\_PSEPK Peptide deformylase 2 (PDF 2) (Polypeptide deformylase 2) gb|AAN70132.1|AE016653\_3: polypeptide deformylase [Pseudomonas putida KT2440] Length = 178
- 4955.4 Best-BlastP=> >nrprot 50% Identities = 132/417 (31%), Positives = 218/417 (52%), Gaps = 9/417 (2%) ref|NP\_221200.1| PROLINE/BETAINE TRANSPORTER (proP6) [Rickettsia prowazekii] pir|D71647| proline/betaine transporter (proP6) RP852 - Rickettsia prowazekii emb|CAA15276.1| PROLINE/BETAINE TRANSPORTER (proP6) [Rickettsia prowazekii] Length = 415
- 4957.2 Best-BlastP=> >nrprot 62% Identities = 53/108 (49%), Positives = 74/108 (68%), Gaps = 3/108 (2%) ref|NP\_251650.1| type 4 fimbrial biogenesis protein PilZ [Pseudomonas aeruginosa PA01] pir|B59241| type 4 fimbriae biogenesis protein [imported] - Pseudomonas aeruginosa gb|AA93519.1| involved in biogenesis of type 4 fimbriae gb|AAG06348.1|AE004722\_4 type 4 fimbrial biogenesis protein PilZ [Pseudomonas aeruginosa PA01] Length = 118
- 4958.3 Best-BlastP=> >nrprot 47% Identities = 90/313 (28%), Positives = 142/313 (45%), Gaps = 20/313 (6%) ref|NP\_819534.1| DNA polymerase III, delta prime subunit [Coxiella burnetii] RSA 493| gb|AAO90048.1| DNA polymerase III, delta prime subunit [Coxiella burnetii] RSA 493| Length = 319
- 496.1 Best-BlastP=> >nrprot No Hits found

- 4960.2 Best-BlastP=> >nrprot No Hits found
- 4961.1 Best-BlastP=> >nrprot 77% Identities = 70/127 (55%), Positives = 99/127 (77%), Gaps = 4/127 (3%) ref|NP\_391517.1| similar to large conductance mechanosensitive channel protein [Bacillus subtilis] sp|P94585|MSEL\_BACSU Large-conductance mechanosensitive channel pir|E70065 large conductance mechanosensitive channel homolog ywpC - Bacillus subtilis emb|CAB05944.1| ywpC [Bacillus subtilis] emb|CAB15653.1| large conductance mechanosensitive channel protein [Bacillus subtilis subsp. subtilis str. 168] Length = 130
- 4962.2 Best-BlastP=> >nrprot No Hits found
- 4965.2 Best-BlastP=> >nrprot 61% Identities = 99/105 (94%), Positives = 102/105 (97%) emb|CAB65201.1| hypothetical protein [Legionella pneumophila] Length = 356
- 4966.2 Best-BlastP=> >nrprot 98% Identities = 586/598 (97%), Positives = 590/598 (98%) emb|CAB65200.1| hypothetical protein [Legionella pneumophila] Length = 598
- 4968.2
- Best-BlastP=> >nrprot 63% Identities = 60/128 (46%), Positives = 83/128 (64%) ref|NP\_439721.1| alanine racemase biosynthetic [Haemophilus influenzae Rd] sp|P45257|ALR\_HAEIN Alanine racemase pir|E64130 alanine racemase (EC 5.1.1.1), biosynthetic - Haemophilus influenzae (strain Rd KW20) gb|AAC23218.1| alanine racemase, biosynthetic (air) [Haemophilus influenzae Rd] Length = 360
- 4969.3
- Best-BlastP=> >nrprot 81% Identities = 117/163 (71%), Positives = 141/163 (86%), Gaps = 1/163 (0%) ref|NP\_719448.1| replicative DNA helicase [Shewanella oneidensis MR-1] gb|AAN56892.1| AE015824\_3 replicative DNA helicase [Shewanella oneidensis MR-1] Length = 468
- 497.1 Best-BlastP=> >nrprot No Hits found
- 4972.3 Best-BlastP=> >nrprot 68% Identities = 111/195 (56%), Positives = 146/195 (74%) ref|ZP\_00091033.1| COG0305: Replicative DNA helicase [Azotobacter vinelandii] Length = 463
- 4974.1 Best-BlastP=> >nrprot 40% Identities = 43/138 (31%), Positives = 71/138 (51%), Gaps = 6/138 (4%) pir|T18332 icmL protein - Legionella pneumophila gb|AAC38190.1| DotL [Legionella pneumophila] emb|CAA75329.1| icmL protein [Legionella pneumophila] emb|CAD43145.1| DotL protein [Legionella pneumophila serogroup 6] Length = 212
- 4977.3 Best-BlastP=> >nrprot No Hits found
- 4979.1 Best-BlastP=> >nrprot 71% Identities = 115/192 (59%), Positives = 144/192 (75%) ref|NP\_246450.1| unknown [Pasteurella multocida] sp|P57947|ENGB\_PASMU Probable GTP-binding protein engB gb|AAK03595.1| unknown [Pasteurella multocida] Length = 205
- 498.4 Best-BlastP=> >nrprot 37% Identities = 78/305 (25%), Positives = 125/305 (40%), Gaps = 56/305 (18%) ref|NP\_421401.1| amine oxidase, flavin-containing [Caulobacter crescentus CB15] pir|E87571 amine oxidase, flavin-containing [imported] - Caulobacter crescentus gb|AAK24569.1| amine oxidase, flavin-containing [Caulobacter crescentus CB15] Length = 454
- 4980.3 Best-BlastP=> >nrprot 69% Identities = 102/206 (49%), Positives = 139/206 (67%), Gaps = 7/206 (3%) ref|NP\_759874.1| Cytochrome c4 [Vibrio vulnificus CMCP6] gb|AAO09401.1| AE016800\_6 Cytochrome c4 [Vibrio vulnificus CMCP6] Length = 205
- 4984.2 Best-BlastP=> >nrprot 73% Identities = 109/166 (65%), Positives = 126/166 (75%), Gaps = 1/166 (0%) gb|AAO38281.1| Lfe115p1 [Leptospirillum ferrooxidans] Length = 178

- 4987.2 Best-BlastP=> >nrprot 77% Identities = 274/490 (55%), Positives = 360/490 (73%), Gaps = 28/490 (5%) ref|NP\_457051.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi] ref|NP\_804211.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] sp|Q8Z4P6|ENGA\_SALT1 Probable GTP-binding protein engA pir|AF0821 probable GTP-binding protein STY2764 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) emb|CAD02722.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO68060.1| putative GTP-binding protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 490
- 499.2 Best-BlastP=> >nrprot 51% Identities = 129/343 (37%), Positives = 196/343 (57%), Gaps = 10/343 (2%) ref|ZP\_00106589.1| COG1680: Beta-lactamase class C and other penicillin binding proteins [Nostoc punctiforme] Length = 393
- 4990.3 Best-BlastP=> >nrprot No Hits found
- 4992.2 Best-BlastP=> >nrprot No Hits found
- 4993.2 Best-BlastP=> >nrprot 36% Identities = 44/89 (49%), Positives = 63/89 (70%) ref|ZP\_00102874.1| hypothetical protein [Desulfotobacterium hafniense] Length = 106
- 4995.1 Best-BlastP=> >nrprot 33% Identities = 42/179 (23%), Positives = 73/179 (40%), Gaps = 36/179 (20%) ref|NP\_229450.1| alpha-amylase, putative [Thermotoga maritima] pir|G7227 hypothetical protein TM1650 - Thermotoga maritima (strain MSB8) gb|AAD36717.1|AE001807\_8 alpha-amylase, putative [Thermotoga maritima] Length = 422
- 4998.2 Best-BlastP=> >nrprot 16% Identities = 47/200 (23%), Positives = 87/200 (43%), Gaps = 16/200 (8%) ref|NP\_036450.1| leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] gb|AAD13138.1| leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] gb|AAH14500.1| Leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] gb|AAH21208.1| Leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens] Length = 739
- 4999.2 Best-BlastP=> >nrprot 77% Identities = 157/241 (65%), Positives = 197/241 (81%), Gaps = 4/241 (1%) ref|NP\_252346.1| 30S ribosomal protein S2 [Pseudomonas aeruginosa PAO1] sp|O82850|RS2\_PSEAE 30S ribosomal protein S2 pir|C83189 30S ribosomal protein S2 PA3656 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07044.1|AE004785\_8 30S ribosomal protein S2 [Pseudomonas aeruginosa PAO1] Length = 246
- 50.1 Best-BlastP=> >nrprot 84% Identities = 76/92 (82%), Positives = 80/92 (86%) emb|CAB60051.1| lvhB2 [Legionella pneumophila] gb|AAM08238.1| putative pilin subunit [Legionella pneumophila] Length = 96
- 500.2 Best-BlastP=> >nrprot 97% Identities = 341/352 (96%), Positives = 346/352 (98%) gb|AAG59860.1|AF299349\_1 major acid phosphatase [Legionella pneumophila] Length = 352
- 5000.3 Best-BlastP=> >nrprot 97% Identities = 131/136 (96%), Positives = 134/136 (98%) emb|CAB09802.1| 16 kD immunogenic protein [Legionella pneumophila] Length = 136
- 5001.1 Best-BlastP=> >nrprot No Hits found
- 5003.2 Best-BlastP=> >nrprot No Hits found
- 5005.3 Best-BlastP=> >nrprot 99% Identities = 454/455 (99%), Positives = 455/455 (100%) gb|AAQ18124.1| CpxA [Legionella pneumophila] Length = 455
- 501.2 Best-BlastP=> >nrprot 30% Identities = 40/167 (23%), Positives = 75/167 (44%), Gaps = 13/167 (7%) dbj|BAC45194.1| kinesin-like protein [Oryza sativa (japonica cultivar-group)] Length = 1967

- 5010.2 Best-BlastP=> >nrprot 18% Identities = 34/117 (29%), Positives = 54/117 (46%), Gaps = 12/117 (10%) emb|CAD90592.1| C3L protein [Cowpox virus] Length = 833
- 5015.2 Best-BlastP=> >nrprot 58% Identities = 43/110 (39%), Positives = 66/110 (60%), Gaps = 3/110 (2%) ref|ZP\_00056081.1| hypothetical protein [Magnetospirillum magnetotacticum] Length = 164
- 5018.2 Best-BlastP=> >nrprot No Hits found
- 5019.1 Best-BlastP=> >nrprot 61% Identities = 87/190 (45%), Positives = 125/190 (65%) gb|AAG10504.1|AF279106\_66 predicted YacE family of P-loop kinases [uncultured marine gamma proteobacterium EBAC31A08] Length = 197
- 502.3 Best-BlastP=> >nrprot No Hits found
- 5021.3 Best-BlastP=> >nrprot 48% Identities = 64/247 (25%), Positives = 120/247 (48%), Gaps = 8/247 (3%) ref|NP\_903494.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 252
- 5022.2 Best-BlastP=> >nrprot 58% Identities = 124/336 (36%), Positives = 204/336 (60%), Gaps = 5/336 (1%) ref|NP\_742592.1| membrane protein, putative [Pseudomonas putida KT2440] gb|AAN66056.1|AE016234\_9 membrane protein, putative [Pseudomonas putida KT2440] Length = 346
- 5026.1 Best-BlastP=> >nrprot 77% Identities = 49/89 (55%), Positives = 70/89 (78%) ref|NP\_250138.1| flagellar biosynthetic protein FliQ [Pseudomonas aeruginosa PA01] ref|ZP\_00139064.1| COG1987: Flagellar biosynthesis pathway, component FliQ [Pseudomonas aeruginosa UCBPP-PA14] pir|A83465 flagellar biosynthetic protein FliQ PA1447 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04836.1|AE004574\_7 flagellar biosynthetic protein FliQ [Pseudomonas aeruginosa PAO1] Length = 89
- 5028.2 Best-BlastP=> >nrprot 70% Identities = 270/528 (51%), Positives = 367/528 (69%), Gaps = 5/528 (0%) ref|NP\_820198.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90712.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 550
- 503.3 Best-BlastP=> >nrprot 55% Identities = 162/399 (40%), Positives = 247/399 (61%), Gaps = 3/399 (0%) ref|ZP\_00065233.1| COG0741: Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) [Microbulbifer degradans 2-40] Length = 543
- 5030.2 Best-BlastP=> >nrprot 84% Identities = 225/326 (69%), Positives = 276/326 (84%) ref|NP\_820836.1| peptide ABC transporter, permease protein [Coxiella burnetii RSA 493] gb|AAO91350.1| peptide ABC transporter, permease protein [Coxiella burnetii RSA 493] Length = 327
- 5031.2 Best-BlastP=> >nrprot 40% Identities = 42/173 (24%), Positives = 75/173 (43%), Gaps = 12/173 (6%) ref|NP\_542876.1| hypothetical protein [Pseudomonas putida] emb|CAC86816.1| hypothetical protein [Pseudomonas putida] Length = 267
- 5032.1 Best-BlastP=> >nrprot No Hits found
- 5033.1 Best-BlastP=> >nrprot No Hits found
- 5037.1 Best-BlastP=> >nrprot 84% Identities = 35/43 (81%), Positives = 38/43 (88%) ref|NP\_300059.1| 50S ribosomal protein L34 [Xylella fastidiosa 9a5c] ref|NP\_780293.1| 50S ribosomal protein L34 [Xylella fastidiosa Temecula1] sp|Q9P9T9|RL34\_XYLFA 50S ribosomal protein L34 pir|B82517 50S ribosomal protein L34 XF2782 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF85567.1|AE004083\_6 50S ribosomal protein L34 [Xylella fastidiosa 9a5c] gb|AAO29942.1| 50S ribosomal protein L34 [Xylella fastidiosa Temecula1] Length = 46

- 5038.1 Best-BlastP=> >nrprot 57% Identities = 45/107 (42%), Positives = 66/107 (61%), Gaps = 2/107 (1%) ref|NP\_290337.1| RNase P, protein component; protein C5; processes tRNA, 4.5S RNA [Escherichia coli O157:H7 EDL933] ref|NP\_312666.1| ribonuclease P protein component [Escherichia coli O157:H7] sp|Q8XB43|RNPA\_ECO57 Ribonuclease P protein component (RNaseP protein) (RNase P protein) (Protein C5) pir|G91208 ribonuclease P protein component [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir|A86055 hypothetical protein mpaA [imported] - Escherichia coli (strain O157:H7, substrain EDL933) gb|AAG58901.1|AE005601\_7 RNase P, protein component; protein C5; processes tRNA, 4.5S RNA [Escherichia coli O157:H7 EDL933] dbj|BAB38062.1| ribonuclease P protein component [Escherichia coli O157:H7] Length = 119
- 5039.2 Best-BlastP=> >nrprot 62% Identities = 38/68 (55%), Positives = 51/68 (75%) ref|ZP\_00134326.1| COG0759: Uncharacterized conserved protein [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 100
- 5040.2 Best-BlastP=> >nrprot 68% Identities = 268/565 (47%), Positives = 381/565 (67%), Gaps = 23/565 (4%) ref|NP\_820897.1| inner-membrane protein, 60kDa [Coxiella burnetii RSA 493] sp|P45650|60IM\_COXBU 60 kDa inner-membrane protein homolog gb|AAO91411.1| inner-membrane protein, 60kDa [Coxiella burnetii RSA 493] Length = 566
- 5041.2 Best-BlastP=> >nrprot 98% Identities = 176/178 (98%), Positives = 176/178 (98%) sp|O34955|PYR\_LEGPN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) gb|AAB84257.1| inorganic pyrophosphatase [Legionella pneumophila] gb|AAC02428.1| inorganic pyrophosphatase [Legionella pneumophila] Length = 178
- 5042.1 Best-BlastP=> >nrprot No Hits found
- 5043.3 Best-BlastP=> >nrprot 70% Identities = 210/415 (50%), Positives = 298/415 (71%), Gaps = 2/415 (0%) ref|NP\_760503.1| Putative Mg2+ and Co2+ transporter CorB [Vibrio vulnificus CMCP6] gb|AAO10030.1|AE016802\_73 Putative Mg2+ and Co2+ transporter CorB [Vibrio vulnificus CMCP6] Length = 425
- 5044.2 Best-BlastP=> >nrprot 73% Identities = 166/299 (55%), Positives = 217/299 (72%), Gaps = 13/299 (4%) ref|NP\_763465.1| Conserved hypothetical protein [Vibrio vulnificus CMCP6] gb|AAO08455.1|AE016813\_207 Conserved hypothetical protein [Vibrio vulnificus CMCP6] Length = 304
- 5046.2 Best-BlastP=> >nrprot 53% Identities = 45/118 (38%), Positives = 73/118 (61%), Gaps = 5/118 (4%) ref|XP\_132330.1| RIKEN cDNA 2810006K23 [Mus musculus] gb|AAH46909.1| Similar to RIKEN cDNA 2810006K23 gene [Mus musculus] Length = 184
- 5047.3 Best-BlastP=> >nrprot 41% Identities = 43/167 (25%), Positives = 80/167 (47%), Gaps = 6/167 (3%) ref|ZP\_00067126.1| COG3009: Uncharacterized protein conserved in bacteria [Microbulifer degradans 2-40] Length = 217
- 505.3 Best-BlastP=> >nrprot No Hits found
- 5050.2 Best-BlastP=> >nrprot 99% Identities = 241/243 (99%), Positives = 242/243 (99%) emb|CAD90952.1| LssA protein [Legionella pneumophila] Length = 243
- 5052.4 Best-BlastP=> >nrprot 97% Identities = 194/201 (96%), Positives = 197/201 (98%) emb|CAD90953.1| LssZ protein [Legionella pneumophila] Length = 204
- 5054.2 Best-BlastP=> >nrprot 33% Identities = 77/161 (47%), Positives = 108/161 (67%) ref|NP\_390248.1| yqkA [Bacillus subtilis] sp|P54564|YQKA\_BACSU Hypothetical protein yqkA pir|C69966 hypothetical protein yqkA - Bacillus subtilis dbj|BAA12633.1| YqkA [Bacillus subtilis] emb|CAB14299.1| yqkA [Bacillus subtilis subsp. subtilis str. 168] Length = 343
- 5056.2 Best-BlastP=> >nrprot 59% Identities = 57/101 (56%), Positives = 67/101 (66%), Gaps = 1/101 (0%) ref|ZP\_00091135.1| COG2852: Uncharacterized protein conserved in bacteria [Azotobacter vinelandii] Length = 150



- 5058.2 Best-BlastP=> >nrprot 57% Identities = 29/66 (43%), Positives = 46/66 (69%), Gaps = 1/66 (1%) dbj|BAA75251.1| Similar to IS1301 of *Neisseria meningitidis* [Actinobacillus actinomycetemcomitans] Length = 255
- 5059.3 Best-BlastP=> >nrprot 44% Identities = 33/70 (47%), Positives = 46/70 (65%) pir|S61903 hypothetical protein 1 - *Neisseria meningitidis* emb|CAA88914.1| orf1 [Neisseria meningitidis] Length = 151
- 506.3 Best-BlastP=> >nrprot No Hits found
- 5060.2 Best-BlastP=> >nrprot 99% Identities = 504/505 (99%), Positives = 504/505 (99%) emb|CAB65195.1| hypothetical protein [Legionella pneumophila] Length = 505
- 5061.4 Best-BlastP=> >nrprot 87% Identities = 468/562 (83%), Positives = 492/562 (87%), Gaps = 16/562 (2%) emb|CAB65194.1| hypothetical protein [Legionella pneumophila] Length = 548
- 5062.3 Best-BlastP=> >nrprot 18% Identities = 24/71 (33%), Positives = 39/71 (54%) gb|AAA21525.1| meiotin-1 Length = 259
- 5064.2 Best-BlastP=> >nrprot No Hits found
- 5065.2 Best-BlastP=> >nrprot 34% Identities = 30/100 (30%), Positives = 54/100 (54%), Gaps = 11/100 (11%) ref|NP\_593310.1| F-box protein [Schizosaccharomyces pombe] sp|P87053|POF1\_SCHPO F-box/WD-repeat protein pof1 (Skl1-binding protein 1) pir|T38932 probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe) emb|CAB08168.1| SPAC57A10.05c [Schizosaccharomyces pombe] dbj|BAA84528.1| Pof1 [Schizosaccharomyces pombe] Length = 605
- 5066.2 Best-BlastP=> >nrprot 57% Identities = 50/121 (41%), Positives = 80/121 (66%), Gaps = 5/121 (4%) ref|NP\_487806.1| two-component response regulator [Nostoc sp. PCC 7120] pir|AG2276 two-component response regulator all3766 [imported] - *Nostoc* sp. (strain PCC 7120) dbj|BAB75465.1| two-component response regulator [Nostoc sp. PCC 7120] Length = 143
- 5068.3 Best-BlastP=> >nrprot 51% Identities = 52/194 (26%), Positives = 98/194 (50%), Gaps = 8/194 (4%) ref|ZP\_00110196.1| hypothetical protein [Nostoc punctiforme] Length = 223
- 5069.3 Best-BlastP=> >nrprot 53% Identities = 48/149 (32%), Positives = 74/149 (49%), Gaps = 25/149 (16%) ref|NP\_812673.1| arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] gb|AAO78867.1| arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] Length = 157
- 507.3 Best-BlastP=> >nrprot 46% Identities = 18/32 (56%), Positives = 22/32 (68%) gb|AAN04217.1| putative transposase Tnp [Aeromonas salmonicida] Length = 383
- 5071.2 Best-BlastP=> >nrprot No Hits found
- 5072.2 Best-BlastP=> >nrprot 26% Identities = 30/85 (35%), Positives = 41/85 (48%) ref|NP\_473229.2| putative protein kinase [Plasmodium falciparum 3D7] emb|CAA15620.3| putative protein kinase [Plasmodium falciparum 3D7] Length = 2515
- 5075.4 Best-BlastP=> >nrprot 11% Identities = 62/172 (36%), Positives = 102/172 (59%), Gaps = 18/172 (10%) ref|NP\_703336.1| P. falciparum RESA-like protein with DnaJ domain [Plasmodium falciparum 3D7] emb|CAD48951.1| P. falciparum RESA-like protein with DnaJ domain [Plasmodium falciparum 3D7] Length = 1451
- 5076.2 Best-BlastP=> >nrprot 54% Identities = 50/158 (31%), Positives = 87/158 (55%), Gaps = 10/158 (6%) ref|NP\_634196.1| Hydrogenase expression/formation protein [Methanosarcina mazei Goe1] emb|CAA62962.1| F420-nonreducing hydrogenase II [Methanosarcina mazei] gb|AAM31868.1| Hydrogenase expression/formation protein [Methanosarcina mazei Goe1] Length = 161
- 5077.3 Best-BlastP=> >nrprot 60% Identities = 198/424 (46%), Positives = 262/424 (61%), Gaps = 2/424 (0%) ref|ZP\_00089783.1| COG3259: Coenzyme F420-reducing hydrogenase, alpha subunit [Azotobacter vinelandii] Length = 442

- 5078.2 Best-BlastP=> >nrprot 76% Identities = 250/432 (57%), Positives = 329/432 (76%), Gaps = 3/432 (0%) ref|NP\_052842.1| hypothetical protein [Coxiella burnetii] gb|AAD33508.1|AF131076\_34 hypothetical protein [Coxiella burnetii] Length = 433
- 5080.4 Best-BlastP=> >nrprot 44% Identities = 121/443 (27%), Positives = 217/443 (48%), Gaps = 26/443 (5%) ref|NP\_903425.1| probable peptide transporter protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61417.1| probable peptide transporter protein [Chromobacterium violaceum ATCC 12472] Length = 495
- 5081.3 Best-BlastP=> >nrprot 50% Identities = 62/173 (35%), Positives = 96/173 (55%) ref|NP\_520208.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD15794.1| CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 194
- 5082.3 Best-BlastP=> >nrprot No Hits found
- 5084.4 Best-BlastP=> >nrprot 30% Identities = 94/351 (26%), Positives = 160/351 (45%), Gaps = 28/351 (7%) ref|ZP\_00087727.1| hypothetical protein [Pseudomonas fluorescens PfO-1] Length = 375
- 5087.2 Best-BlastP=> >nrprot 19% Identities = 37/151 (24%), Positives = 69/151 (45%), Gaps = 11/151 (7%) ref|NP\_705411.1| hypothetical protein, conserved [Plasmodium falciparum 3D7] emb|CAD52648.1| hypothetical protein, conserved [Plasmodium falciparum 3D7] Length = 2533
- 5088.2 Best-BlastP=> >nrprot 53% Identities = 49/131 (37%), Positives = 76/131 (58%), Gaps = 4/131 (3%) ref|NP\_832446.1| Acetyltransferase [Bacillus cereus ATCC 14579] gb|AAP09647.1| Acetyltransferase [Bacillus cereus ATCC 14579] Length = 141
- 509.1 Best-BlastP=> >nrprot 50% Identities = 69/172 (40%), Positives = 99/172 (57%), Gaps = 10/172 (5%) ref|NP\_903527.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ61519.2| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 576
- 5090.2 Best-BlastP=> >nrprot 59% Identities = 148/359 (41%), Positives = 211/359 (58%), Gaps = 12/359 (3%) ref|NP\_662343.1| glutamate 5-kinase [Chlorobium tepidum TLS] sp|Q8KCG4|PROB\_CHL TE Glutamate 5-kinase (Gamma-glutamyl kinase) (GK) gb|AAM72685.1| glutamate 5-kinase [Chlorobium tepidum TLS] Length = 361
- 5092.3 Best-BlastP=> >nrprot No Hits found
- 5093.3 Best-BlastP=> >nrprot 52% Identities = 97/243 (39%), Positives = 128/243 (52%), Gaps = 2/243 (0%) ref|NP\_820472.1| UDP-2,3-diacylglucosamine hydrolase [Coxiella burnetii RSA 493] gb|AAO90986.1| UDP-2,3-diacylglucosamine hydrolase [Coxiella burnetii RSA 493] Length = 243
- 5094.2 Best-BlastP=> >nrprot 55% Identities = 93/209 (44%), Positives = 129/209 (61%), Gaps = 13/209 (6%) ref|ZP\_00085068.1| COG0850: Septum formation inhibitor [Pseudomonas fluorescens PfO-1] Length = 245
- 5097.1 Best-BlastP=> >nrprot 46% Identities = 76/295 (25%), Positives = 139/295 (47%), Gaps = 7/295 (2%) ref|NP\_355292.1| AGR\_C\_4240p [Agrobacterium tumefaciens] ref|NP\_533007.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|D97640 hypothetical protein AGR\_C\_4240 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|AE2863 conserved hypothetical protein Atu2334 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88077.1| AGR\_C\_4240p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL43323.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 302
- 5098.2 Best-BlastP=> >nrprot No Hits found
- 510.2 Best-BlastP=> >nrprot No Hits found

- 5100.2 Best-BlastP=> >nprot 42% Identities = 101/389 (25%), Positives = 173/389 (44%), Gaps = 16/389 (4%) ref|NP\_444149.1| Y4xM [Rhizobium sp. NGR234] sp|P55705|Y4XM\_RHISN HYPOTHETICAL TRANSPORT PROTEIN Y4XM gb|AAB91936.1| Y4xM [Rhizobium sp. NGR234] Length = 404
- 5103.4 Best-BlastP=> >nprot 42% Identities = 25/61 (40%), Positives = 37/61 (60%), Gaps = 1/61 (1%) gb|AAG10082.1|AF295331\_2 outer membrane lipoprotein Pop [Edwardsiella tarda] Length = 155
- 5104.3 Best-BlastP=> >nprot 48% Identities = 203/509 (39%), Positives = 293/509 (57%), Gaps = 9/509 (1%) ref|NP\_896011.1| FAD linked oxidase, N-terminal [Prochlorococcus marinus str. MIT 9313] emb|CAE22361.1| FAD linked oxidase, N-terminal [Prochlorococcus marinus str. MIT 9313] Length = 571
- 5106.3 Best-BlastP=> >nprot 32% Identities = 54/242 (22%), Positives = 111/242 (45%), Gaps = 24/242 (9%) gb|EAA15516.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 585
- 5108.2 Best-BlastP=> >nprot No Hits found
- 5113.3 Best-BlastP=> >nprot No Hits found
- 5114.3 Best-BlastP=> >nprot No Hits found
- 5115.2 Best-BlastP=> >nprot 44% Identities = 77/284 (27%), Positives = 141/284 (49%), Gaps = 19/284 (6%) ref|ZP\_00128740.1| COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Desulfovibrio desulfuricans G20] Length = 326
- 5116.3 Best-BlastP=> >nprot 56% Identities = 71/173 (41%), Positives = 107/173 (61%) ref|NP\_800289.1| hypothetical protein VPA0779 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC62122.1| hypothetical protein [Vibrio parahaemolyticus] Length = 203
- 5123.3 Best-BlastP=> >nprot 57% Identities = 44/78 (56%), Positives = 54/78 (69%) ref|NP\_819379.1| DNA-binding protein Fis [Coxiella burnetii RSA 493] gb|AAO89893.1| DNA-binding protein Fis [Coxiella burnetii RSA 493] Length = 103
- 5124.3 Best-BlastP=> >nprot 78% Identities = 96/151 (63%), Positives = 120/151 (79%) ref|NP\_820809.1| ribose-phosphate pyrophosphokinase [Coxiella burnetii RSA 493] gb|AAO91323.1| ribose-phosphate pyrophosphokinase [Coxiella burnetii RSA 493] Length = 319
- 5127.4 Best-BlastP=> >nprot 77% Identities = 117/162 (72%), Positives = 141/162 (87%) ref|ZP\_00068148.1| COG0462: Phosphoribosylpyrophosphate synthetase [Microbulifer degradans 2-40] Length = 316
- 5129.4 Best-BlastP=> >nprot 76% Identities = 607/1050 (57%), Positives = 799/1050 (76%), Gaps = 12/1050 (1%) ref|NP\_773366.1| AcrB/AcrD/AcrF family protein [Bradyrhizobium japonicum] dbj|BAC51991.1| AcrB/AcrD/AcrF family protein [Bradyrhizobium japonicum USDA 110] Length = 1052
- 5132.3 Best-BlastP=> >nprot No Hits found
- 5133.3 Best-BlastP=> >nprot No Hits found
- 5134.4 Best-BlastP=> >nprot 99% Identities = 308/309 (99%), Positives = 309/309 (100%) gb|AAN63820.1| lysophospholipase A [Legionella pneumophila] Length = 309
- 5135.2 Best-BlastP=> >nprot No Hits found
- 514.5 Best-BlastP=> >nprot 16% Identities = 124/559 (22%), Positives = 243/559 (43%), Gaps = 100/559 (17%) gb|AAB00143.1| putative Length = 1015
- 5146.2 Best-BlastP=> >nprot 55% Identities = 154/418 (36%), Positives = 238/418 (56%), Gaps = 13/418 (3%) gb|AAC44538.1| ProP [Escherichia coli] Length = 500

5147.1	Best-BlastP=> >nrprot No Hits found			
5151.1	Best-BlastP=> >nrprot 56% Identities = 109/295 (36%), Positives = 167/295 (56%), Gaps = 9/295 (3%) ref NP_346934.1  MccF-like protein [Clostridium acetobutylicum] pir  G96935 mccF-like protein [imported] - Clostridium acetobutylicum gb AAK78274.1 AE007544_3 MccF-like protein [Clostridium acetobutylicum] Length = 306			
5152.1	Best-BlastP=> >nrprot 55% Identities = 56/126 (44%), Positives = 72/126 (57%), Gaps = 2/126 (1%) ref NP_107051.1  unknown protein [Mesorhizobium loti] dj  BAB52837.1  unknown protein [Mesorhizobium loti] Length = 274			
5153.1	Best-BlastP=> >nrprot 97% Identities = 141/145 (97%), Positives = 142/145 (97%) gb AAK00280.1 AF288536_2 unknown [Legionella longbeachae] Length = 145			
5154.2	Best-BlastP=> >nrprot 93% Identities = 253/273 (92%), Positives = 259/273 (94%) gb AAK00279.1 AF288536_1 spectinomycin 3' adenylyltransferase [Legionella longbeachae] Length = 274			
5156.1	Best-BlastP=> >nrprot No Hits found			
5159.2	Best-BlastP=> >nrprot 62% Identities = 240/471 (50%), Positives = 313/471 (66%), Gaps = 7/471 (1%) ref NP_900831.1  probable melitin resistance protein [Chromobacterium violaceum ATCC 12472] gb AAQ58836.1  probable melitin resistance protein [Chromobacterium violaceum ATCC 12472] Length = 495			
5162.1	Best-BlastP=> >nrprot No Hits found			
5164.1	Best-BlastP=> >nrprot No Hits found			
5167.4	Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb AAP83334.1 AF469614_2 unknown [Francisella tularensis subsp. tularensis] Length = 94			
5173.1	Best-BlastP=> >nrprot 41% Identities = 195/643 (30%), Positives = 282/643 (43%), Gaps = 44/643 (6%) ref NP_251563.1  hypothetical protein [Pseudomonas aeruginosa PA01] pir  F83287 hypothetical protein PA2873 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06261.1 AE004713_10 hypothetical protein PA2873 [Pseudomonas aeruginosa PAO1] Length = 668			
5174.2	Best-BlastP=> >nrprot No Hits found			
5176.1	Best-BlastP=> >nrprot No Hits found			
5177.2	Best-BlastP=> >nrprot 41% Identities = 61/168 (36%), Positives = 95/168 (56%), Gaps = 1/168 (0%) ref ZP_00144063.1  Outer membrane protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24326.1  Outer membrane protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] Length = 202			
5178.1	Best-BlastP=> >nrprot 98% Identities = 162/163 (99%), Positives = 162/163 (99%) gb AAC38179.1  DotD [Legionella pneumophila] = 163			Length
5180.1	Best-BlastP=> >nrprot 98% Identities = 74/75 (98%), Positives = 75/75 (100%) gb AAN17184.1 AF492466_2 ferrous iron transporter A [Legionella pneumophila] Length = 75			
5188.2	Best-BlastP=> >nrprot 70% Identities = 205/420 (48%), Positives = 305/420 (72%), Gaps = 2/420 (0%) ref ZP_00025967.1  COG1301: Na+/H+-dicarboxylate symporters [Ralstonia metallidurans] Length = 467			
5189.2	Best-BlastP=> >nrprot No Hits found			
519.3	Best-BlastP=> >nrprot 99% Identities = 549/550 (99%), Positives = 549/550 (99%) pir  A41468 60K heat shock protein htpB - Legionella pneumophila Length = 550			

- 5193.2 Best-BlastP=> >nrprot 10% Identities = 49/180 (27%), Positives = 75/180 (41%), Gaps = 40/180 (22%) ref|NP\_229450.1| alpha-amylase, putative [Thermotoga maritima] pir|G72227 hypothetical protein TM1650 - Thermotoga maritima (strain MSB8) gb|AAD36717.1|AE001807\_8 alpha-amylase, putative [Thermotoga maritima] Length = 422
- 5194.1 Best-BlastP=> >nrprot 52% Identities = 74/157 (47%), Positives = 98/157 (62%), Gaps = 5/157 (3%) ref|ZP\_00036504.1| COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Enterococcus faecium] Length = 738
- 5195.2 Best-BlastP=> >nrprot 69% Identities = 237/447 (53%), Positives = 312/447 (69%), Gaps = 4/447 (0%) ref|NP\_718290.1| succinylarginine dihydrolase [Shewanella oneidensis MR-1] gb|AAN55734.1|AE015710\_2 succinylarginine dihydrolase [Shewanella oneidensis MR-1] Length = 444
- 52.1 Best-BlastP=> >nrprot 88% Identities = 52/66 (78%), Positives = 60/66 (90%) emb|CAB60050.1| lvrC [Legionella pneumophila] Length = 67
- 520.1 Best-BlastP=> >nrprot 62% Identities = 67/139 (48%), Positives = 92/139 (66%) ref|NP\_440670.1| hypothetical protein [Synecocystis sp. PCC 6803] sp|P73321|Y194\_SYNY3 Hypothetical protein sir1894 pir|S77503 hypothetical protein sir1894 - Synecocystis sp. (strain PCC 6803) dbj|BAA17350.1| ORF\_ID:sir1894-hypothetical protein [Synecocystis sp. PCC 6803] Length = 156
- 5200.2 Best-BlastP=> >nrprot 77% Identities = 489/756 (64%), Positives = 587/756 (77%), Gaps = 5/756 (0%) ref|NP\_820975.1| DNA topoisomerase I [Coxiella burnetii RSA 493] gb|AAO91489.1| DNA topoisomerase I [Coxiella burnetii RSA 493] Length = 765
- 5201.2 Best-BlastP=> >nrprot 73% Identities = 122/217 (56%), Positives = 165/217 (76%), Gaps = 2/217 (0%) sp|O66188|SCNC\_THITI Thiocyanate hydrolase gamma subunit dbj|BAA28288.1| thiocyanate hydrolase gamma subunit [Thiobacillus thioparus] Length = 243
- 5202.2 Best-BlastP=> >nrprot 55% Identities = 46/92 (50%), Positives = 57/92 (61%), Gaps = 2/92 (2%) sp|O66187|SCNA\_THITI Thiocyanate hydrolase alpha subunit dbj|BAA28287.1| thiocyanate hydrolase alpha subunit [Thiobacillus thioparus] Length = 126
- 5204.2 Best-BlastP=> >nrprot 46% Identities = 56/110 (50%), Positives = 74/110 (67%), Gaps = 1/110 (0%) sp|O66186|SCNB\_THITI Thiocyanate hydrolase beta subunit dbj|BAA28286.1| thiocyanate hydrolase beta subunit [Thiobacillus thioparus] Length = 157
- 5206.1 Best-BlastP=> >nrprot 73% Identities = 212/360 (58%), Positives = 272/360 (75%), Gaps = 2/360 (0%) ref|ZP\_00138670.1| COG1706: Flagellar basal-body P-ring protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 440
- 5208.1 Best-BlastP=> >nrprot 55% Identities = 34/86 (39%), Positives = 57/86 (66%), Gaps = 1/86 (1%) ref|NP\_924146.1| hypothetical protein gs1200 [Gloeobacter violaceus] dbj|BAC89141.1| gs1200 [Gloeobacter violaceus] Length = 96
- 521.2 Best-BlastP=> >nrprot 55% Identities = 239/722 (33%), Positives = 382/722 (52%), Gaps = 53/722 (7%) ref|NP\_773225.1| bl16585 [Bradyrhizobium japonicum] dbj|BAC51850.1| bl16585 [Bradyrhizobium japonicum USDA 110] Length = 861
- 5216.2 Best-BlastP=> >nrprot 64% Identities = 127/282 (45%), Positives = 181/282 (64%), Gaps = 9/282 (3%) ref|NP\_643189.1| pirin [Xanthomonas axonopodis pv. citri str. 306] gb|AAM37725.1| pirin [Xanthomonas axonopodis pv. citri str. 306] Length = 285
- 5217.1 Best-BlastP=> >nrprot 76% Identities = 78/118 (66%), Positives = 95/118 (80%) ref|ZP\_00024696.1| COG1484: DNA replication protein [Ralstonia metallidurans] Length = 268
- 5219.1 Best-BlastP=> >nrprot 50% Identities = 98/254 (38%), Positives = 135/254 (53%), Gaps = 11/254 (4%) gb|AAM90719.1| TraN [Salmonella typhimurium] Length = 617

- 5220.1 Best-BlastP=> >nrprot 26% Identities = 41/119 (34%), Positives = 58/119 (48%), Gaps = 16/119 (13%) ref|NP\_052852.1| hypothetical protein [Coxiella burnetii] pir|S52231 hypothetical protein 160 - Coxiella burnetii emb|CAA59944.1| orf 160 [Coxiella burnetii] gb|AAD33484.1|AF131076\_10 hypothetical protein [Coxiella burnetii] Length = 160
- 5224.2 Best-BlastP=> >nrprot No Hits found
- 5226.2 Best-BlastP=> >nrprot 76% Identities = 117/173 (67%), Positives = 138/173 (79%) ref|NP\_744614.1| translation initiation factor IF-3 [Pseudomonas putida KT2440] gb|AAN68078.1|AE016439\_13 translation initiation factor IF-3 [Pseudomonas putida KT2440] Length = 177
- 5227.2 Best-BlastP=> >nrprot 68% Identities = 34/63 (53%), Positives = 46/63 (73%), Gaps = 1/63 (1%) sp|P13069|RL35\_BACST 50S ribosomal protein L35 pir|R5BS35 ribosomal protein L35 - Bacillus stearothermophilus emb|CAA34313.1| unnamed protein product [Geobacillus stearothermophilus] Length = 66
- 5229.1 Best-BlastP=> >nrprot 81% Identities = 108/142 (76%), Positives = 118/142 (83%) ref|NP\_230221.1| ribosomal protein L13 [Vibrio cholerae O1 biovar eltor str. N16961] pir|B82308 ribosomal protein L13 VC0570 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93738.1| ribosomal protein L13 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 142
- 523.2 Best-BlastP=> >nrprot 48% Identities = 87/267 (32%), Positives = 144/267 (53%), Gaps = 1/267 (0%) ref|NP\_252216.1| probable outer membrane protein [Pseudomonas aeruginosa PA01] pir|D83204 probable outer membrane protein PA3526 [imported] - Pseudomonas aeruginosa (strain PA01) gb|AAG06914.1|AE004773\_3 probable outer membrane protein precursor [Pseudomonas aeruginosa PA01] Length = 321
- 5232.1 Best-BlastP=> >nrprot 39% Identities = 94/302 (31%), Positives = 135/302 (44%), Gaps = 38/302 (12%) ref|ZP\_00065012.1| COG0323: DNA mismatch repair enzyme (predicted ATPase) [Microbulbifer degradans 2-40] Length = 630
- 5238.1 Best-BlastP=> >nrprot 71% Identities = 266/495 (53%), Positives = 354/495 (71%), Gaps = 5/495 (1%) ref|ZP\_00067387.1| COG0138: AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful) [Microbulbifer degradans 2-40] Length = 526
- 524.2 Best-BlastP=> >nrprot 69% Identities = 194/342 (56%), Positives = 241/342 (70%), Gaps = 2/342 (0%) ref|NP\_820684.1| dihydroorotase, homodimeric type [Coxiella burnetii RSA 493] gb|AAO91198.1| dihydroorotase, homodimeric type [Coxiella burnetii RSA 493] Length = 351
- 5242.3 Best-BlastP=> >nrprot No Hits found
- 5243.2 Best-BlastP=> >nrprot No Hits found
- 5247.1 Best-BlastP=> >nrprot 40% Identities = 80/312 (25%), Positives = 141/312 (45%), Gaps = 26/312 (8%) ref|ZP\_00110262.1| hypothetical protein [Nostoc punctiforme] Length = 348
- 5250.2 Best-BlastP=> >nrprot 86% Identities = 234/324 (72%), Positives = 280/324 (86%) ref|NP\_819669.1| dehydrogenase, E1 component, beta subunit, putative [Coxiella burnetii RSA 493] gb|AAO90183.1| dehydrogenase, E1 component, beta subunit, putative [Coxiella burnetii RSA 493] Length = 326
- 5253.1 Best-BlastP=> >nrprot 62% Identities = 92/196 (46%), Positives = 132/196 (67%), Gaps = 3/196 (1%) ref|ZP\_00090036.1| COG4445: Hydroxylase for synthesis of 2-methylthio-cis-ribozeatin in tRNA [Azotobacter vinelandii] Length = 200
- 5254.1 Best-BlastP=> >nrprot 53% Identities = 72/206 (34%), Positives = 121/206 (58%) ref|NP\_820242.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90756.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 206

- 5255.1 Best-BlastP=> >nrprot 54% Identities = 132/378 (34%), Positives = 210/378 (55%), Gaps = 8/378 (2%) ref|ZP\_00087763.1| COG1520: FOG: WD40-like repeat [Pseudomonas fluorescens PfO-1] Length = 440
- 5256.2 Best-BlastP=> >nrprot 98% Identities = 64/64 (100%), Positives = 64/64 (100%) gb|AAG40471.1| global regulator [Legionella pneumophila] Length = 64
- 526.2 Best-BlastP=> >nrprot 97% Identities = 202/207 (97%), Positives = 203/207 (98%) gb|AAM00600.1| Rhase T [Legionella pneumophila] Length = 207
- 5266.2 Best-BlastP=> >nrprot 39% Identities = 212/1088 (19%), Positives = 439/1088 (40%), Gaps = 185/1088 (17%) pir|T14867 interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| interaptin [Dictyostelium discoideum] Length = 1738
- 5268.2 Best-BlastP=> >nrprot 54% Identities = 56/183 (30%), Positives = 107/183 (58%), Gaps = 6/183 (3%) ref|NP\_821059.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO91573.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 192
- 5269.1 Best-BlastP=> >nrprot No Hits found
- 5270.2 Best-BlastP=> >nrprot No Hits found
- 5273.1 Best-BlastP=> >nrprot 55% Identities = 42/101 (41%), Positives = 61/101 (60%), Gaps = 3/101 (2%) ref|NP\_820129.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] gb|AAO90643.1| oligopeptide transporter, OPT family [Coxiella burnetii RSA 493] Length = 669
- 5277.3 Best-BlastP=> >nrprot 60% Identities = 186/328 (56%), Positives = 235/328 (71%), Gaps = 5/328 (1%) ref|NP\_901482.1| dihydroorotate oxidase [Chromobacterium violaceum ATCC 12472] gb|AAQ59486.1| dihydroorotate oxidase [Chromobacterium violaceum ATCC 12472] Length = 344
- 5278.3 Best-BlastP=> >nrprot No Hits found
- 528.2 Best-BlastP=> >nrprot 99% Identities = 200/201 (99%), Positives = 201/201 (100%) gb|AAM00601.1| peroxynitrite reductase [Legionella pneumophila] Length = 201
- 5282.3 Best-BlastP=> >nrprot 44% Identities = 20/54 (37%), Positives = 32/54 (59%) ref|ZP\_00077653.1| COG0693: Putative intracellular protease/amidase [Methanosarcina barkeri] Length = 209
- 5288.1 Best-BlastP=> >nrprot 60% Identities = 60/130 (46%), Positives = 83/130 (63%), Gaps = 4/130 (3%) pir|A60635 glutathione transferase (EC 2.5.1.18), fosfomycin-modifying - Escherichia coli plasmid pSU961 transposon Tn2921 gb|AAA98399.1| fosfomycin-resistance protein [Serratia marcescens] Length = 141
- 5289.2 Best-BlastP=> >nrprot 32% Identities = 49/169 (28%), Positives = 73/169 (43%), Gaps = 19/169 (11%) ref|NP\_819837.1| aminoglycoside N(6')-acetyltransferase [Coxiella burnetii RSA 493] gb|AAO90351.1| aminoglycoside N(6')-acetyltransferase [Coxiella burnetii RSA 493] Length = 188
- 529.2 Best-BlastP=> >nrprot 99% Identities = 105/105 (100%), Positives = 105/105 (100%) gb|AAM00602.1| glutaredoxin-like protein [Legionella pneumophila] Length = 115
- 5295.1 Best-BlastP=> >nrprot 68% Identities = 218/435 (50%), Positives = 309/435 (71%) ref|NP\_253162.1| PmbA protein [Pseudomonas aeruginosa PAO1] pir|B83086 PmbA protein PA4472 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07860.1|AE004861\_1 PmbA protein [Pseudomonas aeruginosa PAO1] Length = 449
- 5297.2 Best-BlastP=> >nrprot No Hits found



- 530.3 Best-BlastP=> >nrprot 50% Identities = 75/162 (46%), Positives = 100/162 (61%), Gaps = 3/162 (1%) ref|ZP\_00129339.1| hypothetical protein [Desulfovibrio desulfuricans G20] Length = 231
- 5307.3 Best-BlastP=> >nrprot 19% Identities = 64/234 (27%), Positives = 111/234 (47%), Gaps = 23/234 (9%) ref|NP\_820063.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90577.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 468
- 5309.1 Best-BlastP=> >nrprot 84% Identities = 196/267 (73%), Positives = 234/267 (87%) ref|NP\_743889.1| septum site-determining protein MinD [Pseudomonas putida KT2440] gb|AAN67353.1|AE016361\_7 septum site-determining protein MinD [Pseudomonas putida KT2440] Length = 270
- 531.4 Best-BlastP=> >nrprot No Hits found
- 5311.1 Best-BlastP=> >nrprot 58% Identities = 43/94 (45%), Positives = 58/94 (61%) ref|ZP\_00090060.1| COG0721: Asp-tRNAAsn/Glu-tRNA<sup>Gln</sup> amidotransferase C subunit [Azotobacter vinelandii] Length = 146
- 5312.2 Best-BlastP=> >nrprot 99% Identities = 206/208 (99%), Positives = 207/208 (99%) gb|AAF05324.2| unknown virulence protein [Legionella pneumophila] Length = 208
- 5313.1 Best-BlastP=> >nrprot 32% Identities = 28/91 (30%), Positives = 46/91 (50%), Gaps = 6/91 (6%) ref|NP\_520202.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD15788.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 176
- 5316.1 Best-BlastP=> >nrprot 41% Identities = 200/203 (98%), Positives = 203/203 (100%) gb|AAF05325.1| unknown virulence protein [Legionella pneumophila] Length = 205
- 5317.2 Best-BlastP=> >nrprot 65% Identities = 94/204 (46%), Positives = 136/204 (66%), Gaps = 1/204 (0%) ref|ZP\_00067804.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 206
- 5318.2 Best-BlastP=> >nrprot 34% Identities = 47/115 (40%), Positives = 72/115 (62%) ref|NP\_790719.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54414.1| conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 249
- 5319.1 Best-BlastP=> >nrprot No Hits found
- 532.2 Best-BlastP=> >nrprot 57% Identities = 132/383 (34%), Positives = 215/383 (56%), Gaps = 24/383 (6%) ref|NP\_718711.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN56155.1|AE015753\_1 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 374
- 5321.1 Best-BlastP=> >nrprot 43% Identities = 27/53 (50%), Positives = 38/53 (71%), Gaps = 2/53 (3%) gb|AAP84173.1| conserved hypothetical protein [Pseudomonas aeruginosa] Length = 744
- 5322.1 Best-BlastP=> >nrprot 58% Identities = 36/102 (35%), Positives = 61/102 (59%), Gaps = 3/102 (2%) ref|NP\_816469.1| conserved domain protein [Enterococcus faecalis V583] gb|AAO82539.1| conserved domain protein [Enterococcus faecalis V583] Length = 104
- 5324.1 Best-BlastP=> >nrprot 51% Identities = 72/194 (37%), Positives = 113/194 (58%), Gaps = 2/194 (1%) ref|NP\_719033.1| AcrB/AcrD/AcrF family protein [Shewanella oneidensis MR-1] gb|AAN56477.1|AE015784\_10 AcrB/AcrD/AcrF family protein [Shewanella oneidensis MR-1] Length = 1046

- 5328.1 Best-BlastP=> >nrprot 41% Identities = 34/123 (27%), Positives = 62/123 (50%), Gaps = 4/123 (3%) ref|NP\_692567.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] dbj|BAC13602.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] Length = 402
- 533.2 Best-BlastP=> >nrprot 64% Identities = 122/264 (46%), Positives = 172/264 (65%), Gaps = 8/264 (3%) ref|NP\_246208.1| AroE [Pasteurella multocida] sp|P57932|AROE\_PASMU Shikimate 5-dehydrogenase gb|AAK03355.1| AroE [Pasteurella multocida] Length = 269
- 5334.1 Best-BlastP=> >nrprot 32% Identities = 70/121 (57%), Positives = 83/121 (68%), Gaps = 9/121 (7%) gb|AAQ82687.1| Epa5p [Candida glabrata] Length = 1218
- 5337.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 5338.2 Best-BlastP=> >nrprot 30% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180
- 5340.1 Best-BlastP=> >nrprot 14% Identities = 40/136 (29%), Positives = 73/136 (53%), Gaps = 19/136 (13%) gb|AAA67447.1| P120 Length = 232
- 5341.1 Best-BlastP=> >nrprot No Hits found
- 5342.2 Best-BlastP=> >nrprot 60% Identities = 87/178 (48%), Positives = 113/178 (63%), Gaps = 5/178 (2%) ref|NP\_819838.1| transcriptional regulator, TetR family [Coxiella burnetii RSA 493] gb|AAO90352.1| transcriptional regulator, TetR family [Coxiella burnetii RSA 493] Length = 193
- 5344.2 Best-BlastP=> >nrprot 21% Identities = 36/77 (46%), Positives = 48/77 (62%), Gaps = 1/77 (1%) ref|ZP\_00028865.1| hypothetical protein [Burkholderia fungorum] Length = 123
- 5349.3 Best-BlastP=> >nrprot 15% Identities = 65/306 (21%), Positives = 140/306 (45%), Gaps = 40/306 (13%) dbj|BAC86266.1| unnamed protein product [Homo sapiens] Length = 486
- 5354.3 Best-BlastP=> >nrprot No Hits found
- 5359.2 Best-BlastP=> >nrprot 43% Identities = 22/59 (37%), Positives = 36/59 (61%) ref|NP\_637282.1| flagellar protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM41206.1| flagellar protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 135
- 536.3 Best-BlastP=> >nrprot 69% Identities = 459/876 (52%), Positives = 600/876 (68%), Gaps = 23/876 (2%) ref|NP\_744167.1| aminopeptidase N [Pseudomonas putida KT2440] gb|AAN67631.1|AE016392\_12 aminopeptidase N [Pseudomonas putida KT2440] Length = 885
- 5360.2 Best-BlastP=> >nrprot No Hits found
- 5361.2 Best-BlastP=> >nrprot 68% Identities = 179/380 (47%), Positives = 261/380 (68%), Gaps = 3/380 (0%) ref|NP\_746466.1| flagellar biosynthetic protein FlhB [Pseudomonas putida KT2440] gb|AAN69930.1|AE016632\_1 flagellar biosynthetic protein FlhB [Pseudomonas putida KT2440] Length = 380

- 5369.2 Best-BlastP=> >nrprot 72% Identities = 47/68 (69%), Positives = 58/68 (85%) ref|NP\_639162.1| 30S ribosomal protein S21 [Xanthomonas campestris pv. campestris str. ATCC 33913] ref|NP\_644178.1| 30S ribosomal protein S21 [Xanthomonas axonopodis pv. citri str. 306] sp|Q8NL04|RS21\_XANAC 30S ribosomal protein S21 gb|AAM38714.1| 30S ribosomal protein S21 [Xanthomonas axonopodis pv. citri str. 306] gb|AAM43491.1| 30S ribosomal protein S21 [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 71
- 537.2 Best-BlastP=> >nrprot No Hits found
- 5370.1 Best-BlastP=> >nrprot 97% Identities = 142/147 (96%), Positives = 144/147 (97%), Gaps = 1/147 (0%) gb|AAB09541.1| LporfX Length = 146
- 5373.1 Best-BlastP=> >nrprot No Hits found
- 5376.2 Best-BlastP=> >nrprot 25% Identities = 185/917 (20%), Positives = 352/917 (38%), Gaps = 160/917 (17%) gb|EAA15312.1| hypothetical protein [Plasmodium yoelii yoelii] Length = 1527
- 5377.2 Best-BlastP=> >nrprot No Hits found
- 538.1 Best-BlastP=> >nrprot No Hits found
- 5380.3 Best-BlastP=> >nrprot 49% Identities = 52/160 (32%), Positives = 91/160 (56%), Gaps = 5/160 (3%) ref|NP\_248967.1| hypothetical protein [Pseudomonas aeruginosa PA01] pir|D83612 hypothetical protein PA0276 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG03665.1|AE004465\_11 hypothetical protein PA0276 [Pseudomonas aeruginosa PAO1] Length = 171
- 5381.1 Best-BlastP=> >nrprot No Hits found
- 5382.1 Best-BlastP=> >nrprot No Hits found
- 5386.1 Best-BlastP=> >nrprot 67% Identities = 170/327 (51%), Positives = 225/327 (68%), Gaps = 3/327 (0%) ref|NP\_844883.1| oxidoreductase, NAD-binding [Bacillus anthracis str. Ames] gb|AAP26369.1| oxidoreductase, NAD-binding [Bacillus anthracis str. Ames] Length = 341
- 5387.1 Best-BlastP=> >nrprot 67% Identities = 128/249 (51%), Positives = 169/249 (67%), Gaps = 2/249 (0%) gb|AAM51645.1| putative transposase [Francisella tularensis subsp. tularensis] Length = 247
- 5388.1 Best-BlastP=> >nrprot No Hits found
- 539.3 Best-BlastP=> >nrprot 61% Identities = 107/144 (74%), Positives = 123/144 (85%) emb|CAB46580.1| IS1400 transposase B [Yersinia enterocolitica] Length = 294
- 5390.1 Best-BlastP=> >nrprot 41% Identities = 30/89 (33%), Positives = 51/89 (57%) ref|NP\_716406.1| conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN53851.1|AE015522\_6 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 100
- 5391.2 Best-BlastP=> >nrprot 58% Identities = 192/471 (40%), Positives = 283/471 (60%), Gaps = 5/471 (1%) ref|NP\_840383.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] emb|CAD84207.1| conserved hypothetical protein [Nitrosomonas europaea ATCC 19718] Length = 510
- 5398.3 Best-BlastP=> >nrprot 66% Identities = 173/351 (49%), Positives = 237/351 (67%) ref|ZP\_00084264.1| COG4972: Tfp pilus assembly protein, ATPase PilM [Pseudomonas fluorescens PfO-1] Length = 354
- 540.3 Best-BlastP=> >nrprot 72% Identities = 58/101 (57%), Positives = 78/101 (77%) emb|CAB46580.1| IS1400 transposase B [Yersinia enterocolitica] Length = 294

- 5402.1 Best-BlastP=> >nrprot No Hits found
- 5404.2 Best-BlastP=> >nrprot No Hits found
- 5405.2 Best-BlastP=> >nrprot 98% Identities = 314/322 (97%), Positives = 319/322 (99%) gb|AAM00613.1| chemiosmotic efflux system protein B-like protein [Legionella pneumophila] Length = 322
- 5406.1 Best-BlastP=> >nrprot 34% Identities = 109/300 (36%), Positives = 175/300 (58%), Gaps = 15/300 (5%) ref|NP\_902623.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] gb|AAQ60621.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 1390
- 5412.1 Best-BlastP=> >nrprot 72% Identities = 190/322 (59%), Positives = 232/322 (72%), Gaps = 6/322 (1%) ref|NP\_638907.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42831.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 323
- 5413.1 Best-BlastP=> >nrprot No Hits found
- 5417.1 Best-BlastP=> >nrprot 59% Identities = 50/137 (36%), Positives = 82/137 (59%), Gaps = 9/137 (6%) ref|NP\_487806.1| two-component response regulator [Nostoc sp. PCC 7120] pir|JAG2276 two-component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB75465.1| two-component response regulator [Nostoc sp. PCC 7120] Length = 143
- 5420.1 Best-BlastP=> >nrprot 49% Identities = 42/134 (31%), Positives = 67/134 (50%), Gaps = 20/134 (14%) gb|AAH41716.1| Similar to myosin, heavy polypeptide 4, skeletal muscle [Xenopus laevis] Length = 1170
- 5421.1 Best-BlastP=> >nrprot No Hits found
- 5422.1 Best-BlastP=> >nrprot No Hits found
- 5423.1 Best-BlastP=> >nrprot 64% Identities = 36/75 (48%), Positives = 50/75 (66%) ref|NP\_252731.1| exodeoxyribonuclease VII small subunit [Pseudomonas aeruginosa PA01] ref|ZP\_00137487.1| COG1722: Exonuclease VII small subunit [Pseudomonas aeruginosa PA14] sp|Q9HWY5|EX7S\_PSEAE Probable exodeoxyribonuclease VII small subunit (Exonuclease VII small subunit) pir|E83139 exodeoxyribonuclease VII small subunit PA4042 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07429.1| AE004821\_2 exodeoxyribonuclease VII small subunit [Pseudomonas aeruginosa PAO1] Length = 80
- 5424.2 Best-BlastP=> >nrprot No Hits found
- 5426.2 Best-BlastP=> >nrprot 71% Identities = 86/142 (60%), Positives = 109/142 (76%), Gaps = 2/142 (1%) ref|NP\_820558.1| tolR protein [Coxiella burnetii RSA 493] gb|AAO91072.1| tolR protein [Coxiella burnetii RSA 493] Length = 147
- 5427.1 Best-BlastP=> >nrprot 68% Identities = 114/225 (50%), Positives = 154/225 (68%), Gaps = 4/225 (1%) ref|ZP\_00082839.1| COG0811: Biopolymer transport proteins [Pseudomonas fluorescens PfO-1] Length = 231
- 5428.1 Best-BlastP=> >nrprot 53% Identities = 48/116 (41%), Positives = 70/116 (60%), Gaps = 1/116 (0%) ref|NP\_404733.1| conserved hypothetical protein [Yersinia pestis] ref|NP\_670358.1| hypothetical protein [Yersinia pestis KIM] pir|JAH0137 conserved hypothetical protein YPO1120 [imported] - Yersinia pestis (strain CO92) emb|CAC89963.1| conserved hypothetical protein [Yersinia pestis CO92] gb|AAM86609.1| AE013907\_3 hypothetical protein [Yersinia pestis KIM] Length = 133
- 5429.1 Best-BlastP=> >nrprot 56% Identities = 33/73 (45%), Positives = 45/73 (61%), Gaps = 2/73 (2%) ref|NP\_819889.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90403.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 82
- 543.1 Best-BlastP=> >nrprot No Hits found

- 5437.2 Best-BlastP=> >nrprot No Hits found
- 5438.1 Best-BlastP=> >nrprot 73% Identities = 114/187 (60%), Positives = 144/187 (77%) ref|ZP\_00065453.1| COG1207: N-acetylglucosamine-1-phosphate uridylyltransferase (contains nucleotidyltransferase and l-patch acetyltransferase domains) [Microbulbifer degradans 2-40] Length = 451
- 544.2 Best-BlastP=> >nrprot 76% Identities = 265/446 (59%), Positives = 337/446 (75%), Gaps = 5/446 (1%) ref|ZP\_00138105.1| COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Pseudomonas aeruginosa UCBPP-PA14] Length = 597
- 5440.1 Best-BlastP=> >nrprot No Hits found
- 5446.3 Best-BlastP=> >nrprot 62% Identities = 188/449 (41%), Positives = 279/449 (62%), Gaps = 12/449 (2%) gb|AAP74578.1| kynurenine 3-monooxygenase [Polaribacter filamentus] Length = 469
- 5447.1 Best-BlastP=> >nrprot 51% Identities = 88/224 (39%), Positives = 129/224 (57%), Gaps = 8/224 (3%) ref|NP\_484370.1| unknown protein [Nostoc sp. PCC 7120] pir|AE1847 hypothetical protein al0326 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB72284.1| ORF\_ID:al0326~unknown protein [Nostoc sp. PCC 7120] Length = 224
- 5448.1 Best-BlastP=> >nrprot 35% Identities = 36/120 (30%), Positives = 61/120 (50%), Gaps = 7/120 (5%) sp|P45790|GSPC\_AERHY GENERAL SECRETION PATHWAY PROTEIN C emb|CAA47125.1| ExeC [Aeromonas hydrophila] Length = 290
- 5453.2 Best-BlastP=> >nrprot 68% Identities = 171/344 (49%), Positives = 242/344 (70%), Gaps = 1/344 (0%) ref|NP\_819316.1| major facilitator family transporter [Coxiella burnetii RSA 493] gb|AAO89830.1| major facilitator family transporter [Coxiella burnetii RSA 493] Length = 458
- 5455.1 Best-BlastP=> >nrprot 64% Identities = 71/152 (46%), Positives = 101/152 (66%) ref|ZP\_00140766.1| COG5528: Predicted integral membrane protein [Pseudomonas aeruginosa UCBPP-PA14] Length = 155
- 5456.1 Best-BlastP=> >nrprot 99% Identities = 225/226 (99%), Positives = 226/226 (100%) gb|AAQ18123.1| CpxR [Legionella pneumophila] Length = 226
- 5457.1 Best-BlastP=> >nrprot 57% Identities = 52/117 (44%), Positives = 77/117 (65%) ref|NP\_384234.1| PUTATIVE CYTIDINE DEAMINASE PROTEIN [Sinorhizobium meliloti] emb|CAC41515.1| PUTATIVE CYTIDINE DEAMINASE PROTEIN [Sinorhizobium meliloti] Length = 152
- 5458.1 Best-BlastP=> >nrprot 53% Identities = 32/96 (33%), Positives = 52/96 (54%), Gaps = 2/96 (2%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180
- 5460.1 Best-BlastP=> >nrprot 56% Identities = 147/325 (45%), Positives = 206/325 (63%), Gaps = 10/325 (3%) ref|NP\_189431.2| DegP protease [Arabidopsis thaliana] gb|AAK62640.1| K16N12.18/K16N12.18 [Arabidopsis thaliana] gb|AAM47381.1| At3g27925/K16N12.18 [Arabidopsis thaliana] Length = 439
- 5462.2 Best-BlastP=> >nrprot 66% Identities = 270/541 (49%), Positives = 367/541 (67%), Gaps = 6/541 (1%) ref|NP\_819168.1| penicillin-binding protein 3 [Coxiella burnetii RSA 493] gb|AAO89682.1| penicillin-binding protein 3 [Coxiella burnetii RSA 493] Length = 548
- 5467.1 Best-BlastP=> >nrprot No Hits found

- 5469.1 Best-BlastP=> >nrrprot 70% Identities = 24/55 (43%), Positives = 40/55 (72%) ref|NP\_438830.1| hypothetical protein [Haemophilus influenzae Rd] sp|P44814|DTD\_HAEIN D-tyrosyl-tRNA(Tyr) deacylase pir|E64156 hypothetical protein HI0670 - Haemophilus influenzae (strain Rd KW20) pdb|1J7G|A Chain A, Structure Of Yhz From Haemophilus influenzae (HI0670), A D- Tyr-Trna(Tyr) Deacylase gb|AAC22330.1| conserved hypothetical protein [Haemophilus influenzae Rd] Length = 144
- 5470.1 Best-BlastP=> >nrrprot 76% Identities = 58/83 (69%), Positives = 65/83 (78%) ref|ZP\_00083364.1| COG1490: D-Tyr-tRNA<sup>Tyr</sup> deacylase [Pseudomonas fluorescens PfO-1] Length = 145
- 5471.2 Best-BlastP=> >nrrprot 59% Identities = 30/57 (52%), Positives = 41/57 (71%) ref|NP\_773232.1| bsr6592 [Bradyrhizobium japonicum] dbj|BAC51857.1| bsr6592 [Bradyrhizobium japonicum USDA 110] Length = 95
- 5473.1 Best-BlastP=> >nrrprot 73% Identities = 154/270 (57%), Positives = 197/270 (72%), Gaps = 5/270 (1%) ref|ZP\_00029131.1| COG3243: Poly(3-hydroxyalkanoate) synthetase [Burkholderia fungorum] Length = 642
- 5474.2 Best-BlastP=> >nrrprot 42% Identities = 44/134 (32%), Positives = 73/134 (54%), Gaps = 2/134 (1%) ref|ZP\_00027817.1| COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Burkholderia fungorum] Length = 174
- 5476.1 Best-BlastP=> >nrrprot 54% Identities = 48/106 (45%), Positives = 67/106 (63%), Gaps = 1/106 (0%) ref|NP\_759432.1| HesB family protein [Vibrio vulnificus CMCP6] gb|AAO08959.1|AE016798\_119 HesB family protein [Vibrio vulnificus CMCP6] Length = 107
- 5477.1 Best-BlastP=> >nrrprot 57% Identities = 36/84 (42%), Positives = 55/84 (65%), Gaps = 1/84 (1%) ref|NP\_873022.1| DNA-binding protein [Haemophilus ducreyi 35000HP] gb|AAP95411.1| DNA-binding protein [Haemophilus ducreyi 35000HP] Length = 98
- 5478.2 Best-BlastP=> >nrrprot 28% Identities = 30/102 (29%), Positives = 47/102 (46%), Gaps = 13/102 (12%) sp|Q9W751|PIX1\_XENLA Pituitary homeobox 1 (X-PITX-1) (xPitx1) gb|AAD45292.1|AF155206\_1 homeodomain transcription factor Pitx-1 [Xenopus laevis] Length = 305
- 5479.2 Best-BlastP=> >nrrprot 51% Identities = 62/169 (36%), Positives = 102/169 (60%), Gaps = 2/169 (1%) gb|AAN46162.1| unknown protein [Synechococcus sp. PCC 7942] Length = 208
- 548.3 Best-BlastP=> >nrrprot No Hits found
- 5481.1 Best-BlastP=> >nrrprot 50% Identities = 143/306 (46%), Positives = 192/306 (62%), Gaps = 1/306 (0%) ref|ZP\_00043253.1| COG0790: FOG: TPR repeat, SEL1 subfamily [Magnetococcus sp. MC-1] Length = 831
- 5482.2 Best-BlastP=> >nrrprot 41% Identities = 75/284 (26%), Positives = 124/284 (43%), Gaps = 17/284 (5%) sp|O57809|1A1D\_PYRHO Putative 1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) pdb|1J0A|A Chain A, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb|1J0A|B Chain B, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb|1J0A|C Chain C, Crystal Structure Analysis Of The Acc Deaminase Homologue pdb|1J0B|A Chain A, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|B Chain B, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|C Chain C, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|D Chain D, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|E Chain E, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|F Chain F, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|G Chain G, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor pdb|1J0B|H Chain H, Crystal Structure Analysis Of The Acc Deaminase Homologue Complexed With Inhibitor
- 5484.4 Best-BlastP=> >nrrprot No Hits found

5489.2

Best-BlastP=> >nrprot 52% Identities = 64/189 (33%), Positives = 107/189 (56%), Gaps = 8/189 (4%) ref|NP\_882264.1| putative exported protein [Bordetella pertussis] ref|NP\_886390.1| putative exported protein [Bordetella parapertussis] ref|NP\_891381.1| putative exported protein [Bordetella bronchiseptica] emb|CAE44018.1| putative exported protein [Bordetella pertussis] emb|CAE39540.1| putative exported protein [Bordetella parapertussis] emb|CAE35211.1| putative exported protein [Bordetella bronchiseptica] Length = 207

549.5 Best-BlastP=> >nrprot 27% Identities = 60/253 (23%), Positives = 108/253 (42%), Gaps = 12/253 (4%) ref|NP\_638097.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb|AAM42021.1| conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913] Length = 618

5492.2 Best-BlastP=> >nrprot 77% Identities = 105/178 (58%), Positives = 145/178 (81%) ref|NP\_251274.1| CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Pseudomonas aeruginosa PAO1] pir|B83322 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase PA2584 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05972.1|AE004687\_1 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Pseudomonas aeruginosa PAO1] Length = 186

5496.2 Best-BlastP=> >nrprot 95% Identities = 168/175 (96%), Positives = 171/175 (97%) emb|CAB65201.1| hypothetical protein [Legionella pneumophila] Length = 356

5497.1 Best-BlastP=> >nrprot 98% Identities = 328/334 (98%), Positives = 330/334 (98%) emb|CAB65202.1| WecA protein [Legionella pneumophila] Length = 334

5498.1 Best-BlastP=> >nrprot 99% Identities = 317/318 (99%), Positives = 318/318 (100%) emb|CAB65203.1| hypothetical protein [Legionella pneumophila] Length = 318

5499.1 Best-BlastP=> >nrprot 99% Identities = 291/291 (100%), Positives = 291/291 (100%) emb|CAB65204.1| RmlA protein [Legionella pneumophila] Length = 291

55.1 Best-BlastP=> >nrprot 98% Identities = 125/128 (97%), Positives = 127/128 (99%) gb|AAM08236.1| LvrB [Legionella pneumophila] Length = 150

5500.1 Best-BlastP=> >nrprot 98% Identities = 484/494 (97%), Positives = 486/494 (98%), Gaps = 2/494 (0%) sp|Q9RDY2|G6PI\_LEGPN Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) emb|CAB65205.1| Gpi protein [Legionella pneumophila] Length = 497

5504.4 Best-BlastP=> >nrprot No Hits found

551.2 Best-BlastP=> >nrprot 64% Identities = 122/243 (50%), Positives = 163/243 (67%), Gaps = 3/243 (1%) ref|ZP\_00039313.1| COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Xylella fastidiosa Dixon] Length = 245

5514.2 Best-BlastP=> >nrprot 32% Identities = 56/241 (23%), Positives = 110/241 (45%), Gaps = 36/241 (14%) gb|EAA16038.1| repeat organellar protein-related [Plasmodium yoelii yoelii] Length = 1441

5515.2 Best-BlastP=> >nrprot 78% Identities = 149/249 (59%), Positives = 197/249 (79%) ref|NP\_251642.1| electron transfer flavoprotein beta-subunit [Pseudomonas aeruginosa PAO1] pir|C83277 electron transfer flavoprotein beta-subunit PA2952 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06340.1|AE004721\_8 electron transfer flavoprotein beta-subunit [Pseudomonas aeruginosa PAO1] Length = 249



- 5517.1 Best-BlastP=> >nrprot 50% Identities = 47/123 (38%), Positives = 65/123 (52%), Gaps = 14/123 (11%) ref|ZP\_00087881.1| COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Pseudomonas fluorescens PfO-1] Length = 138
- 5520.1 Best-BlastP=> >nrprot 38% Identities = 31/125 (24%), Positives = 57/125 (45%), Gaps = 4/125 (3%) ref|NP\_716604.1| hypothetical protein [Shewanella oneidensis MR-1] Length = 474
- 5521.1 Best-BlastP=> >nrprot 61% Identities = 47/133 (35%), Positives = 83/133 (62%), Gaps = 1/133 (0%) ref|NP\_903590.1| conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] Length = 144
- 5523.2 Best-BlastP=> >nrprot 60% Identities = 157/327 (48%), Positives = 203/327 (62%), Gaps = 9/327 (2%) ref|ZP\_00086640.1| COG1612: Uncharacterized protein required for cytochrome oxidase assembly [Pseudomonas fluorescens PfO-1] Length = 359
- 5524.1 Best-BlastP=> >nrprot 43% Identities = 46/180 (25%), Positives = 76/180 (42%), Gaps = 25/180 (13%) ref|NP\_800052.1| hypothetical protein VPA0542 [Vibrio parahaemolyticus RIMD 2210633] dbj|BAC61885.1| hypothetical protein [Vibrio parahaemolyticus] Length = 178
- 5526.2 Best-BlastP=> >nrprot 30% Identities = 42/141 (29%), Positives = 64/141 (45%), Gaps = 2/141 (1%) ref|ZP\_00081004.1| COG3637: Opacity protein and related surface antigens [Geobacter metallireducens] Length = 219
- 5527.2 Best-BlastP=> >nrprot 69% Identities = 91/170 (53%), Positives = 120/170 (70%) ref|NP\_743494.1| UDP-N-acetylmuramoylalanine--D-glutamate ligase [Pseudomonas putida KT2440] gb|AAN66958.1|AE016324\_8 UDP-N-acetylmuramoylalanine--D-glutamate ligase [Pseudomonas putida KT2440] Length = 450
- 5528.2 Best-BlastP=> >nrprot 99% Identities = 239/239 (100%), Positives = 239/239 (100%) emb|CAB65196.1| hypothetical protein [Legionella pneumophila] Length = 239
- 553.1 Best-BlastP=> >nrprot No Hits found
- 5530.2 Best-BlastP=> >nrprot 68% Identities = 119/231 (51%), Positives = 161/231 (69%) ref|NP\_767647.1| bll1007 [Bradyrhizobium japonicum] dbj|BAC46272.1| bll1007 [Bradyrhizobium japonicum USDA 110] Length = 345
- 5532.2 Best-BlastP=> >nrprot 50% Identities = 86/270 (31%), Positives = 146/270 (54%), Gaps = 11/270 (4%) ref|ZP\_00117263.1| COG3781: Predicted membrane protein [Cytophaga hutchinsonii] Length = 290
- 5533.2 Best-BlastP=> >nrprot 43% Identities = 28/84 (33%), Positives = 35/84 (41%), Gaps = 16/84 (19%) gb|AAO52009.1| similar to exonuclease ii [Schizosaccharomyces pombe] [Dictyostelium discoideum] Length = 1749
- 5534.2 Best-BlastP=> >nrprot 98% Identities = 486/494 (98%), Positives = 489/494 (98%) gb|AAK35046.1|AF330136\_2 type II protein secretion ATPase LspE [Legionella pneumophila] Length = 494
- 5535.1 Best-BlastP=> >nrprot No Hits found
- 5538.2 Best-BlastP=> >nrprot 75% Identities = 95/159 (59%), Positives = 121/159 (76%), Gaps = 1/159 (0%) ref|NP\_819315.1| single-strand binding protein [Coxiella burnetii RSA 493] gb|AAO89829.1| single-strand binding protein [Coxiella burnetii RSA 493] Length = 158
- 5539.1 Best-BlastP=> >nrprot No Hits found

- 5540.1 Best-BlastP=> >nprot 81% Identities = 90/126 (71%), Positives = 104/126 (82%) ref|NP\_252927.1| 50S ribosomal protein L17 [Pseudomonas aeruginosa PAO1] sp|O52761|RL17\_PSEAE 50S ribosomal protein L17 pir|C83113 50S ribosomal protein L17 PA4237 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAC03117.1| ribosomal large subunit protein L17 [Pseudomonas aeruginosa] gb|AAG07625.1|AE004841\_3 50S ribosomal protein L17 [Pseudomonas aeruginosa PAO1] Length = 129
- 5542.3 Best-BlastP=> >nprot 70% Identities = 120/255 (47%), Positives = 183/255 (71%), Gaps = 1/255 (0%) ref|NP\_831729.1| Aminoglycoside 6-adenylyltransferase [Bacillus cereus ATCC 14579] gb|AAP08930.1| Aminoglycoside 6-adenylyltransferase [Bacillus cereus ATCC 14579] Length = 290
- 5546.1 Best-BlastP=> >nprot 73% Identities = 65/107 (60%), Positives = 79/107 (73%), Gaps = 1/107 (0%) ref|NP\_820379.1| ErfKYbiSYcfSYnhG family protein [Coxiella burnetii RSA 493] gb|AAO90893.1| ErfKYbiSYcfSYnhG family protein [Coxiella burnetii RSA 493] Length = 175
- 5548.1 Best-BlastP=> >nprot No Hits found
- 5549.2 Best-BlastP=> >nprot 73% Identities = 134/229 (58%), Positives = 172/229 (75%), Gaps = 3/229 (1%) ref|ZP\_00065236.1| COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Microbulbifer degradans 2-40] Length = 238
- 555.2 Best-BlastP=> >nprot 53% Identities = 110/317 (34%), Positives = 171/317 (53%), Gaps = 11/317 (3%) ref|NP\_442295.1| hypothetical protein [Synechocystis sp. PCC 6803] sp|Q55724|Y644\_SYNY3 Hypothetical protein slr0644 pir|S76519 hypothetical protein - Synechocystis sp. (strain PCC 6803) db|JBA10365.1| ORF\_ID:slr0644-hypothetical protein [Synechocystis sp. PCC 6803] Length = 355
- 5550.3 Best-BlastP=> >nprot 80% Identities = 334/503 (66%), Positives = 412/503 (81%), Gaps = 2/503 (0%) ref|NP\_819973.1| cytochrome d ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] gb|AAO90487.1| cytochrome d ubiquinol oxidase, subunit I [Coxiella burnetii RSA 493] Length = 521
- 5552.2 Best-BlastP=> >nprot 75% Identities = 232/378 (61%), Positives = 287/378 (75%), Gaps = 2/378 (0%) gb|AAG01153.1|AF284438\_4 cytochrome d oxidase subunit [Brucella melitensis biovar Abortus] Length = 384
- 5554.2 Best-BlastP=> >nprot No Hits found
- 5555.2 Best-BlastP=> >nprot No Hits found
- 5556.1 Best-BlastP=> >nprot No Hits found
- 5557.2 Best-BlastP=> >nprot 42% Identities = 113/561 (20%), Positives = 251/561 (44%), Gaps = 65/561 (11%) db|BAB40921.2| myosin heavy chain 2x [Bos taurus] Length = 1938
- 5559.3 Best-BlastP=> >nprot No Hits found
- 5560.3 Best-BlastP=> >nprot 54% Identities = 68/232 (29%), Positives = 116/232 (50%), Gaps = 21/232 (9%) ref|NP\_923239.1| probable carbonyl reductase [Gloeobacter violaceus] db|JAC88234.1| glr0293 [Gloeobacter violaceus] Length = 243
- 5563.1 Best-BlastP=> >nprot 54% Identities = 57/145 (39%), Positives = 84/145 (57%), Gaps = 3/145 (2%) ref|NP\_841440.1| GCN5-related N-acetyltransferase [Nitrosomonas europaea ATCC 19718] emb|CAD85310.1| GCN5-related N-acetyltransferase [Nitrosomonas europaea ATCC 19718] Length = 157
- 5564.1 Best-BlastP=> >nprot 81% Identities = 322/475 (67%), Positives = 387/475 (81%), Gaps = 2/475 (0%) ref|NP\_819499.1| dihydrolipoamide dehydrogenase [Coxiella burnetii RSA 493] gb|AAO90013.1| dihydrolipoamide dehydrogenase [Coxiella burnetii RSA 493] Length = 474

- 5566.1 Best-BlastP=> >nprot 75% Identities = 38/55 (69%), Positives = 45/55 (81%) ref|NP\_523225.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] emb|CAD18817.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum] Length = 72
- 5569.1 Best-BlastP=> >nprot No Hits found
- 557.2 Best-BlastP=> >nprot 75% Identities = 517/898 (57%), Positives = 675/898 (75%), Gaps = 15/898 (1%) ref|NP\_820774.1| DNA polymerase I [Coxiella burnetii RSA 493] gb|AAO91288.1| DNA polymerase I [Coxiella burnetii RSA 493] Length = 895
- 5576.3 Best-BlastP=> >nprot 26% Identities = 61/216 (28%), Positives = 87/216 (40%), Gaps = 25/216 (11%) ref|NP\_662329.1| hypothetical protein [Chlorobium tepidum TLS] gb|AAM72671.1| hypothetical protein [Chlorobium tepidum TLS] Length = 325
- 558.2 Best-BlastP=> >nprot 34% Identities = 31/95 (32%), Positives = 53/95 (55%), Gaps = 9/95 (9%) gb|AAM15532.1|AF482691\_1 probable sensor/response regulator hybrid [Pseudomonas aeruginosa] Length = 469
- 5582.4 Best-BlastP=> >nprot 88% Identities = 584/737 (79%), Positives = 653/737 (88%), Gaps = 3/737 (0%) gb|AAM00624.1| putative copper efflux ATPase [Legionella pneumophila] Length = 736
- 5584.2 Best-BlastP=> >nprot 52% Identities = 188/189 (99%), Positives = 188/189 (99%) emb|CAC33489.1| hypothetical protein [Legionella pneumophila] Length = 189
- 5586.1 Best-BlastP=> >nprot 37% Identities = 32/76 (42%), Positives = 48/76 (63%) ref|NP\_217688.1| hypothetical protein Rv3172c [Mycobacterium tuberculosis H37Rv] ref|NP\_337786.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] ref|NP\_856842.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] pir|B70948 hypothetical protein Rv3172c - Mycobacterium tuberculosis (strain H37RV) emb|CAA16637.1| hypothetical protein Rv3172c [Mycobacterium tuberculosis H37Rv] gb|AAK47600.1| hypothetical protein [Mycobacterium tuberculosis CDC1551] emb|CAD95289.1| HYPOTHETICAL PROTEIN [Mycobacterium bovis subsp. bovis AF2122/97] Length = 160
- 5587.3 Best-BlastP=> >nprot 61% Identities = 132/276 (47%), Positives = 173/276 (62%) ref|NP\_229753.1| 4-hydroxybenzoate octaprenyltransferase [Vibrio cholerae O1 biovar eltor str. N16961] pir|C82365 4-hydroxybenzoate octaprenyltransferase VC0094 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93272.1| 4-hydroxybenzoate octaprenyltransferase [Vibrio cholerae O1 biovar eltor str. N16961] Length = 284
- 5588.2 Best-BlastP=> >nprot 67% Identities = 33/98 (33%), Positives = 65/98 (66%), Gaps = 4/98 (4%) ref|NP\_819561.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90075.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 96
- 559.2 Best-BlastP=> >nprot 83% Identities = 78/107 (72%), Positives = 92/107 (85%) ref|NP\_862496.1| hypothetical protein [Pseudomonas sp. ADP] gb|AAK50291.1|U66917\_59 hypothetical protein [Pseudomonas sp. ADP] Length = 152
- 5592.2 Best-BlastP=> >nprot 81% Identities = 150/229 (65%), Positives = 188/229 (82%) ref|ZP\_00134926.1| COG0081: Ribosomal protein L1 [Actinobacillus pleuropneumoniae serovar 1 str. 4074] Length = 229
- 5593.1 Best-BlastP=> >nprot 40% Identities = 30/79 (37%), Positives = 45/79 (56%) ref|NP\_755977.1| Hypothetical protein [Escherichia coli CFT073] gb|AAN82551.1|AE016767\_311 Hypothetical protein [Escherichia coli CFT073] Length = 144
- 5595.2 Best-BlastP=> >nprot 72% Identities = 112/174 (64%), Positives = 127/174 (72%), Gaps = 18/174 (10%) ref|ZP\_00123239.1| COG0049: Ribosomal protein S7 [Haemophilus somnus 129PT] ref|ZP\_00131785.1| hypothetical protein [Haemophilus somnus 2336] Length = 156

- 5596.3 Best-BlastP=> >nrprot 90% Identities = 109/123 (88%), Positives = 115/123 (93%) ref|NP\_799152.1| ribosomal protein S12 [Vibrio parahaemolyticus RIMD 2210633] sp|Q87L43|RS12\_VIBPA 30S ribosomal protein S12 dbj|BAC61036.1| ribosomal protein S12 [Vibrio parahaemolyticus] Length = 124
- 5598.2 Best-BlastP=> >nrprot 66% Identities = 189/394 (47%), Positives = 264/394 (67%), Gaps = 2/394 (0%) ref|NP\_820522.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] gb|AAO91036.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] Length = 426
- 5600.2 Best-BlastP=> >nrprot 72% Identities = 45/66 (68%), Positives = 55/66 (83%) ref|NP\_747188.1| ribosomal protein L31 [Pseudomonas putida KT2440] gb|AAN70652.1|AE016709\_4 ribosomal protein L31 [Pseudomonas putida KT2440] Length = 100
- 5602.3 Best-BlastP=> >nrprot 65% Identities = 60/155 (38%), Positives = 102/155 (65%), Gaps = 7/155 (4%) ref|NP\_069835.1| conserved hypothetical protein [Archaeoglobus fulgidus DSM 4304] pir|B69375 phosphohistidine phosphatase (EC3.1.3.-) sixA-related [similarity] - Archaeoglobus fulgidus gb|AAB90241.1| conserved hypothetical protein [Archaeoglobus fulgidus DSM 4304] Length = 151
- 5605.2 Best-BlastP=> >nrprot No Hits found
- 5606.2 Best-BlastP=> >nrprot No Hits found
- 5607.2 Best-BlastP=> >nrprot 64% Identities = 221/475 (46%), Positives = 306/475 (64%), Gaps = 6/475 (1%) ref|NP\_654832.1| hypothetical protein predicted by GeneMark [Bacillus anthracis A2012] ref|NP\_843400.1| algininate O-acetyltransferase, putative [Bacillus anthracis str. Ames] gb|AAP24886.1| algininate O-acetyltransferase, putative [Bacillus anthracis str. Ames] Length = 471
- 5609.1 Best-BlastP=> >nrprot 70% Identities = 60/84 (71%), Positives = 67/84 (79%) ref|NP\_819512.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90026.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 92
- 561.3 Best-BlastP=> >nrprot 80% Identities = 305/432 (70%), Positives = 352/432 (81%), Gaps = 2/432 (0%) ref|NP\_901046.1| probable ATPase associated with chromosome architecture [Chromobacterium violaceum ATCC 12472] gb|AAQ59051.1| probable ATPase associated with chromosome architecture [Chromobacterium violaceum ATCC 12472] Length = 443
- 5610.1 Best-BlastP=> >nrprot 60% Identities = 47/109 (43%), Positives = 67/109 (61%), Gaps = 1/109 (0%) ref|NP\_00092417.1| hypothetical protein [Azotobacter vinelandii] Length = 137
- 5611.1 Best-BlastP=> >nrprot 43% Identities = 35/61 (57%), Positives = 47/61 (77%) ref|NP\_00092427.1| hypothetical protein [Azotobacter vinelandii] Length = 838
- 5615.1 Best-BlastP=> >nrprot 67% Identities = 115/242 (47%), Positives = 150/242 (61%), Gaps = 31/242 (12%) ref|NP\_00090468.1| COG0582: Integrase [Azotobacter vinelandii] Length = 399
- 562.1 Best-BlastP=> >nrprot 59% Identities = 78/206 (37%), Positives = 120/206 (58%), Gaps = 6/206 (2%) ref|NP\_00091807.1| COG2834: Outer membrane lipoprotein-sorting protein [Azotobacter vinelandii] Length = 207
- 5620.3 Best-BlastP=> >nrprot 51% Identities = 28/61 (45%), Positives = 39/61 (63%) ref|NP\_600458.1| predicted transcriptional regulator [Corynebacterium glutamicum ATCC 13032] dbj|BAB98628.1| Predicted transcriptional regulators [Corynebacterium glutamicum ATCC 13032] Length = 75
- 5621.1 Best-BlastP=> >nrprot 35% Identities = 72/345 (20%), Positives = 148/345 (42%), Gaps = 30/345 (8%) ref|NP\_00118987.1| COG0477: Permeases of the major facilitator superfamily [Cytophaga hutchinsonii] Length = 441

- 5623.2 Best-BlastP=> >nrprot 24% Identities = 57/252 (22%), Positives = 114/252 (45%), Gaps = 15/252 (5%) ref|NP\_484762.1| unknown protein [Nostoc sp. PCC 7120] pir|AE1896 hypothetical protein alr0719 [imported] - Nostoc sp. (strain PCC 7120) dbj|BAB72676.1| ORF\_ID:alr0719-unknown protein [Nostoc sp. PCC 7120] Length = 393
- 5626.2 Best-BlastP=> >nrprot 56% Identities = 119/291 (40%), Positives = 169/291 (58%), Gaps = 10/291 (3%) ref|ZP\_00091084.1| COG0582: Integrase [Azotobacter vinelandii] Length = 287
- 5630.1 Best-BlastP=> >nrprot 42% Identities = 47/154 (30%), Positives = 72/154 (46%), Gaps = 24/154 (15%) ref|NP\_519620.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] emb|CAD15201.1| HYPOTHETICAL PROTEIN [Ralstonia solanacearum] Length = 233
- 5633.2 Best-BlastP=> >nrprot 68% Identities = 143/273 (52%), Positives = 190/273 (69%), Gaps = 1/273 (0%) ref|NP\_790075.1| diaminopimelate epimerase [Pseudomonas syringae pv. tomato str. DC3000] sp|Q88B09|DAPF\_PSESM Diaminopimelate epimerase (DAP epimerase) gb|AAO53770.1| diaminopimelate epimerase [Pseudomonas syringae pv. tomato str. DC3000] Length = 276
- 5634.2 Best-BlastP=> >nrprot 58% Identities = 16/32 (50%), Positives = 25/32 (78%) ref|ZP\_00068204.1| hypothetical protein [Microbulbifer degradans 2-40] Length = 57
- 5636.1 Best-BlastP=> >nrprot No Hits found
- 5637.1 Best-BlastP=> >nrprot 58% Identities = 86/198 (43%), Positives = 126/198 (63%), Gaps = 4/198 (2%) ref|NP\_840924.1| Phospholipase/Carboxylesterase [Nitrosomonas europaea ATCC 19718] emb|CAD84761.1| Phospholipase/Carboxylesterase [Nitrosomonas europaea ATCC 19718] Length = 224
- 5638.2 Best-BlastP=> >nrprot No Hits found
- 564.2 Best-BlastP=> >nrprot 68% Identities = 417/792 (52%), Positives = 546/792 (68%), Gaps = 28/792 (3%) ref|NP\_251305.1| cell division protein FtsK [Pseudomonas aeruginosa PAO1] sp|Q9I0M3|FTSK\_PSEAE DNA translocase ftsK pir|E83318 cell division protein FtsK PA2615 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06003.1|AE004690\_3 cell division protein FtsK [Pseudomonas aeruginosa PAO1] Length = 811
- 5642.1 Best-BlastP=> >nrprot No Hits found
- 5644.3 Best-BlastP=> >nrprot 47% Identities = 193/498 (38%), Positives = 268/498 (53%), Gaps = 78/498 (15%) ref|NP\_233251.1| hemagglutinin/protease [Vibrio cholerae O1 biovar eltor str. N16961] sp|P24153|HAPT\_VIBCH Hemagglutinin/proteinase precursor (HA/protease) (Vibriolysin) pir|A42358 vibriolysin (EC 3.4.24.-) precursor [validated] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAA27579.1| HA/protease gb|AAF96763.1| hemagglutinin/protease [Vibrio cholerae O1 biovar eltor str. N16961] Length = 609
- 5645.2 Best-BlastP=> >nrprot 82% Identities = 520/752 (69%), Positives = 622/752 (82%), Gaps = 9/752 (1%) ref|NP\_251310.1| ATP-binding protease component ClpA [Pseudomonas aeruginosa PAO1] pir|B83319 ATP-binding proteinase component ClpA PA2620 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06008.1|AE004690\_8 ATP-binding protease component ClpA [Pseudomonas aeruginosa PAO1] Length = 758
- 5647.1 Best-BlastP=> >nrprot 62% Identities = 55/80 (68%), Positives = 70/80 (87%) ref|NP\_642326.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] sp|Q8PL06|CLPS\_XANAC ATP-dependent Clp protease adaptor protein clpS gb|AAM36862.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 106

- 5648.1 Best-BlastP=> >nrprot 60% Identities = 42/112 (37%), Positives = 68/112 (60%) ref|NP\_753425.1| Hypothetical protein [Escherichia coli CFT073] gbl|AAN79985.1|AE016759\_259 Hypothetical protein [Escherichia coli CFT073] Length = 393
- 5649.1 Best-BlastP=> >nrprot 88% Identities = 327/418 (78%), Positives = 371/418 (88%) ref|NP\_746141.1| isocitrate dehydrogenase, NADP-dependent, prokaryotic-type [Pseudomonas putida KT2440] gbl|AAN69605.1|AE016594\_2 isocitrate dehydrogenase, NADP-dependent, prokaryotic-type [Pseudomonas putida KT2440] Length = 418
- 5650.3 Best-BlastP=> >nrprot 45% Identities = 67/239 (28%), Positives = 107/239 (44%), Gaps = 43/239 (17%) ref|NP\_924301.1| unknown protein [Gloeobacter violaceus] dbj|BAC89296.1| gl|1355 [Gloeobacter violaceus] Length = 278
- 5652.2 Best-BlastP=> >nrprot No Hits found
- 5654.2 Best-BlastP=> >nrprot No Hits found
- 5655.2 Best-BlastP=> >nrprot 58% Identities = 73/131 (55%), Positives = 94/131 (71%) ref|ZP\_00108601.1| COG2193: Bacterioferritin (cytochrome b1) [Nostoc punctiforme] Length = 144
- 5656.2 Best-BlastP=> >nrprot 15% Identities = 23/70 (32%), Positives = 37/70 (52%), Gaps = 1/70 (1%) ref|NP\_171674.2| expressed protein [Arabidopsis thaliana] pir|F86147 hypothetical protein T1N6.5 [imported] - Arabidopsis thaliana gbl|AAF78398.1|AC009273\_4 Contains similarity to a putative protein T2J13.100 gl|6522560 from Arabidopsis thaliana BAC T2J13 gb|AL132967 Length = 308
- 5660.1 Best-BlastP=> >nrprot 37% Identities = 69/275 (25%), Positives = 124/275 (45%), Gaps = 24/275 (8%) ref|NP\_692096.1| hypothetical protein [Oceanobacillus ihavensis HTE831] dbj|BAC13131.1| hypothetical conserved protein [Oceanobacillus ihavensis HTE831] Length = 314
- 5662.1 Best-BlastP=> >nrprot 65% Identities = 92/150 (61%), Positives = 116/150 (77%) ref|NP\_819966.1| conserved hypothetical protein [Coxiella burnetii RSA 493] gbl|AAO90480.1| conserved hypothetical protein [Coxiella burnetii RSA 493] Length = 414
- 5668.2 Best-BlastP=> >nrprot 28% Identities = 100/406 (24%), Positives = 167/406 (41%), Gaps = 82/406 (20%) ref|NP\_220907.1| unknown [Rickettsia prowazekii] pir|E71657 hypothetical protein RP534 - Rickettsia prowazekii emb|CAA14983.1| unknown [Rickettsia prowazekii] Length = 598
- 5669.2 Best-BlastP=> >nrprot 43% Identities = 125/540 (23%), Positives = 240/540 (44%), Gaps = 44/540 (8%) ref|ZP\_00044012.1| hypothetical protein [Magnetococcus sp. MC-1] Length = 725
- 567.5 Best-BlastP=> >nrprot 46% Identities = 236/953 (24%), Positives = 425/953 (44%), Gaps = 81/953 (8%) ref|NP\_052976.1| 93% identical to sp:TRG1\_ECOLI.gp:FPLTRAH\_3[TraG of plasmid F, responsible for pilus biogenesis and stabilization of mating pairs] [Plasmid R100] gbl|AAD28728.1|AF112468\_7 inner membrane and periplasmic mating pair stabilization protein TraG [Salmonella typhimurium] dbj|BAA78880.1| 93% identical to sp:TRG1\_ECOLI.gp:FPLTRAH\_3[TraG of plasmid F, responsible for pilus biogenesis and stabilization of mating pairs] [Plasmid R100] Length = 940
- 5671.2 Best-BlastP=> >nrprot 74% Identities = 73/123 (59%), Positives = 94/123 (76%), Gaps = 3/123 (2%) ref|ZP\_00122793.1| COG1607: Acyl-CoA hydrolase [Haemophilus somnus 129PT] ref|ZP\_00133225.1| hypothetical protein [Haemophilus somnus 2336] Length = 154
- 5672.1 Best-BlastP=> >nrprot No Hits found
- 5675.2 Best-BlastP=> >nrprot 52% Identities = 113/338 (33%), Positives = 186/338 (55%), Gaps = 23/338 (6%) ref|NP\_767510.1| bl|0870 [Bradyrhizobium japonicum] dbj|BAC46135.1| bl|0870 [Bradyrhizobium japonicum USDA 110] Length = 329

- 5677.2 Best-BlastP=> >nrprot 34% Identities = 42/164 (25%), Positives = 70/164 (42%), Gaps = 21/164 (12%) gb|EAA22028.1| putative yir4 protein [Plasmodium yoelii yoelii] Length = 299
- 568.2 Best-BlastP=> >nrprot 83% Identities = 380/535 (71%), Positives = 448/535 (83%) ref|ZP\_00082147.1| COG4799: Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta) [Geobacter metallireducens] Length = 535
- 5685.2 Best-BlastP=> >nrprot 99% Identities = 405/410 (98%), Positives = 408/410 (99%) gb|AAM00606.1| unknown [Legionella pneumophila] Length = 421
- 5686.2 Best-BlastP=> >nrprot 70% Identities = 85/154 (55%), Positives = 112/154 (72%) ref|NP\_252654.1| probable transcriptional regulator [Pseudomonas aeruginosa PAO1] ref|ZP\_00137402.1| COG1522: Transcriptional regulators [Pseudomonas aeruginosa UCBPP-PA14] pir|F83150 probable transcription regulator PA3965 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG07352.1|AE004814\_7 probable transcriptional regulator [Pseudomonas aeruginosa PAO1] Length = 169
- 5687.1 Best-BlastP=> >nrprot No Hits found
- 5688.2 Best-BlastP=> >nrprot 39% Identities = 38/170 (22%), Positives = 75/170 (44%), Gaps = 33/170 (19%) gb|EAA16038.1| repeat organellar protein related [Plasmodium yoelii yoelii] Length = 1441
- 569.2 Best-BlastP=> >nrprot 64% Identities = 136/258 (52%), Positives = 170/258 (65%), Gaps = 1/258 (0%) ref|ZP\_00082146.1| COG1024: Enoyl-CoA hydratase/carnithine racemase [Geobacter metallireducens] Length = 263
- 5690.2 Best-BlastP=> >nrprot 70% Identities = 75/146 (51%), Positives = 99/146 (67%), Gaps = 9/146 (6%) ref|NP\_641722.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] gb|AAM36258.1| conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306] Length = 149
- 5694.2 Best-BlastP=> >nrprot 64% Identities = 70/152 (46%), Positives = 103/152 (67%), Gaps = 3/152 (1%) ref|NP\_719482.1| mce-related protein [Shewanella oneidensis MR-1] gb|AAN56926.1|AE015826\_11 mce-related protein [Shewanella oneidensis MR-1] Length = 157
- 5695.1 Best-BlastP=> >nrprot 77% Identities = 152/259 (58%), Positives = 202/259 (77%) ref|NP\_931230.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16405.1| unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 260
- 5696.2 Best-BlastP=> >nrprot 77% Identities = 168/258 (65%), Positives = 205/258 (79%) ref|NP\_794201.1| toluene tolerance ABC transporter, ATP-binding protein, putative [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO57896.1| toluene tolerance ABC transporter, ATP-binding protein, putative [Pseudomonas syringae pv. tomato str. DC3000] Length = 269
- 57.1 Best-BlastP=> >nrprot 96% Identities = 272/289 (94%), Positives = 279/289 (96%) gb|AAM08235.1| LvrA [Legionella pneumophila] Length = 289
- 5701.2 Best-BlastP=> >nrprot 67% Identities = 179/375 (47%), Positives = 250/375 (66%), Gaps = 9/375 (2%) ref|NP\_519920.1| PUTATIVE DIHYDROLIPOAMIDE ACETYLTRANSFERASE (COMPONENT E2 OF PYRUVATE DEHYDROGENASE COMPLEX) PROTEIN [Ralstonia solanacearum] emb|CAD15501.1| PUTATIVE DIHYDROLIPOAMIDE ACETYLTRANSFERASE (COMPONENT E2 OF PYRUVATE DEHYDROGENASE COMPLEX) PROTEIN [Ralstonia solanacearum] Length = 372
- 571.2 Best-BlastP=> >nrprot 67% Identities = 336/671 (50%), Positives = 440/671 (65%), Gaps = 23/671 (3%) ref|ZP\_00082145.1| COG4770: Acetyl/propionyl-CoA carboxylase, alpha subunit [Geobacter metallireducens] Length = 668
- 5711.2 Best-BlastP=> >nrprot No Hits found



- 5719.2 Best-BlastP=> >nrprot 66% Identities = 116/246 (47%), Positives = 167/246 (67%), Gaps = 1/246 (0%) ref|ZP\_00123187.1| COG0149: Triosephosphate isomerase [Haemophilus somnus 129PT] Length = 255
- 572.2 Best-BlastP=> >nrprot 38% Identities = 161/480 (33%), Positives = 219/480 (45%), Gaps = 84/480 (17%) pir|JC4908 alkaline serine proteinase (EC 3.4.-.-) | precursor - Alteromonas sp Length = 715
- 5720.1 Best-BlastP=> >nrprot No Hits found
- 5723.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 5724.2 Best-BlastP=> >nrprot No Hits found
- 573.1 Best-BlastP=> >nrprot 79% Identities = 52/94 (55%), Positives = 75/94 (79%) ref|NP\_820064.1| hypothetical protein [Coxiella burnetii RSA 493] gb|AAO90578.1| hypothetical protein [Coxiella burnetii RSA 493] Length = 94
- 5730.1 Best-BlastP=> >nrprot No Hits found
- 5735.2 Best-BlastP=> >nrprot 63% Identities = 181/388 (46%), Positives = 251/388 (64%), Gaps = 2/388 (0%) ref|NP\_820522.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] gb|AAO91036.1| tryptophan/tyrosine permease family protein [Coxiella burnetii RSA 493] Length = 426
- 5739.3 Best-BlastP=> >nrprot 31% Identities = 357/1425 (25%), Positives = 551/1425 (38%), Gaps = 320/1425 (22%) ref|NP\_772111.1| bl|5471 [Bradyrhizobium japonicum] db|BAC50736.1| bl|5471 [Bradyrhizobium japonicum USDA 110] Length = 4210
- 574.2 Best-BlastP=> >nrprot No Hits found
- 5741.1 Best-BlastP=> >nrprot 60% Identities = 76/174 (43%), Positives = 116/174 (66%) ref|ZP\_00043325.1| COG0398: Uncharacterized conserved protein [Magnetococcus sp. MC-1] Length = 222
- 5743.1 Best-BlastP=> >nrprot No Hits found
- 5747.1 Best-BlastP=> >nrprot No Hits found
- 5761.1 Best-BlastP=> >nrprot 25% Identities = 26/72 (36%), Positives = 38/72 (52%), Gaps = 1/72 (1%) ref|NP\_902894.1| probable dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ60890.1| probable dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 417
- 5765.1 Best-BlastP=> >nrprot 53% Identities = 39/100 (39%), Positives = 62/100 (62%) ref|NP\_795325.1| ParB family protein [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO59020.1| ParB family protein [Pseudomonas syringae pv. tomato str. DC3000] Length = 290
- 5766.1 Best-BlastP=> >nrprot 34% Identities = 39/142 (27%), Positives = 62/142 (43%), Gaps = 18/142 (12%) ref|NP\_464180.1| lmo0653 [Listeria monocytogenes EGD-e] pir|AE1156 hypothetical protein lmo0653 [imported] - Listeria monocytogenes (strain EGD-e) emb|CAC98731.1| lmo0653 [Listeria monocytogenes] Length = 306
- 5767.1 Best-BlastP=> >nrprot No Hits found
- 5769.2 Best-BlastP=> >nrprot 58% Identities = 52/126 (41%), Positives = 77/126 (61%), Gaps = 4/126 (3%) ref|NP\_251491.1| hypothetical protein [Pseudomonas aeruginosa PAO1] pir|A83296 hypothetical protein PA2801 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06189.1|AE004707\_8 hypothetical protein PA2801 [Pseudomonas aeruginosa PAO1] Length = 134

- 577.2 Best-BlastP=> >nrprot 37% Identities = 58/180 (32%), Positives = 107/180 (59%), Gaps = 1/180 (0%) ref|NP\_624053.1| predicted transposase [Thermoanaerobacter tengcongensis] gb|AAM25657.1| predicted transposase [Thermoanaerobacter tengcongensis] Length = 267
- 5774.2 Best-BlastP=> >nrprot No Hits found
- 5776.1 Best-BlastP=> >nrprot No Hits found
- 5780.1
- Best-BlastP=> >nrprot 61% Identities = 56/79 (70%), Positives = 63/79 (79%) ref|NP\_246141.1| HisF [Pasteurella multocida] sp|Q9CLM0|HIS6\_PASMU Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF) gb|AAK03288.1| HisF [Pasteurella multocida] Length = 256
- 5796.3 Best-BlastP=> >nrprot 46% Identities = 61/195 (31%), Positives = 92/195 (47%), Gaps = 26/195 (13%) ref|NP\_890659.1| putative ring-hydroxylating dioxygenase large subunit [Bordetella bronchiseptica] emb|CAE34488.1| putative ring-hydroxylating dioxygenase large subunit [Bordetella bronchiseptica] Length = 438
- 58.1 Best-BlastP=> >nrprot 95% Identities = 211/227 (92%), Positives = 217/227 (95%) gb|AAM08234.1| putative phage repressor [Legionella pneumophila] Length = 227
- 5804.1 Best-BlastP=> >nrprot 53% Identities = 55/137 (40%), Positives = 76/137 (55%), Gaps = 12/137 (8%) ref|NP\_229825.1| cytochrome c5 [Vibrio cholerae O1 biovar eltor str. N16961] pir|F82355 cytochrome c5 VC0168 [imported] - Vibrio cholerae (strain N16961) gb|AAF93344.1| cytochrome c5 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 135
- 5806.2 Best-BlastP=> >nrprot 75% Identities = 54/87 (62%), Positives = 67/87 (77%) ref|NP\_00125359.1| COG0268: Ribosomal protein S20 [Pseudomonas syringae pv. syringae B728a] ref|NP\_790649.1| ribosomal protein S20 [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO54344.1| ribosomal protein S20 [Pseudomonas syringae pv. tomato str. DC3000] Length = 92
- 5807.1 Best-BlastP=> >nrprot 66% Identities = 48/113 (42%), Positives = 76/113 (67%) sp|Q43948|HYPA\_AZOCH Hydrogenase nickel incorporation protein hypA (Protein hypA) pir|JN0646 hydrogenase expression/formation protein HupA - Azotobacter chroococcum gb|AAA22132.1| hydrogenase accessory protein HupA Length = 113
- 5808.1 Best-BlastP=> >nrprot 48% Identities = 59/180 (32%), Positives = 87/180 (48%), Gaps = 13/180 (7%) gb|AAA25680.1| aminoglycoside 6'-N-acetyltransferase Length = 180
- 5809.1 Best-BlastP=> >nrprot No Hits found
- 5812.1 Best-BlastP=> >nrprot 60% Identities = 57/154 (37%), Positives = 95/154 (61%), Gaps = 6/154 (3%) emb|CAB60049.1| lvrB [Legionella pneumophila] Length = 157
- 5813.1 Best-BlastP=> >nrprot 65% Identities = 30/57 (52%), Positives = 43/57 (75%) emb|CAB60050.1| lvrC [Legionella pneumophila] Length = 67
- 5814.1 Best-BlastP=> >nrprot 45% Identities = 38/121 (31%), Positives = 66/121 (54%), Gaps = 6/121 (4%) gb|AAL05416.1| PilL [Yersinia pseudotuberculosis] Length = 356
- 5816.1
- Best-BlastP=> >nrprot 69% Identities = 52/96 (54%), Positives = 79/96 (82%) ref|ZP\_00122751.1| COG0718: Uncharacterized protein conserved in bacteria [Haemophilus somnus 129PT] ref|ZP\_00132634.1| hypothetical protein [Haemophilus somnus 2336] Length = 109
- 5818.1 Best-BlastP=> >nrprot No Hits found

- 5821.1 Best-BlastP=> >nprot No Hits found
- 5822.1 Best-BlastP=> >nprot No Hits found
- 5823.2 Best-BlastP=> >nprot 49% Identities = 125/369 (33%), Positives = 198/369 (53%), Gaps = 33/369 (8%) ref|NP\_899726.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] gb|AAQ57736.1| probable aminopeptidase [Chromobacterium violaceum ATCC 12472] Length = 415
- 5824.1 Best-BlastP=> >nprot 56% Identities = 43/67 (64%), Positives = 53/67 (79%) ref|NP\_773113.1| bl|6473 [Bradyrhizobium japonicum] dbj|BAC51738.1| bl|6473 [Bradyrhizobium japonicum USDA 110] Length = 345
- 5829.2 Best-BlastP=> >nprot 50% Identities = 67/218 (30%), Positives = 124/218 (56%), Gaps = 1/218 (0%) ref|NP\_880554.1| putative glutamine-binding periplasmic protein precursor [Bordetella pertussis] emb|CAE42138.1| putative glutamine-binding periplasmic protein precursor [Bordetella pertussis] Length = 247
- 583.2 Best-BlastP=> >nprot 82% Identities = 128/198 (64%), Positives = 164/198 (82%), Gaps = 1/198 (0%) ref|NP\_743801.1| trp repressor binding protein [Pseudomonas putida KT2440] gb|AAN67265.1| AE016353\_5 trp repressor binding protein [Pseudomonas putida KT2440] Length = 201
- 5844.1 Best-BlastP=> >nprot 65% Identities = 66/135 (48%), Positives = 88/135 (65%), Gaps = 5/135 (3%) ref|NP\_044227.1| KlcA [Enterobacter aerogenes] ref|NP\_862440.1| KlcA protein [Pseudomonas sp. ADP] sp|P52602|KLA1\_ECOLI Antirestriction protein klcA pir|T08486 probable anti-restriction protein klcA - Enterobacter aerogenes plasmid R751 gb|AAC64430.1| KlcA [Enterobacter aerogenes] gb|AAK50236.1| U66917\_3 KlcA protein [Pseudomonas sp. ADP] Length = 142
- 5846.2 Best-BlastP=> >nprot No Hits found
- 5848.1 Best-BlastP=> >nprot No Hits found
- 585.2
- Best-BlastP=> >nprot 72% Identities = 62/118 (52%), Positives = 85/118 (72%), Gaps = 1/118 (0%) ref|NP\_274848.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir|A81035 conserved hypothetical protein NMB1852 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF42186.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 129
- 5856.1 Best-BlastP=> >nprot 42% Identities = 20/43 (46%), Positives = 27/43 (62%), Gaps = 1/43 (2%) ref|ZP\_00141162.1| COG0617: tRNA nucleotidyltransferase/poly(A) polymerase [Pseudomonas aeruginosa UCBPP-PA14] Length = 467
- 5857.1 Best-BlastP=> >nprot 64% Identities = 65/139 (46%), Positives = 92/139 (66%) ref|NP\_735626.1| Unknown [Streptococcus agalactiae NEM316] emb|CAD46839.1| Unknown [Streptococcus agalactiae NEM316] Length = 162
- 5867.1 Best-BlastP=> >nprot No Hits found
- 587.2 Best-BlastP=> >nprot 74% Identities = 149/254 (58%), Positives = 194/254 (76%), Gaps = 1/254 (0%) gb|EAA20230.1| exodeoxyribonuclease III [Plasmodium yoelii yoelii] Length = 271
- 5871.3 Best-BlastP=> >nprot 46% Identities = 94/364 (25%), Positives = 174/364 (47%), Gaps = 21/364 (5%) ref|NP\_691531.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] ref|NP\_692364.1| hypothetical protein [Oceanobacillus ihayensis HTE831] ref|NP\_693263.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] dbj|BAC12566.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] dbj|BAC13399.1| hypothetical conserved protein [Oceanobacillus ihayensis HTE831] dbj|BAC14298.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] Length = 402
- 5872.1 Best-BlastP=> >nprot No Hits found

- 5874.1 Best-BlastP=> >nrprot 71% Identities = 96/178 (53%), Positives = 128/178 (71%), Gaps = 1/178 (0%) ref|ZP\_00024697.1| COG4584: Transposase and inactivated derivatives [Ralstonia metalidurans] Length = 343
- 5875.1 Best-BlastP=> >nrprot 43% Identities = 28/90 (31%), Positives = 44/90 (48%) gb|AAAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180
- 5876.2 Best-BlastP=> >nrprot 71% Identities = 121/219 (55%), Positives = 165/219 (75%), Gaps = 1/219 (0%) ref|NP\_791574.1| cytidylate kinase [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO55269.1| cytidylate kinase [Pseudomonas syringae pv. tomato str. DC3000] Length = 229
- 588.3 Best-BlastP=> >nrprot 72% Identities = 146/252 (57%), Positives = 186/252 (73%) ref|NP\_840124.1| Exodeoxyribonuclease III:Exodeoxyribonuclease III xth [Nitrosomonas europaea ATCC 19718] emb|CAD83934.1| Exodeoxyribonuclease III:Exodeoxyribonuclease III xth [Nitrosomonas europaea ATCC 19718] Length = 254
- 5890.1 Best-BlastP=> >nrprot No Hits found
- 5892.1 Best-BlastP=> >nrprot 73% Identities = 59/99 (59%), Positives = 73/99 (73%) ref|NP\_742622.1| ribosomal protein L23 [Pseudomonas putida KT2440] gb|AAAN66086.1|AE016238\_4 ribosomal protein L23 [Pseudomonas putida KT2440] Length = 99
- 5894.3 Best-BlastP=> >nrprot 82% Identities = 202/275 (73%), Positives = 229/275 (83%) ref|ZP\_00067989.1| COG0090: Ribosomal protein L2 [Microbulbifer degradans 2-40] Length = 275
- 5895.3 Best-BlastP=> >nrprot 86% Identities = 65/90 (72%), Positives = 80/90 (88%) ref|NP\_882398.1| 30S ribosomal protein S19 [Bordetella parapertussis] ref|NP\_886586.1| 30S ribosomal protein S19 [Bordetella bronchiseptica] emb|CAE39774.1| 30S ribosomal protein S19 [Bordetella parapertussis] emb|CAE30535.1| 30S ribosomal protein S19 [Bordetella bronchiseptica] Length = 91
- 5896.1 Best-BlastP=> >nrprot 62% Identities = 42/115 (36%), Positives = 75/115 (65%) ref|NP\_286169.1| putative transport protein [Escherichia coli O157:H7 EDL933] ref|NP\_308508.1| putative transport protein [Escherichia coli O157:H7] pir|A90689 probable transport protein ECs0481 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir|E85539 probable transport protein yajR [imported] - Escherichia coli (strain O157:H7, substrain EDL933) gb|AAG54777.1|AE005222\_2 putative transport protein [Escherichia coli O157:H7 EDL933] dbj|BAB33904.1| putative transport protein [Escherichia coli O157:H7] Length = 456
- 5897.1 Best-BlastP=> >nrprot 55% Identities = 41/73 (56%), Positives = 51/73 (69%) ref|NP\_931085.1| hypothetical protein [Photobacterium luminescens subsp. laumondii TTO1] emb|CAE16252.1| unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1] Length = 459
- 5898.2 Best-BlastP=> >nrprot 97% Identities = 266/271 (98%), Positives = 268/271 (98%) gb|AAC83338.1| major outer membrane protein precursor [Legionella pneumophila] gb|AAC83342.1| major outer membrane protein precursor [Legionella pneumophila] Length = 289
- 5899.1 Best-BlastP=> >nrprot No Hits found
- 59.1 Best-BlastP=> >nrprot 95% Identities = 137/145 (94%), Positives = 142/145 (97%) gb|AAM08233.1| unknown [Legionella pneumophila] Length = 243
- 590.4 Best-BlastP=> >nrprot 17% Identities = 93/427 (21%), Positives = 182/427 (42%), Gaps = 50/427 (11%) ref|NP\_603419.1| Exonuclease SBCC [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94718.1| Exonuclease SBCC [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 921
- 5900.3 Best-BlastP=> >nrprot No Hits found

- 5901.3 Best-BlastP=> >nrprot 17% Identities = 49/177 (27%), Positives = 85/177 (48%), Gaps = 27/177 (15%) ref[NP\_001259.1] RCC1-like G exchanging factor RLG [Homo sapiens] pir|T50663 RCC1-like G exchanging factor RLG [imported] - human gb|AAC79987.1| RCC1-like G exchanging factor RLG [Homo sapiens] gb|AAH29052.1| RCC1-like G exchanging factor RLG [Homo sapiens] gb|AAP88928.1| chromosome condensation 1-like [Homo sapiens] Length = 551
- 5903.2 Best-BlastP=> >nrprot 76% Identities = 191/318 (60%), Positives = 247/318 (77%) ref[NP\_819776.1] KpsF/GutQ family protein [Coxiella burnetii RSA 493] gb|AAO90290.1| KpsF/GutQ family protein [Coxiella burnetii RSA 493] Length = 324
- 5904.2 Best-BlastP=> >nrprot 21% Identities = 25/100 (25%), Positives = 46/100 (46%), Gaps = 6/100 (6%) ref[NP\_283688.1] hypothetical protein NMA0899 [Neisseria meningitidis Z2491] pir|D81936 hypothetical protein NMA0899 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB84177.1| hypothetical protein NMA0899 [Neisseria meningitidis Z2491] Length = 124
- 5905.1 Best-BlastP=> >nrprot 53% Identities = 118/304 (38%), Positives = 165/304 (54%), Gaps = 7/304 (2%) ref[NP\_902888.1] probable translation initiation protein, Sua5/YciO/YrdC family [Chromobacterium violaceum ATCC 12472] gb|AAQ60884.1| probable translation initiation protein, Sua5/YciO/YrdC family [Chromobacterium violaceum ATCC 12472] Length = 321
- 5906.1 Best-BlastP=> >nrprot 100% Identities = 138/138 (100%), Positives = 138/138 (100%) emb|CAA67994.1| oxaloacetate decarboxylase alpha-chain [Legionella pneumophila] Length = 596
- 5907.1 Best-BlastP=> >nrprot 56% Identities = 20/31 (64%), Positives = 30/31 (96%) ref[NP\_283131.1] hypothetical protein NMA0292 [Neisseria meningitidis Z2491] pir|G82024 hypothetical protein NMA0292 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB83599.1| hypothetical protein NMA0292 [Neisseria meningitidis Z2491] Length = 94
- 591.3 Best-BlastP=> >nrprot 74% Identities = 156/258 (60%), Positives = 198/258 (76%) ref[XP\_00024696.1] COG1484: DNA replication protein [Ralstonia metallidurans] Length = 268
- 5910.1 Best-BlastP=> >nrprot No Hits found
- 592.3 Best-BlastP=> >nrprot 96% Identities = 531/559 (94%), Positives = 540/559 (96%) gb|AAM00619.1| unknown [Legionella pneumophila] Length = 559
- 5920.2 Best-BlastP=> >nrprot 46% Identities = 94/364 (25%), Positives = 174/364 (47%), Gaps = 21/364 (5%) ref[NP\_691531.1] transposase for IS652 [Oceanobacillus ihayensis HTE831] ref[NP\_692364.1] hypothetical protein [Oceanobacillus ihayensis HTE831] ref[NP\_693263.1] transposase for IS652 [Oceanobacillus ihayensis HTE831] dbj|BAC12566.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] dbj|BAC13399.1| hypothetical conserved protein [Oceanobacillus ihayensis HTE831] dbj|BAC14298.1| transposase for IS652 [Oceanobacillus ihayensis HTE831] Length = 402
- 5926.1 Best-BlastP=> >nrprot 59% Identities = 36/74 (48%), Positives = 47/74 (63%) ref[NP\_355900.1] AGR\_L\_236p [Agrobacterium tumefaciens] ref[NP\_535243.1] conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] pir|C98145 hypothetical protein AGR\_L\_236 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) pir|A13142 conserved hypothetical protein Atu4765 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) gb|AAK88685.1| AGR\_L\_236p [Agrobacterium tumefaciens str. C58 (Cereon)] gb|AAL45559.1| conserved hypothetical protein [Agrobacterium tumefaciens str. C58 (U. Washington)] Length = 507
- 593.2 Best-BlastP=> >nrprot No Hits found
- 5935.1 Best-BlastP=> >nrprot No Hits found

594.1	Best-BlastP=> >nrprot 97% Identities = 145/150 (96%), Positives = 147/150 (98%) gb AAM00620.1  chemiosmotic efflux system C protein A [Legionella pneumophila] Length = 150	
5944.1	Best-BlastP=> >nrprot No Hits found	
5947.1	Best-BlastP=> >nrprot 65% Identities = 17/39 (43%), Positives = 30/39 (76%) ref NP_469382.1  similar to E. coli DedA protein [Listeria innocua] pir AD1437 E. coli DedA protein homolog lin0035 [imported] - Listeria innocua (strain Clip11262) emb CAC95268.1  lin0035 [Listeria innocua] Length = 219	
5950.1	Best-BlastP=> >nrprot No Hits found	
5952.1	Best-BlastP=> >nrprot 79% Identities = 49/52 (94%), Positives = 49/52 (94%) gb AAM00633.1  unknown [Legionella pneumophila] Length = 176	
5953.1	Best-BlastP=> >nrprot 87% Identities = 48/57 (84%), Positives = 50/57 (87%) sp Q48815 HELA_LEGPN Protein heIA gb AAB05679.1  HeIA Length = 1052	
5957.1	Best-BlastP=> >nrprot 68% Identities = 162/270 (60%), Positives = 214/270 (79%) ref ZP_00122424.1  COG1185: Polyrribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) [Haemophilus somnus 129PT] Length = 713	
596.3	Best-BlastP=> >nrprot 73% Identities = 314/570 (55%), Positives = 419/570 (73%), Gaps = 5/570 (0%) ref NP_819843.1  malate oxidoreductase [Coxiella burnetii RSA 493] gb AAO90357.1  malate oxidoreductase [Coxiella burnetii RSA 493] Length = 565	
597.2	Best-BlastP=> >nrprot 37% Identities = 29/80 (36%), Positives = 46/80 (57%), Gaps = 1/80 (1%) ref NP_820267.1  hypothetical protein [Coxiella burnetii RSA 493] gb AAO90781.1  hypothetical protein [Coxiella burnetii RSA 493] Length = 160	
5978.2	Best-BlastP=> >nrprot 68% Identities = 92/166 (55%), Positives = 126/166 (75%) ref NP_931234.1  hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16409.1  unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] Length = 187	
5979.1	Best-BlastP=> >nrprot No Hits found	
598.2	Best-BlastP=> >nrprot 46% Identities = 36/101 (35%), Positives = 49/101 (48%), Gaps = 15/101 (14%) ref NP_249404.1  hypothetical protein [Pseudomonas aeruginosa PA01] pir A83555 hypothetical protein PA0713 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04102.1 AE004507_1 hypothetical protein PA0713 [Pseudomonas aeruginosa PAO1] Length = 97	
5983.1	Best-BlastP=> >nrprot No Hits found	
5985.1	Best-BlastP=> >nrprot 44% Identities = 29/106 (27%), Positives = 56/106 (52%), Gaps = 4/106 (3%) ref NP_692567.1  transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj BAC13602.1  transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 402	
5986.2	Best-BlastP=> >nrprot No Hits found	
5987.1	Best-BlastP=> >nrprot No Hits found	
5988.1	Best-BlastP=> >nrprot 35% Identities = 27/55 (49%), Positives = 31/55 (56%), Gaps = 3/55 (5%) dbj BAC94688.1  hypothetical protein [Vibrio vulnificus YJ016] Length = 343	
5996.1	Best-BlastP=> >nrprot 51% Identities = 67/159 (42%), Positives = 90/159 (56%), Gaps = 3/159 (1%) ref NP_742500.1  conserved hypothetical protein [Pseudomonas putida KT2440] gb AAN65964.1 AE016224_8 conserved hypothetical protein [Pseudomonas putida KT2440] Length = 166	

- 5999.1 Best-BlastP=> >nrprot 69% Identities = 49/91 (53%), Positives = 68/91 (74%) gb|AAP83334.1|AF469614\_2 unknown [Francisella tularensis subsp. tularensis] Length = 94
- 60.1 Best-BlastP=> >nrprot No Hits found
- 600.3 Best-BlastP=> >nrprot 73% Identities = 117/172 (68%), Positives = 137/172 (79%) ref|NP\_220600.1|ABC TRANSPORTER ATP-BINDING PROTEIN (abcT3) [Rickettsia prowazekii] pir|F71732 ABC transporter ATP-binding protein (abcT3) RP214 - Rickettsia prowazekii emb|CAA14677.1|ABC TRANSPORTER ATP-BINDING PROTEIN (abcT3) [Rickettsia prowazekii] Length = 548
- 6002.1 Best-BlastP=> >nrprot 30% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1|ORF1 transposase [Acinetobacter baumannii] Length = 180
- 6004.1 Best-BlastP=> >nrprot No Hits found
- 6007.1 Best-BlastP=> >nrprot No Hits found
- 601.4
- Best-BlastP=> >nrprot 45% Identities = 97/361 (26%), Positives = 180/361 (49%), Gaps = 13/361 (3%) ref|NP\_359923.1|multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] pir|F97735 hypothetical protein abcT3 [imported] - Rickettsia conorii (strain Malish 7) gb|AAL02824.1|multidrug resistance ABC transporter ATP-binding protein [Rickettsia conorii] Length = 589
- 6015.1 Best-BlastP=> >nrprot No Hits found
- 6016.1 Best-BlastP=> >nrprot 40% Identities = 31/71 (43%), Positives = 42/71 (59%), Gaps = 1/71 (1%) ref|NP\_774998.1|putative protein [Citrobacter freundii] gb|AAN87662.1|putative protein [Citrobacter freundii] Length = 112
- 6018.1 Best-BlastP=> >nrprot No Hits found
- 6019.1
- Best-BlastP=> >nrprot 56% Identities = 67/145 (46%), Positives = 100/145 (68%) ref|NP\_635334.1|transcriptional regulator, AraC family [Methanosarcina mazei Goe1] gb|AAM33006.1|transcriptional regulator, AraC family [Methanosarcina mazei Goe1] Length = 209
- 602.4 Best-BlastP=> >nrprot 39% Identities = 64/253 (25%), Positives = 125/253 (49%), Gaps = 21/253 (8%) ref|NP\_834835.1|Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] gb|AAP12036.1|Transcriptional regulator, MerR family [Bacillus cereus ATCC 14579] Length = 254
- 6029.1 Best-BlastP=> >nrprot 70% Identities = 31/48 (64%), Positives = 39/48 (81%) ref|NP\_520567.1|PROBABLE 50S RIBOSOMAL SUBUNIT PROTEIN L33 [Ralstonia solanacearum] sp|Q8XWM8|RL33\_RALSO 50S ribosomal protein L33 emb|CAD16153.1|PROBABLE 50S RIBOSOMAL SUBUNIT PROTEIN L33 [Ralstonia solanacearum] Length = 56
- 6036.1 Best-BlastP=> >nrprot 99% Identities = 110/110 (100%), Positives = 110/110 (100%) emb|CAC33488.1|hypothetical protein [Legionella pneumophila] Length = 110
- 6037.1 Best-BlastP=> >nrprot 47% Identities = 33/78 (42%), Positives = 54/78 (69%) sp|P04928|SANT\_PLAFN S-ANTIGEN PROTEIN PRECURSOR pir|YAZQN7 S-antigen precursor - malaria parasite (Plasmodium falciparum) (strain NF7/Ghana) gb|AAA29758.1|S antigen precursor Length = 309
- 6038.1 Best-BlastP=> >nrprot No Hits found



6039.1

Best-BlastP=> >nprot 82% Identities = 366/558 (65%), Positives = 460/558 (82%), Gaps = 3/558 (0%) ref[NP\_251852.1] 30S ribosomal protein S1 [Pseudomonas aeruginosa PAO1] pir||C83250 30S ribosomal protein S1 PA3162 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06550.1|AE004740\_3 30S ribosomal protein S1 [Pseudomonas aeruginosa PAO1] Length = 559

604.3

Best-BlastP=> >nprot 55% Identities = 104/249 (41%), Positives = 138/249 (55%), Gaps = 6/249 (2%) ref[NP\_419511.1] transcriptional regulator SkgA [Caulobacter crescentus CB15] sp|Q9RP67|SKGA\_CAUCR Transcriptional regulator skgA (Stationary-phase regulation of katG protein) pir||C87335 transcription regulator SkgA [imported] - Caulobacter crescentus gb|AAF01797.1|AF170912\_1 putative helix-turn-helix transcriptional regulator SkgA [Caulobacter crescentus] gb|AAK22679.1|transcriptional regulator SkgA [Caulobacter crescentus CB15] Length = 255

6040.1

Best-BlastP=> >nprot 71% Identities = 54/92 (58%), Positives = 72/92 (78%) ref[NP\_819558.1] 3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA 493] gb|AAO90072.1|3-phosphoshikimate 1-carboxyvinyltransferase [Coxiella burnetii RSA 493] Length = 438

6042.1

Best-BlastP=> >nprot 69% Identities = 105/209 (50%), Positives = 149/209 (71%), Gaps = 2/209 (0%) ref|ZP\_00122964.1| COG0125: Thymidylate kinase [Haemophilus somnus 129PT] Length = 210

6044.1

Best-BlastP=> >nprot No Hits found

6049.1

Best-BlastP=> >nprot 74% Identities = 123/208 (59%), Positives = 155/208 (74%), Gaps = 2/208 (0%) ref[NP\_903586.1] probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] gb|AAQ61577.1| probable electron-transferring-flavoprotein dehydrogenase [Chromobacterium violaceum ATCC 12472] Length = 539

6052.1

Best-BlastP=> >nprot 47% Identities = 55/162 (33%), Positives = 91/162 (56%), Gaps = 2/162 (1%) ref[NP\_719829.1] conserved hypothetical protein [Shewanella oneidensis MR-1] gb|AAN57273.1|AE015863\_2 conserved hypothetical protein [Shewanella oneidensis MR-1] Length = 191

606.3

Best-BlastP=> >nprot 56% Identities = 199/513 (38%), Positives = 301/513 (58%), Gaps = 6/513 (1%) ref[NP\_819600.1] amino acid permease family protein [Coxiella burnetii RSA 493] gb|AAO90114.1| amino acid permease family protein [Coxiella burnetii RSA 493] Length = 560

6061.1

Best-BlastP=> >nprot No Hits found

6062.1

Best-BlastP=> >nprot 62% Identities = 75/166 (45%), Positives = 108/166 (65%), Gaps = 2/166 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180

6064.1

Best-BlastP=> >nprot No Hits found

6066.1

Best-BlastP=> >nprot 35% Identities = 34/122 (27%), Positives = 58/122 (47%), Gaps = 10/122 (8%) ref[NP\_242278.1] transposase (01) [Bacillus halodurans] pir||D83826 transposase (01) BH1412 [imported] - Bacillus halodurans (strain C-125) dbj|BAB05131.1| transposase (01) [Bacillus halodurans] Length = 405

6070.1

Best-BlastP=> >nprot 65% Identities = 59/121 (48%), Positives = 85/121 (70%) ref[NP\_781505.1] 2-hydroxyacid dehydrogenase [Clostridium tetani E88] gb|AAO35442.1| 2-hydroxyacid dehydrogenase [Clostridium tetani E88] Length = 357

6071.1

Best-BlastP=> >nprot 43% Identities = 23/67 (34%), Positives = 31/67 (46%) gb|AAK61303.1| putative transposase [Xanthomonas oryzae pv. oryzae] Length = 344

- 6072.1 Best-BlastP=> >nrprot 45% Identities = 18/43 (41%), Positives = 29/43 (67%) gb|AAB38861.1| putative transposase [Burkholderia cepacia]  
Length = 345
- 6074.1 Best-BlastP=> >nrprot 49% Identities = 48/175 (27%), Positives = 84/175 (48%), Gaps = 14/175 (8%) ref|NP\_692337.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] ref|NP\_693308.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC13372.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC14343.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 397
- 6079.1 Best-BlastP=> >nrprot 44% Identities = 35/96 (36%), Positives = 49/96 (51%) gb|AAB97874.1| surface antigen [Trypanosoma cruzi]  
Length = 722
- 6081.1 Best-BlastP=> >nrprot 45% Identities = 24/44 (54%), Positives = 32/44 (72%) dbj|BAC93915.1| L-asparaginase I [Vibrio vulnificus YJ016]  
Length = 337
- 6083.1 Best-BlastP=> >nrprot No Hits found
- 6086.1 Best-BlastP=> >nrprot 98% Identities = 102/104 (98%), Positives = 103/104 (99%) gb|AAM00607.1| unknown [Legionella pneumophila]  
Length = 121
- 6087.1 Best-BlastP=> >nrprot No Hits found
- 6089.1 Best-BlastP=> >nrprot 49% Identities = 48/175 (27%), Positives = 84/175 (48%), Gaps = 14/175 (8%) ref|NP\_692337.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] ref|NP\_693308.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC13372.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] dbj|BAC14343.1| transposase for IS652 [Oceanobacillus iheyensis HTE831] Length = 397
- 6093.1 Best-BlastP=> >nrprot No Hits found
- 6094.1 Best-BlastP=> >nrprot No Hits found
- 6097.1 Best-BlastP=> >nrprot 41% Identities = 1129/1221 (92%), Positives = 1163/1221 (95%), Gaps = 16/1221 (1%) gb|AAD41583.1|AF057703.1 structural toxin protein RtxA [Legionella pneumophila] Length = 1208
- 6098.1 Best-BlastP=> >nrprot 50% Identities = 41/74 (55%), Positives = 53/74 (71%) ref|NP\_927457.1| DNA adenine methylase (Deoxyadenosyl-methyltransferase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE12382.1| DNA adenine methylase (Deoxyadenosyl-methyltransferase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 270
- 61.1 Best-BlastP=> >nrprot No Hits found
- 6106.1 Best-BlastP=> >nrprot 37% Identities = 20/56 (35%), Positives = 32/56 (57%) ref|NP\_051664.1| transposase, putative [Deinococcus radiodurans] pir|A75633 probable transposase - Deinococcus radiodurans (strain R1) gb|AAF12606.1|AE001826\_75 transposase, putative [Deinococcus radiodurans] Length = 327
- 6107.1 Best-BlastP=> >nrprot No Hits found
- 6108.1 Best-BlastP=> >nrprot 63% Identities = 76/169 (44%), Positives = 110/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180
- 6110.1 Best-BlastP=> >nrprot 85% Identities = 74/77 (96%), Positives = 74/77 (96%) emb|CAB65201.1| hypothetical protein [Legionella pneumophila]  
Length = 356
- 6117.1 Best-BlastP=> >nrprot 11% Identities = 83/277 (29%), Positives = 126/277 (45%), Gaps = 51/277 (18%) ref|XP\_300615.1| similar to hypothetical protein [Homo sapiens] Length = 423

- 6119.1 Best-BlastP=> >nrprot 41% Identities = 34/123 (27%), Positives = 62/123 (50%), Gaps = 4/123 (3%) ref|NP\_692567.1| transposase for IS652 [Oceanobacillus ihbensis HTE831] dbj|BAC13602.1| transposase for IS652 [Oceanobacillus ihbensis HTE831] Length = 402
- 612.2 Best-BlastP=> >nrprot 97% Identities = 696/721 (96%), Positives = 706/721 (97%) gb|AAC64361.1| catalase-peroxidase KatB [Legionella pneumophila] Length = 721
- 6121.1 Best-BlastP=> >nrprot 52% Identities = 51/199 (25%), Positives = 100/199 (50%), Gaps = 21/199 (10%) gb|AAB05879.1| putative transposase Length = 424
- 6122.1 Best-BlastP=> >nrprot No Hits found
- 6123.1 Best-BlastP=> >nrprot No Hits found
- 6125.1 Best-BlastP=> >nrprot 98% Identities = 51/51 (100%), Positives = 51/51 (100%) pir|T42167 Rep protein - Escherichia coli plasmid pO157 gb|AAC70135.1| Rep protein E1 [Escherichia coli O157:H7] Length = 51
- 6128.1 Best-BlastP=> >nrprot 99% Identities = 388/388 (100%), Positives = 388/388 (100%) ref|NP\_061425.1| 100 pct identical to gp:FPLMCG\_6[SopA of plasmid F] [Plasmid F] gb|AAA24902.1| Protein A dbj|BAA97916.1| 100 pct identical to gp:FPLMCG\_6[SopA of plasmid F] [Plasmid F] emb|CAC79981.1| orf1176 [Escherichia coli] gb|AAO61293.1| Para [BAC cloning vector pEBAC190G] emb|CAD50597.1| SopA protein [Cloning vector pUvBBAC] Length = 391
- 6130.1 Best-BlastP=> >nrprot 99% Identities = 323/323 (100%), Positives = 323/323 (100%) ref|NP\_061426.1| 100 pct identical to sp:SOPB\_ECOLI[SopB of plasmid F] [Plasmid F] ref|NP\_052641.1| SopB protein [Escherichia coli O157:H7] sp|P08867|SOPB\_ECOLI SopB protein [Plasmid partition protein B] pir|T00244 sopB protein - Escherichia coli plasmids pO157 and F emb|CAA28296.1| unnamed protein product [Escherichia coli] gb|AAA24903.1| Protein B gb|AAC53637.1| SopB dbj|BAA31791.1| SopB protein [Escherichia coli] gb|AAC70137.1| plasmid partitioning protein [Escherichia coli O157:H7] dbj|BAA97917.1| 100 pct identical to sp:SOPB\_ECOLI[SopB of plasmid F] [Plasmid F] emb|CAC79980.1| orf972 [Escherichia coli] gb|AAO61294.1| ParB [BAC cloning vector pEBAC190G] emb|CAD50598.1| SopB protein [Cloning vector pUvBBAC] Length = 323
- 6131.1 Best-BlastP=> >nrprot 47% Identities = 239/927 (25%), Positives = 368/927 (39%), Gaps = 188/927 (20%) ref|NP\_772111.1| bl|5471 [Bradyrhizobium japonicum] dbj|BAC50736.1| bl|5471 [Bradyrhizobium japonicum USDA 110] Length = 4210
- 6132.1 Best-BlastP=> >nrprot 37% Identities = 21/57 (36%), Positives = 33/57 (57%) ref|NP\_051664.1| transposase, putative [Deinococcus radiodurans] pir|A75633 probable transposase - Deinococcus radiodurans (strain R1) gb|AAF12606.1| AE001826\_75 transposase, putative [Deinococcus radiodurans] Length = 327
- 6133.1 Best-BlastP=> >nrprot 67% Identities = 44/80 (55%), Positives = 59/80 (73%) ref|NP\_273113.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir|B81244 conserved hypothetical protein NMB0047 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF40518.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 94
- 6134.1 Best-BlastP=> >nrprot 54% Identities = 78/169 (46%), Positives = 111/169 (65%), Gaps = 2/169 (1%) gb|AAN34371.1| ORF1 transposase [Acinetobacter baumannii] Length = 180
- 615.5 Best-BlastP=> >nrprot 53% Identities = 58/230 (25%), Positives = 114/230 (49%), Gaps = 26/230 (11%) ref|NP\_603496.1| Transposase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb|AAL94795.1| Transposase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] Length = 428

- 616.4 Best-BlastP=> >nrprot 67% Identities = 179/333 (53%), Positives = 231/333 (69%), Gaps = 4/333 (1%) ref|ZP\_00024697.1| COG4584: Transposase and inactivated derivatives [Ralstonia metallidurans] Length = 343
- 618.3 Best-BlastP=> >nrprot 55% Identities = 48/125 (38%), Positives = 77/125 (61%), Gaps = 2/125 (1%) ref|NP\_867668.1| probable acyl carrier protein [Pirellula sp.] emb|CAD75215.1| probable acyl carrier protein [Pirellula sp.] Length = 129
- 619.1 Best-BlastP=> >nrprot 19% Identities = 32/118 (27%), Positives = 58/118 (49%), Gaps = 2/118 (1%) ref|NP\_785252.1| (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase [Lactobacillus plantarum WCFS1] sp|Q88WG9|FABZ\_LACPL (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (3R)-hydroxymyristoyl ACP dehydratase emb|CAD64100.1| (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase [Lactobacillus plantarum WCFS1] Length = 147
- 621.5 Best-BlastP=> >nrprot 62% Identities = 195/428 (45%), Positives = 269/428 (62%), Gaps = 17/428 (3%) ref|NP\_214178.1| 3-oxoacyl-[acyl-carrier protein] synthase II [Aquifex aeolicus] pir|B70448 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus gb|AAC07574.1| 3-oxoacyl-[acyl-carrier-protein] synthase II [Aquifex aeolicus VF5] Length = 415
- 622.3 Best-BlastP=> >nrprot 69% Identities = 412/793 (51%), Positives = 556/793 (70%), Gaps = 12/793 (1%) ref|NP\_820864.1| penicillin-binding protein 1A [Coxiella burnetii RSA 493] gb|AAO91378.1| penicillin-binding protein 1A [Coxiella burnetii RSA 493] Length = 793
- 623.2 Best-BlastP=> >nrprot 77% Identities = 253/370 (68%), Positives = 289/370 (78%) ref|ZP\_00013240.1| COG0686: Alanine dehydrogenase [Rhodospirillum rubrum] Length = 372
- 627.1 Best-BlastP=> >nrprot 39% Identities = 110/214 (51%), Positives = 138/214 (64%), Gaps = 14/214 (6%) ref|NP\_612899.1| hypothetical protein [Stx2 converting bacteriophage I] dbj|BAB87868.1| hypothetical protein [Stx2 converting bacteriophage I] Length = 678
- 628.3 Best-BlastP=> >nrprot No Hits found
- 63.1 Best-BlastP=> >nrprot No Hits found
- 630.4 Best-BlastP=> >nrprot 73% Identities = 577/1040 (55%), Positives = 773/1040 (74%), Gaps = 1/1040 (0%) ref|ZP\_00055701.1| hypothetical protein [Magnetospirillum magnetotacticum] Length = 1059
- 632.2 Best-BlastP=> >nrprot 71% Identities = 136/258 (52%), Positives = 189/258 (73%), Gaps = 1/258 (0%) ref|NP\_760580.1| Dihydropteroate synthase [Vibrio vulnificus CMCP6] gb|AAO10107.1|AE016802\_150 Dihydropteroate synthase [Vibrio vulnificus CMCP6] Length = 259
- 633.3 Best-BlastP=> >nrprot 75% Identities = 282/442 (63%), Positives = 344/442 (77%), Gaps = 1/442 (0%) ref|NP\_406959.1| probable phosphoglucosyltransferase/phosphomannomutase [Yersinia pestis] ref|NP\_668021.1| mrsa protein [Yersinia pestis KIM] pir|AE0425 probable phosphoglucosyltransferase/phosphomannomutase [imported] - Yersinia pestis (strain CO92) emb|CAC92729.1| probable phosphoglucosyltransferase/phosphomannomutase [Yersinia pestis CO92] gb|AAM84272.1|AE013670\_9 mrsa protein [Yersinia pestis KIM] Length = 446
- 634.4 Best-BlastP=> >nrprot 51% Identities = 85/166 (51%), Positives = 93/166 (56%) emb|CAB44711.1| hypothetical protein (P4(21)n) [Mus musculus] Length = 400
- 635.5 Best-BlastP=> >nrprot 83% Identities = 278/398 (69%), Positives = 332/398 (83%), Gaps = 14/398 (3%) ref|NP\_819191.1| cell division protein FisZ [Coxiella burnetii RSA 493] gb|AAO89705.1| cell division protein FisZ [Coxiella burnetii RSA 493] Length = 386
- 636.2 Best-BlastP=> >nrprot 77% Identities = 198/287 (68%), Positives = 236/287 (82%) ref|ZP\_00090126.1| COG0774: UDP-3-O-acetyl-N-acetylglucosamine deacetylase [Azotobacter vinelandii] Length = 303

- 637.3 Best-BlastP=> >nrprot 62% Identities = 261/623 (41%), Positives = 396/623 (63%), Gaps = 5/623 (0%) ref|NP\_616924.1| endothelin converting enzyme homolog PepO [Methanosarcina acetivorans str. C2A] gb|AAM05404.1| endothelin converting enzyme homolog PepO [Methanosarcina acetivorans str. C2A] Length = 665
- 64.3 Best-BlastP=> >nrprot No Hits found
- 640.2 Best-BlastP=> >nrprot 51% Identities = 102/309 (33%), Positives = 157/309 (50%), Gaps = 8/309 (2%) ref|NP\_103911.1| hypothetical protein [Mesorhizobium loti] dbj|BAB49697.1| hypothetical protein [Mesorhizobium loti] Length = 345
- 641.3 Best-BlastP=> >nrprot 74% Identities = 416/663 (62%), Positives = 506/663 (76%), Gaps = 5/663 (0%) ref|NP\_931190.1| 2,4-dienoyl-CoA reductase [NADPH] (2,4-dienoyl coenzyme A reductase) [Photorhabdus luminescens subsp. laumondii TTO1] emb|CAE16362.1| 2,4-dienoyl-CoA reductase [NADPH] (2,4-dienoyl coenzyme A reductase) [Photorhabdus luminescens subsp. laumondii TTO1] Length = 673
- 643.3 Best-BlastP=> >nrprot 59% Identities = 208/462 (45%), Positives = 287/462 (62%), Gaps = 10/462 (2%) ref|NP\_284769.1| UDP-N-acetylmuramyl-tripeptide synthetase [Neisseria meningitidis Z2491] sp|Q9JSZ0|MURE\_NEIMA UDP-N-acetylmuramyl-D-glutamate--2,6-diaminopimelate ligase (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase) pir|A81778 UDP-N-acetylmuramyl-D-glutamate-2,6-diamino-pimelate ligase (EC 6.3.2.13) NMA2071 [similarity] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB85288.1| UDP-N-acetylmuramyl-tripeptide synthetase [Neisseria meningitidis Z2491] Length = 492
- 644.2 Best-BlastP=> >nrprot 52% Identities = 113/344 (32%), Positives = 185/344 (53%), Gaps = 10/344 (2%) ref|NP\_820791.1| erythronate-4-phosphate dehydrogenase, putative [Coxiella burnetii RSA 493] gb|AAO91305.1| erythronate-4-phosphate dehydrogenase, putative [Coxiella burnetii RSA 493] Length = 375
- 645.4 Best-BlastP=> >nrprot 66% Identities = 107/219 (48%), Positives = 147/219 (67%), Gaps = 5/219 (2%) ref|NP\_820725.1| membrane protein, putative [Coxiella burnetii RSA 493] gb|AAO91239.1| membrane protein, putative [Coxiella burnetii RSA 493] Length = 230
- 647.5 Best-BlastP=> >nrprot 49% Identities = 55/179 (30%), Positives = 107/179 (59%), Gaps = 1/179 (0%) gb|AAQ75156.1| Pap2 superfamily protein [Alvinella pompejana epibiont 7G3] Length = 202
- 65.1 Best-BlastP=> >nrprot No Hits found
- 650.3 Best-BlastP=> >nrprot 72% Identities = 211/372 (56%), Positives = 272/372 (73%), Gaps = 2/372 (0%) ref|ZP\_00029745.1| COG2170: Uncharacterized conserved protein [Burkholderia fungorum] Length = 388
- 651.2 Best-BlastP=> >nrprot 73% Identities = 70/130 (53%), Positives = 98/130 (75%) ref|ZP\_00079460.1| COG1832: Predicted CoA-binding protein [Geobacter metallireducens] Length = 136
- 652.1 Best-BlastP=> >nrprot 62% Identities = 144/267 (53%), Positives = 179/267 (67%), Gaps = 5/267 (1%) ref|NP\_404647.1| conserved hypothetical protein [Yersinia pestis] ref|NP\_670446.1| hypothetical protein [Yersinia pestis KIM] pir|A10126 conserved hypothetical protein YPO1034 [imported] - Yersinia pestis (strain CO92) emb|CAC89876.1| conserved hypothetical protein [Yersinia pestis CO92] gb|AAM86697.1|AE013915\_6 hypothetical protein [Yersinia pestis KIM] Length = 281
- 656.3 Best-BlastP=> >nrprot No Hits found

- 657.3 Best-BlastP=> >nrprot 6% Identities = 39/123 (31%), Positives = 64/123 (52%), Gaps = 11/123 (8%) ref|NP\_828913.1| serine/threonine-protein kinase [Chlamydomonas caviae GPIC] gb|AAP04791.1| serine/threonine-protein kinase [Chlamydomonas caviae GPIC] Length = 501
- 659.2 Best-BlastP=> >nrprot 31% Identities = 56/209 (26%), Positives = 100/209 (47%), Gaps = 11/209 (5%) ref|NP\_843168.1| conserved hypothetical protein [Bacillus anthracis str. Ames] gb|AAP24654.1| conserved hypothetical protein [Bacillus anthracis str. Ames] Length = 323
- 660.1 Best-BlastP=> >nrprot 61% Identities = 83/178 (46%), Positives = 117/178 (65%) ref|NP\_794412.1| acetyltransferase, GNAT family [Pseudomonas syringae pv. tomato str. DC3000] gb|AAO58107.1| acetyltransferase, GNAT family [Pseudomonas syringae pv. tomato str. DC3000] Length = 189
- 661.3 Best-BlastP=> >nrprot 20% Identities = 51/148 (34%), Positives = 76/148 (51%), Gaps = 10/148 (6%) ref|ZP\_00109305.1| COG1670: Acetyltransferases, including N-acetylases of ribosomal proteins [Nostoc punctiforme] Length = 191
- 663.2 Best-BlastP=> >nrprot 49% Identities = 193/671 (28%), Positives = 325/671 (48%), Gaps = 62/671 (9%) gb|AAL77346.1| AF443847\_2 putative O-acetyltransferase WavN [Vibrio cholerae] Length = 663
- 665.2 Best-BlastP=> >nrprot 69% Identities = 43/78 (55%), Positives = 62/78 (79%) ref|NP\_273842.1| conserved hypothetical protein [Neisseria meningitidis MC58] pir|G81157 conserved hypothetical protein NMB0800 [imported] - Neisseria meningitidis (strain MC58 serogroup B) gb|AAF41213.1| conserved hypothetical protein [Neisseria meningitidis MC58] Length = 94
- 666.2 Best-BlastP=> >nrprot 76% Identities = 120/204 (58%), Positives = 158/204 (77%) ref|ZP\_00126281.1| COG0293: 23S rRNA methylase [Pseudomonas syringae pv. syringae B728a] Length = 216
- 667.3 Best-BlastP=> >nrprot 32% Identities = 68/178 (38%), Positives = 71/178 (39%) pir|A40215 TcD antigen - Trypanosoma cruzi Length = 207
- 668.4 Best-BlastP=> >nrprot 99% Identities = 1026/1048 (97%), Positives = 1040/1048 (99%) pir|T18334 icmE protein - Legionella pneumophila emb|CAA75331.1| icmE protein [Legionella pneumophila] Length = 1048
- 670.1 Best-BlastP=> >nrprot 66% Identities = 213/471 (45%), Positives = 308/471 (65%), Gaps = 18/471 (3%) ref|ZP\_00107537.1| COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydroliipoamide dehydrogenase (E3) component, and related enzymes [Nostoc punctiforme] Length = 472
- 673.3 Best-BlastP=> >nrprot 42% Identities = 123/548 (22%), Positives = 218/548 (39%), Gaps = 102/548 (18%) ref|NP\_458664.1| putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] pir|A1031 probable membrane protein STY4579 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) emb|CAD09354.1| putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi] gb|AAO71734.1| putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi Ty2] Length = 501
- 675.6 Best-BlastP=> >nrprot No Hits found
- 677.6 Best-BlastP=> >nrprot 58% Identities = 258/683 (37%), Positives = 389/683 (56%), Gaps = 39/683 (5%) gb|AAN62290.1| AF440524\_77 conserved hypothetical protein [Pseudomonas aeruginosa] Length = 724
- 678.3 Best-BlastP=> >nrprot No Hits found

- 680.3 Best-BlastP=> >nrprot 53% Identities = 57/132 (43%), Positives = 83/132 (62%), Gaps = 2/132 (1%) ref|NP\_283256.1| patch repair protein [Neisseria meningitidis Z2491] sp|Q9JWD6|VSR\_NEIMA Putative very-short-patch-repair endonuclease pir|H81959 patch repair protein (EC 3.1.-) NMA0429 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) emb|CAB83728.1| patch repair protein [Neisseria meningitidis Z2491] Length = 140
- 681.3 Best-BlastP=> >nrprot No Hits found
- 682.2 Best-BlastP=> >nrprot 76% Identities = 191/295 (64%), Positives = 229/295 (77%), Gaps = 7/295 (2%) sp|Q59603|MTB1\_NEIGO Modification methylase NgoBI (Cytosine-specific methyltransferase NgoBI) (M.NgoBI) gb|AAB03206.2| cytosine DNA methylase M.Ngol [Neisseria gonorrhoeae] Length = 317
- 683.2 Best-BlastP=> >nrprot 64% Identities = 200/443 (45%), Positives = 289/443 (65%), Gaps = 11/443 (2%) ref|NP\_819174.1| UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase [Coxiella burnetii RSA 493] gb|AAO89688.1| UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase [Coxiella burnetii RSA 493] Length = 446
- 684.5 Best-BlastP=> >nrprot 48% Identities = 73/253 (28%), Positives = 127/253 (50%), Gaps = 40/253 (15%) ref|NP\_819573.1| cell division protein ZipA, putative [Coxiella burnetii RSA 493] gb|AAO90087.1| cell division protein ZipA, putative [Coxiella burnetii RSA 493] Length = 225
- 687.5 Best-BlastP=> >nrprot 47% Identities = 120/426 (28%), Positives = 204/426 (47%), Gaps = 29/426 (6%) ref|ZP\_00082430.1| COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Geobacter metallireducens] Length = 410
- 688.1 Best-BlastP=> >nrprot 48% Identities = 71/266 (26%), Positives = 138/266 (51%), Gaps = 11/266 (4%) ref|NP\_908017.1| LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolinetia succinogenes] emb|CAE10917.1| LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolinetia succinogenes] Length = 300
- 692.1 Best-BlastP=> >nrprot No Hits found
- 693.1 Best-BlastP=> >nrprot 71% Identities = 96/172 (55%), Positives = 128/172 (74%) ref|NP\_299266.1| conserved hypothetical protein [Xylella fastidiosa 9a5c] pir|C82613 conserved hypothetical protein XF1984 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF84786.1|AE004018\_2 conserved hypothetical protein [Xylella fastidiosa 9a5c] Length = 187
- 694.3 Best-BlastP=> >nrprot 72% Identities = 239/453 (52%), Positives = 330/453 (72%), Gaps = 9/453 (1%) dbj|BAB33285.1| glutathione reductase [Acinetobacter sp. M-1] Length = 450
- 696.2 Best-BlastP=> >nrprot 74% Identities = 92/143 (64%), Positives = 107/143 (74%), Gaps = 13/143 (9%) ref|NP\_230222.1| ribosomal protein S9 [Vibrio cholerae O1 biovar eltor str. N16961] sp|Q9KUF0|RS9\_VIBCH 30S ribosomal protein S9 pir|C82308 ribosomal protein S9 VC0571 [imported] - Vibrio cholerae (strain N16961 serogroup O1) gb|AAF93739.1| ribosomal protein S9 [Vibrio cholerae O1 biovar eltor str. N16961] Length = 130
- 697.1 Best-BlastP=> >nrprot 74% Identities = 111/188 (59%), Positives = 142/188 (75%), Gaps = 3/188 (1%) ref|NP\_840883.1| Rieske iron-sulfur protein 2Fe-2S subunit [Nitrosomonas europaea ATCC 19718] emb|CAD84720.1| Rieske iron-sulfur protein 2Fe-2S subunit [Nitrosomonas europaea ATCC 19718] Length = 201
- 698.2 Best-BlastP=> >nrprot 81% Identities = 273/401 (68%), Positives = 332/401 (82%) ref|NP\_743478.1| ubiquinol--cytochrome c reductase, cytochrome b [Pseudomonas putida KT2440] gb|AAN66942.1|AE016322\_9 ubiquinol--cytochrome c reductase, cytochrome b [Pseudomonas putida KT2440] Length = 403